



STIC Search Report

Biotech-Chem Library

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TO: Jeffrey Parkin
Location: REM-3D39&3C18
Art Unit: 1648
May 19, 2004
Case Serial Number: 10/072301

From: P. Sheppard
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Search Notes

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STIC-Biotech/ChemLib

121855

From: Parkin, Jeffrey
Sent: Wednesday, May 12, 2004 11:32 AM
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Would you please search the following SEQ ID NOS.: vis-à-vis the aforementioned application (U.S. 10/072,301) v. all relevant databases: 8, 17, 25, 19, 27, 21, 29, 23, and 31.

Provide a hard copy of the results.

Thanks!

JSP
AU 1648
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2-0908

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Searcher: _____
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Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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CC indicate slower progression of the disease. The detection of CCR5
 CC variants may be used to identify individuals at lower risk of infection
 CC relative to the general population who, if infected, may exhibit slower
 CC progression to AIDS. Probes and primers (see AAV84127-36) are provided
 CC for use in diagnostic methods for detecting the presence of such
 CC variants. A method is provided for inhibiting HIV-1 infection of a cell
 CC encoding a CCR5 receptor. This involves introducing a nucleic acid
 CC functional CCR5 molecules present on the cell surface
 CC
 XX Sequence 100 AA;

Query Match Best Local Similarity 100.0%; Score 190; DB 2; Length 100;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPL 36
 DB 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPL 36

RESULT 2

AAW27406
 ID AAW27406 standard; protein; 184 AA.
 AC AAW27406;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Inactive human CCR5.
 XX

KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW predisposition; resistance; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX

OS Homo sapiens.
 XX

PN MO9732019-A2.
 XX

PD 04-SEP-1997.
 XX

PF 28-FEB-1997; 97WO-BE000023.
 XX

PR 01-MAR-1996; 96EP-00870021.
 XX

PR 06-AUG-1996; 96EP-00870102.
 XX

PA (EURO-) EUROSCREEN SA.
 XX

PI Samson M, Parmentier M, Vassart G, Libert F;
 XX

DR WPI; 1997-479829/44.
 XX

DR N-PSDB; AAT90116.
 XX

PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX

PS Claim 1; Fig 1a; 94bp; English.
 XX

CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1
 CC or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat
 CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
 CC viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders. Subjects that express the
 CC inactive receptor have a predisposition, or resistance to HIV-1 and/or
 CC HIV-2
 XX

Sequence 184 AA;

Query Match Best Local Similarity 100.0%; Score 190; DB 2; Length 184;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPL 36
 DB 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPL 36

RESULT 3

AAW27408
 ID AAW27408 standard; protein; 215 AA.
 AC AAW27408;
 XX

DT 14-APR-1998 (first entry)
 XX

DE Inactive human CCR5.
 XX

KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW predisposition; resistance; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX

OS Homo sapiens.
 XX

PN MO9732019-A2.
 XX

PD 04-SEP-1997.
 XX

PF 28-FEB-1997; 97WO-BE000023.
 XX

PR 01-MAR-1996; 96EP-00870021.
 XX

PR 06-AUG-1996; 96EP-00870102.
 XX

PA (EURO-) EUROSCREEN SA.
 XX

PI Samson M, Parmentier M, Vassart G, Libert F;
 XX

DR WPI; 1997-479829/44.
 XX

DR N-PSDB; AAT90118.
 XX

PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX

PS Claim 7; Fig 1d-e; 94bp; English.
 XX

CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which lacks the last 3 transmembrane regions and the regions
 CC involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,
 CC treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
 CC viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders. Subjects that express the
 CC inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2
 XX

Sequence 215 AA;

Query Match Best Local Similarity 100.0%; Score 190; DB 2; Length 215;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPL 36
 DB 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPL 36

RESULT 4

AAW88238
ID AAW88238 standard; protein; 215 AA.
XX
AC AAW88238;
XX
DT 15-MAR-1999 (first entry)
XX
DE HIV-1 co-receptor CCR5 variant CCR5-delta32.
XX
KM HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
XX gene therapy; human.
XX Homo sapiens.
XX
FH Key location/Qualifiers
FT Domain 32..56
FT Domain /note="transmembrane domain 1"
FT Domain 67..87
FT Domain /note="transmembrane domain 2"
FT Domain 103..124
FT Domain /note="transmembrane domain 3"
FT Domain 142..167
FT Domain /note="transmembrane domain 4"
XX
PN WO9854317-A1.
XX
PD 03-DEC-1998.
XX
PF 29-MAY-1998; 98WO-EP003437.
XX
PR 30-MAY-1997; 97US-0048057P.
XX
PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX Beretta A, Quillent C, Arenzana Siededós F, Braun J;
XX MPI, 1999-059835/05.
DR N-PSDB; AAV84159.
XX
PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX resistance of CCR5-expressing cells to HIV-1 infection.
XX
PS Disclosure; Page 38-39; 55pp; English.
XX
CC This is the amino acid sequence of a CCR5 variant protein, designated
CC CCR5-delta32, that includes the first 4 transmembrane domains of wild-
CC type CCR5 (see AAW88232), but lacks transmembrane domains 5-7. CCR5
CC serves as a co-receptor for infection by macrophage-tropic (M-tropic)
CC strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation
CC are resistant to HIV-1 infection, but heterozygous individuals are
CC susceptible. The invention additionally relates to the identification of
CC variant CCR5m303 (see AAW88231), which lacks transmembrane domains 3-7 of
CC CCR5. The detection of CCR5 variants may be used to identify individuals
CC at lower risk of infection relative to the general population who, if
CC infected, may exhibit slower progression to AIDS. Probes and primers (see
CC AAW84127-36) are provided for use in diagnostic methods for detecting the
CC presence of such variants. A method is provided for inhibiting HIV-1
CC infection of a cell expressing the CCR5 receptor. This involves
CC introducing a nucleic acid encoding a CCR5 variant into the cell, thereby
CC reducing the number of functional CCR5 molecules present on the cell
CC surface
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 190; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 4,4e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYTSRCCCKINVKQIAARLLPL 36
1 |||||
DB 1 MDYVSSPIYDINNTYTSRCCCKINVKQIAARLLPL 36

RESULT 5
ID ADCl0142
ADCl0142 standard; protein; 268 AA.
XX
AC ADCl0142;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human NOVX polypeptide SEQ ID NO: 162.
XX
KM cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
XX antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
XX pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
XX inflammatory disorder; chromosome mapping; tissue typing;
XX predictive medicine.
XX
OS Homo sapiens.
XX
PN WO200300842-A2.
XX
PD 03-JAN-2003.
XX
PF 04-JUN-2002; 2002WO-US017443.
XX
PR 04-JUN-2001; 2001US-0295607P.
PR 04-JUN-2001; 2001US-0295661P.
PR 06-JUN-2001; 2001US-0296404P.
PR 06-JUN-2001; 2001US-0296418P.
PR 07-JUN-2001; 2001US-0296575P.
PR 11-JUN-2001; 2001US-0297414P.
PR 12-JUN-2001; 2001US-0295573P.
PR 12-JUN-2001; 2001US-0297567P.
PR 14-JUN-2001; 2001US-0298285P.
PR 15-JUN-2001; 2001US-0298528P.
PR 18-JUN-2001; 2001US-0299133P.
PR 19-JUN-2001; 2001US-0299230P.
PR 21-JUN-2001; 2001US-0299494P.
PR 22-JUN-2001; 2001US-0300177P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308890P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324668P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358656P.
PR 21-FEB-2002; 2002US-0359123P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359644P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363678P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Agge ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eissen A, Ellerman K, Gangolli EA;
PI Gerlach VV, Gorman L, Guo X, Hermann JM, Hjalte T, Ji W, Kekuda R;
PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Miller I;
PI Kr T, Padigan M, Patlutanjan M, Pena CRA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DU, Vernet CM, Zhong H, Zhong W, Alsbrook JP;
PI Burgess CE, Lepley DM;
XX MPI, 2003-210149/20.

DR N-PSDB; ADC10141.

XX New isolated NOX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
XX or CNS diseases.

PS Claim 1; SEQ ID NO 162; 772pp; English.

CC The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOX
CC with the polypeptide is useful for treating or preventing a pathology associated
CC or activity of the polypeptide e.g. disorders associated with aberrant expression
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to one of the
XX polypeptides of the invention.

XX Sequence 268 AA;

Query Match Best Local Similarity 100.0%; Score 190; DB 7; Length 268;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYGVSSPIYDINYTSRPOCKINVKQIAARLLPPL 36
DB 1 MDYGVSSPIYDINYTSRPOCKINVKQIAARLLPPL 36

RESULT 6

AAW27407 ID AAW27407 standard; protein; 352 AA.

AC AAW27407;

DT 14-APR-1998 (first entry)

DE Human CCR5.

XX Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
XX atherosclerosis; autoimmune disorder.

OS Homo sapiens.

PN MO9732019-A2.

PD 04-SEP-1997.

PF 28-FEB-1997; 97MO-BE000023.

PR 01-MAR-1996; 96EP-00870021.

PR 06-AUG-1996; 96EP-00870102.

PA (EURO-) EUROSCREEN SA.

PI Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

DR N-PSDB; AAT90117.

PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
XX disease and viral infection.

PS Claim 4; Fig 1b-c; 94pp; English.

XX The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but

CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to
CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
XX atherosclerosis and autoimmune disorders

XX Sequence 352 AA;

Query Match Best Local Similarity 100.0%; Score 190; DB 2; Length 352;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYGVSSPIYDINYTSRPOCKINVKQIAARLLPPL 36
DB 1 MDYGVSSPIYDINYTSRPOCKINVKQIAARLLPPL 36

RESULT 7

AAW27123 ID AAW27123 standard; protein; 352 AA.

AC AAW27123;

DT 14-DEC-1997 (first entry)

DE Human chemokine receptor 88C.

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody; human.

OS Homo sapiens.

XX Key

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

New nucleic acid encoding chemokine receptors 88-28 and 88C - used to
modulate leukocyte trafficking, e.g. for treatment of inflammation.

Query Match	100.0%	Score 190;	DB 2;	Length 352;
Best Local Similarity	100.0%	Fried. No. 7,9e-20;		
Matches 36;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1 MDYVSSPIVDINYYTSEPCCKINVKQIAARLLPPL 36				
1 MDYVSSPIVDINYYTSEPCCKINVKQIAARLLPPL 36				
<p>RESULT 9</p> <p>AAW88232</p> <p>ID AAW88232 standard; protein: 352 AA.</p> <p>XX AAW88232;</p> <p>XX AC</p> <p>XX DT</p> <p>XX 15-MAR-1999 (first entry)</p> <p>XX DB</p> <p>XX HIV-1 co-receptor CCR5.</p> <p>XX KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;</p> <p>XX gene therapy; human.</p> <p>XX OS</p> <p>XX Homo sapiens.</p> <p>XX Key</p> <p>XX Location/Qualifiers</p> <p>XX FH 32..56</p> <p>XX FT /note= "transmembrane domain 1"</p> <p>XX FT 67..87</p> <p>XX FT /note= "transmembrane domain 2"</p> <p>XX FT 101</p> <p>XX FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA</p> <p>XX FT (Stop) in CCR5m303"</p> <p>XX FT 103..124</p> <p>XX FT /note= "transmembrane domain 3"</p> <p>XX FT 142..167</p> <p>XX FT /note= "transmembrane domain 4"</p> <p>XX FT 200..223</p> <p>XX FT /note= "transmembrane domain 5"</p> <p>XX Domain</p>				

FT Domain 236..260
 FT /note="transmembrane domain 6"
 FT 275..301
 FT /note="transmembrane domain 7"
 PN MO9654317-A1.
 XX 03-DEC-1998.
 PD 29-MAY-1998; 98WO-EP003437.
 XX 30-MAY-1997; 97US-0048057P.
 PR (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PA Beretta A, Quillent C, Arenzana Siededós F, Braun J;
 XX WPI; 1999-059835/05.
 DR N-PSDB; AAV64126.
 XX
 PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 PS Disclosure; Page 34-35; 55pp; English.
 XX
 CC This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAM68231) designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV64127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 190; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 7.9e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYGVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36
 DB 1 MDYGVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36
 XX
 RESULT 10
 ID AAE07048 standard; protein; 352 AA.
 AC AAE07048;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCRS) HDGNR10 protein #2.
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytoskeletal; immunosuppressive; neurotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

OS Homo sapiens.
 XX
 PN WO200158916-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004153.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 XX 03-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-48966/53.
 DR N-PSDB; AAD13299.
 XX
 PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT neurodegenerative disorders.
 PS Example 40; Page 504-505; 518pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCRS)
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergy, autoimmune
 CC disease, multiple sclerosis, rheumatoid arthritis, diabetes mellitus, Crohn's
 CC disease, cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 190; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 7.9e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYGVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36
 DB 1 MDYGVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36
 XX
 RESULT 11
 ID AAG80111 standard; protein; 352 AA.
 AC AAG80111;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CCR5 protein.
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;

KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiaesthetic; immunosuppressive; dermatological;
KW antirheumatic; antiaesthetic.
OS Homo sapiens.
XX
XX WO200172830-A2.
XX
XX 04-OCT-2001.
XX
XX 02-APR-2001; 2001WO-EP003708.
XX
XX 31-MAR-2000; 2000DE-01016013.
XX
XX (IIPP-) IPP PHARM GMBH.
XX (FORS/) FORSMANN U.
XX
XX Forssmann W, Adersmann K, Heitland A, Spodberg N;
PI WPI; 2001-626256/72.
XX
XX
XX Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
XX
XX Disclosure; Page 10; 26pp; German.
XX
XX This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiaesthetic,
CC immunosuppressive, dermatological, antirheumatic, antiaesthetic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CCR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 190; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.9e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYGVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36
Db 1 MDYGVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36
RESULT 12
AAE04321
ID AAE04321 standard; protein; 352 AA.
XX
XX AAE04321;
AC
XX
XX 04-SEP-2001 (first entry)
XX
XX Human chemokine receptor (CCR), CC-CR-5 related protein #2.
XX
XX Human; transformed mammalian cell; CD4; reporter gene; translocation;
KW human immunodeficiency virus; HIV; long terminal repeat; LTR; therapy;
KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
KW CC-CR-5; envelope glycoprotein; anti-HIV.
XX
XX Homo sapiens.
OS
XX
XX US6258527-B1.
FN

XX
XX 10-JUL-2001.
PD
XX
XX 21-MAY-1997; 97US-00861105.
XX
XX 20-MAY-1996; 96US-0017157P.
PR
XX 19-JUN-1996; 96US-0020043P.
PR
XX 19-MAY-1997; 97US-00858660.
XX
XX (AARO-) AARON DIAMOND AIDS RES CENT.
PA (UTNY) UNIV NEW YORK STATE.
XX
XX
XX Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;
PI WPI; 2001-417127/44.
XX
XX N-PSDB; AAD08577.
DR
XX
XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
PT and HIV LTR for identification of drugs and antibodies for treatment of
PT HIV.
XX
XX
XX Disclosure; Col 47-50; 37pp; English.
XX
XX The present invention relates to a transformed mammalian cell that
CC contains a gene encoding CD4, a construct encoding a reporter gene under
CC the regulation of an human immunodeficiency virus (HIV) long terminal
CC repeat (LTR) and that has been transduced with a vector encoding a human
CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
CC cell surface of transformed mammalian cell. The invention is useful for
CC identifying drugs or antibodies that interfere with the translocation of
CC HIV into transformed mammalian cell or for identifying a human chemokine
CC receptor that facilitates the infection of a particular HIV strain into
CC the transformed mammalian cell. Compounds identified can be used to treat
CC cellular dysfunction and to prevent or combat HIV infection. The present
CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.
CC CC-CR-5 is the principal cofactor for entry mediated by the envelope
CC glycoproteins of primary macrophage-tropic strains of HIV-1
XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 190; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.9e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYGVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36
Db 1 MDYGVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36
RESULT 13
AAE07039
ID AAE07039 standard; protein; 352 AA.
XX
XX AAE07039;
AC
XX
XX 16-OCT-2001 (first entry)
XX
XX Human G-protein chemokine receptor (CCRS) HDGNR10 protein #2.
XX
XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW human immunodeficiency virus; antimitochondrial; vasodilator; vulnery;
KW cytostatic; immunosuppressive; neurotrophic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW cardiovascular disorder; myocardial ischaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200158915-A2.
FN

PD 16-AUG-2001.
 XX 09-FEB-2001; 2001MO-US004152.
 PF 09-FEB-2000; 2000US-018125BP.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Roachke V, Li Y, Ruben SM;
 PI WPI: 2001-488965/53.
 DR N-PSDB; AAD13198.
 XX
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT neurodegenerative disorders.
 PS
 PS Example 40; Page 486-487; 495pp; English.
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation, preventing or
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital), immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis), cardiovascular
 CC disorders (myocardial ischaemia) and wound healing
 CC
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 190; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 7.9e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYVSSPIVDINVTSEPCQKINVKQIARLLPPL 36
 DB 1 MDYVSSPIVDINVTSEPCQKINVKQIARLLPPL 36
 ID AAB46858 standard; protein; 352 AA.
 AC AAB46858;
 XX
 XX 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX
 DE Human HDGNR10 protein.
 XX
 XX HDGNR10; human: G-protein chemokine receptor; antiinflammatory;
 KW immunomodulatory; anticoagulant; antifibrotic; immunosuppressive;
 KW cytostatic; antiparasitic; antiproliferative; antirheumatic; antiallergic;
 KW vasorelaxant; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;

KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; eosinophilia; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vullerary.
 OS Homo sapiens.
 XX
 XX US2001000241-A1.
 PN
 PD 12-APR-2001.
 XX
 XX 29-NOV-2000; 2000US-00725285.
 PF
 PR 06-JUN-1995; 95US-00466343.
 PR 18-JUN-1998; 98US-00195662.
 PR 25-JUN-1999; 99US-00339912.
 XX
 XX (LIYY/) LI Y.
 PA (RUBEN/) RUBEN S M.
 XX
 XX Li Y, Ruben SM;
 PI WPI: 2001-226317/23.
 DR N-PSDB; AAF26390.
 XX
 XX New human G-protein chemokine receptor polypeptides and polynucleotides,
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
 PT
 PT Claim 1a; Page 15; 22pp; English.
 PS
 PS This invention describes a novel receptor polypeptide (I) selected from
 CC (i) a fully defined 339 amino acid sequence (ii) fully disclosed in the
 CC specification; and (iii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC anticoagulant, antifibrotic, immunosuppressive, antiviral, cytostatic,
 CC antiparasitic, antiproliferative, antirheumatic, antiallergic, and
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDGNR10, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, psoriasis, and
 CC cell mediated autoimmune diseases, parasitic infections, leukemia, T-
 CC stimulating growth factor activity. HDGNR10 is useful for treating
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC sarcoidosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)
 CC
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 190; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 7.9e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYVSSPIVDINVTSEPCQKINVKQIARLLPPL 36
 DB 1 MDYVSSPIVDINVTSEPCQKINVKQIARLLPPL 36
 ID ABB56342 standard; protein; 352 AA.
 AC ABB56342;
 XX
 XX 18-FEB-2002 (first entry)
 DT
 DT
 XX
 DE Non-endogenous human GPCR protein, SEQ ID NO: 477.
 XX

KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.

XX
 OS Homo sapiens.
 OS Synthetic.

XX WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US011098.

XX 07-APR-2000; 2000US-0195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Brunema K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

XX N-PSDB; ABI97978.

PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.

PS Claim 1; Page 277-278; 394pp; English.

CC The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR

XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 190; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 7.9e-20;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36

Db 1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36

Search completed: May 13, 2004, 15:00:53
 Job time : 9.40971 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 : Search time 1.97476 Seconds
(without alignments)
941.146 Million cell updates/sec

Title: US-10-072-301-8

Perfect score: 190

Sequence: 1 MDYQVSPIDYINYYTSEPCQKINKYQIAARLLPPL 36

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

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- 2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	100.0	87	US-09-087-232A-18	Sequence 18, Appl
2	190	100.0	100	US-09-087-232A-15	Sequence 15, Appl
3	190	100.0	184	US-08-833-752-4	Sequence 4, Appl
4	190	100.0	215	US-09-087-232A-17	Sequence 17, Appl
5	190	100.0	215	US-08-833-752-6	Sequence 6, Appl
6	190	100.0	352	US-09-087-232A-13	Sequence 13, Appl
7	190	100.0	352	US-08-861-105-14	Sequence 14, Appl
8	190	100.0	352	US-08-575-967A-2	Sequence 2, Appl
9	190	100.0	352	US-08-833-752-5	Sequence 5, Appl
10	190	100.0	352	US-09-502-783A-2	Sequence 2, Appl
11	190	100.0	352	US-09-796-202-1	Sequence 1, Appl
12	185	97.4	352	US-09-045-583-52	Sequence 52, Appl
13	185	97.4	352	US-09-534-185-52	Sequence 52, Appl
14	184	96.8	352	US-08-466-343D-2	Sequence 2, Appl
15	170	89.5	354	US-09-517-605-5	Sequence 5, Appl
16	131	68.9	354	US-08-724-984A-2	Sequence 2, Appl
17	123	64.7	22	US-08-861-105-4	Sequence 4, Appl
18	113	59.5	20	US-08-889-291-32	Sequence 32, Appl
19	113	59.5	20	US-09-098-244-32	Sequence 32, Appl
20	113	59.5	20	US-09-375-314-32	Sequence 32, Appl
21	113	59.5	20	US-09-767-395-32	Sequence 32, Appl
22	105	55.3	28	US-08-861-105-6	Sequence 6, Appl
23	83.5	43.9	26	US-09-131-827A-14	Sequence 14, Appl
24	75	39.5	83	US-09-131-827A-13	Sequence 13, Appl
25	75	39.5	329	US-09-502-783A-9	Sequence 9, Appl
26	75	39.5	344	US-08-466-343D-9	Sequence 9, Appl
27	75	39.5	347	US-08-461-244-3	Sequence 3, Appl

28	75	39.5	360	1	US-08-450-393A-4	Sequence 4, Appl
29	75	39.5	360	3	US-08-446-669-4	Sequence 4, Appl
30	75	39.5	360	3	US-09-045-583-50	Sequence 50, Appl
31	75	39.5	360	3	US-09-045-583-51	Sequence 51, Appl
32	75	39.5	360	4	US-09-534-185-50	Sequence 50, Appl
33	75	39.5	360	4	US-09-534-185-51	Sequence 51, Appl
34	75	39.5	360	4	US-08-833-752-7	Sequence 7, Appl
35	75	39.5	360	4	US-09-131-827A-2	Sequence 2, Appl
36	75	39.5	360	4	US-09-131-827A-2	Sequence 2, Appl
37	75	39.5	360	5	PCT-US95-00476-4	Sequence 20, Appl
38	75	39.5	374	1	US-08-450-393A-2	Sequence 2, Appl
39	75	39.5	374	3	US-08-446-669-2	Sequence 2, Appl
40	75	39.5	374	5	PCT-US95-00476-2	Sequence 2, Appl
41	74.5	39.2	355	1	US-08-012-988A-2	Sequence 2, Appl
42	74.5	39.2	355	1	US-08-450-393A-5	Sequence 5, Appl
43	74.5	39.2	355	3	US-08-446-669-5	Sequence 5, Appl
44	74.5	39.2	355	4	US-09-239-938-1	Sequence 1, Appl
45	74.5	39.2	355	4	US-08-833-752-9	Sequence 9, Appl

ALIGNMENTS

```
RESULT 1
US-09-087-232A-18
; Sequence 18, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Baker & Botte, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-087-232A-18

Query Match      100.0%; Score 190; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches      36; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

QY 1 MDYQVSPIDYINYYTSEPCQKINKYQIAARLLPPL 36
|||||
DB 1 MDYQVSPIDYINYYTSEPCQKINKYQIAARLLPPL 36

RESULT 2

US-09-087-232A-15
Sequence 15, Application US/09087232A
Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Quillient et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
NUMBER OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
CORRESPONDENCE ADDRESS: 23
ADDRESS: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-15

Query Match

Best Local Similarity 100.0%; Score 190; DB 3; Length 100;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36
DB 1 MDYVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36

RESULT 3

US-08-833-752-4
Sequence 4, Application US/08833752
Patent No. 6448375

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
CORRESPONDENCE ADDRESS: 17
ADDRESS: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 4:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-4

Query Match
Best Local Similarity 100.0%; Score 190; DB 4; Length 184;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36
DB 1 MDYVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36

RESULT 4

US-09-087-232A-17
Sequence 17, Application US/09087232A
Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Quillient et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
NUMBER OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
CORRESPONDENCE ADDRESS: 23
ADDRESS: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-17

Query Match 100.0%; Score 190; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYTSSEPCCKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDINYTSSEPCCKINVKQIAARLLPPL 36

RESULT 5

US-08-833-752-6
Sequence 6, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbé, Martens, Olsson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-6

Query Match 100.0%; Score 190; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYTSSEPCCKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDINYTSSEPCCKINVKQIAARLLPPL 36

US-09-087-232A-13
Sequence 13, Application US/09087232A
Patent No. 6153431

GENERAL INFORMATION:
APPLICANT: Quillient et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-13

Query Match 100.0%; Score 190; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.7e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYTSSEPCCKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDINYTSSEPCCKINVKQIAARLLPPL 36

RESULT 7

US-08-861-105-14
Sequence 14, Application US/08861105
Patent No. 6258527
GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
APPLICANT: DENG, HONGKUI
APPLICANT: ELMEIER, WILFRIED
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-861-105-14

Query Match Best Local Similarity 100.0%; Score 190; DB 3; Length 352;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36
DB 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

RESULT 8
US-08-575-967A-2
Sequence 2, Application US/08575967A
Patent No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 190; DB 3; Length 352;

Best Local Similarity 100.0%; Pred No. 6.7e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36
DB 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

RESULT 9
US-08-833-752-5
Sequence 5, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-5

Query Match Best Local Similarity 100.0%; Score 190; DB 4; Length 352;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36
DB 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

RESULT 10
US-09-502-783A-2
Sequence 2, Application US/09502783A
Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS
FILE REFERENCE: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0

SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match
Best Local Similarity 100.0%; Score 190; DB 4; Length 352;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

RESULT 11
US-09-796-202-1
Sequence 1, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
US-09-796-202-1

Query Match
Best Local Similarity 100.0%; Score 190; DB 4; Length 352;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

RESULT 12
US-09-045-583-52
Sequence 52, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52

Query Match
Best Local Similarity 97.4%; Score 185; DB 3; Length 352;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

RESULT 13
US-09-534-185-52
Sequence 52, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match
Best Local Similarity 97.2%; Score 185; DB 4; Length 352;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

Db 1 MDYQVSSPIYDIDYTSSEPCQKINVKQIAARLLPPL 36

RESULT 14
US-08-466-343D-2
Sequence 2, Application US/08466343D
Patent No. 6025154
GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2640
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-343D-2

Query Match
Best Local Similarity 96.8%; Score 184; DB 3; Length 352;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDIDYTSSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDIDYTSSEPCQKINVKQIAARLLPPL 36

RESULT 15
US-09-517-605-5
Sequence 5, Application US/09517605
Patent No. 6391567
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Geijtenbeek, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens

US-09-517-605-5

Query Match
Best Local Similarity 89.5%; Score 170; DB 4; Length 352;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDIDYTSSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDIDYTSSEPCQKINVKQIAARLLPPL 36

Search completed: May 13, 2004, 15:10:44
Job time: 1.97476 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 5.3301 Seconds
(without alignments)
1879.405 Million cell updates/sec

Title: US-10-072-301-8

Perfect score: 190

Sequence: 1 MDQVSSPIYDINITYTSRPOCKINVKQIAARLPL 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	36	14	US-10-072-301-8
2	190	100.0	36	14	US-10-071-866-8
3	190	100.0	36	15	US-10-360-828-8
4	190	100.0	184	9	US-09-938-719-4
5	190	100.0	184	9	US-09-939-226-4
6	190	100.0	184	9	US-09-938-703-4
7	190	100.0	215	9	US-09-938-719-6
8	190	100.0	215	9	US-09-939-226-6
9	190	100.0	215	9	US-09-938-703-6
10	190	100.0	352	9	US-09-725-285-2
11	190	100.0	352	9	US-09-759-841-2
12	190	100.0	352	9	US-09-779-879A-22
13	190	100.0	352	9	US-09-779-880A-22
14	190	100.0	352	9	US-09-813-653-15
15	190	100.0	352	9	US-09-813-653-17

16	190	100.0	352	9	US-09-796-202-1	Sequence 1, Appli
17	190	100.0	352	9	US-09-195-662A-2	Sequence 2, Appli
18	190	100.0	352	9	US-09-339-912A-2	Sequence 2, Appli
19	190	100.0	352	9	US-09-938-719-5	Sequence 5, Appli
20	190	100.0	352	9	US-09-939-226-5	Sequence 5, Appli
21	190	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
22	190	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
23	190	100.0	352	10	US-09-734-221A-14	Sequence 14, App
24	190	100.0	352	11	US-09-826-509-477	Sequence 477, App
25	190	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
26	190	100.0	352	14	US-10-232-686-2	Sequence 2, Appli
27	190	100.0	352	14	US-10-086-814-1	Sequence 1, Appli
28	190	100.0	352	14	US-10-067-800-22	Sequence 22, Appli
29	190	100.0	352	14	US-10-290-058A-6	Sequence 352, App
30	190	100.0	352	14	US-10-225-567A-352	Sequence 352, App
31	190	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
32	190	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
33	190	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
34	190	100.0	352	14	US-10-135-839-22	Sequence 22, Appli
35	190	100.0	352	14	US-10-239-423-67	Sequence 67, Appli
36	190	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
37	190	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
38	190	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
39	185	97.4	352	14	US-10-164-649-52	Sequence 52, Appli
40	184	96.8	352	9	US-09-779-879A-2	Sequence 2, Appli
41	184	96.8	352	9	US-09-779-880A-2	Sequence 2, Appli
42	184	96.8	352	14	US-10-067-800-2	Sequence 2, Appli
43	184	96.8	352	14	US-10-135-839-2	Sequence 2, Appli
44	180	94.7	352	13	US-10-106-623-20	Sequence 20, Appli
45	172	90.5	33	10	US-09-913-238-70	Sequence 70, Appli

ALIGNMENTS

RESULT 1
US-10-072-301-8
; Sequence 8, Application US/100722301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072.301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-8

Query Match 100.0%; Score 190; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDQVSSPIYDINITYTSRPOCKINVKQIAARLPL 36
DB 1 MDQVSSPIYDINITYTSRPOCKINVKQIAARLPL 36

RESULT 2
US-10-071-866-8
; Sequence 8, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li

;; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
;; FILE REFERENCE: 25636-717
;; CURRENT APPLICATION NUMBER: US/10/071,866
;; CURRENT FILING DATE: 2002-02-08
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 8
;; LENGTH: 36
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-071-866-8

Query Match 100.0%; Score 190; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1,1e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDYOVSSPIYDINYYTSPCKINKVQIAARLLPPL 36
1 MDYOVSSPIYDINYYTSPCKINKVQIAARLLPPL 36

RESULT 3
US-10-360-828-8
; Sequence 8, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-360-828-8

Query Match 100.0%; Score 190; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1,1e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDYOVSSPIYDINYYTSPCKINKVQIAARLLPPL 36
1 MDYOVSSPIYDINYYTSPCKINKVQIAARLLPPL 36

RESULT 4
US-09-938-719-4
; Sequence 4, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach

;; STATE: CA
;; COUNTRY: U.S.A.
;; ZIP: 92660
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/938,719
;; FILING DATE: 24-Aug-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/626,939
;; FILING DATE: 27-JULY-2000
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Altman, Daniel E
;; REGISTRATION NUMBER: 34,115
;; REFERENCE/DOCKET NUMBER: <Unknown>
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 184 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4

Query Match 100.0%; Score 190; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 7,2e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDYOVSSPIYDINYYTSPCKINKVQIAARLLPPL 36
1 MDYOVSSPIYDINYYTSPCKINKVQIAARLLPPL 36

RESULT 5
US-09-939-226-4
; Sequence 4, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4

Query Match 100.0%; Score 190; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 7,2e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36
|||
DB 1 MDYVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

RESULT 6
US-09-938-703-4
Sequence 4, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

Query Match 100.0%; Score 190; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 7,2e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36
|||
DB 1 MDYVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

RESULT 7
US-09-938-719-6
Sequence 6, Application US/09938719

Patent No. US20020106742A1
GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-July-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

Query Match 100.0%; Score 190; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8,6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36
|||
DB 1 MDYVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

RESULT 8
US-09-939-226-6
Sequence 6, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: 1linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6

Query Match 100.0%; Score 190; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36
1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

Db 1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

RESULT 9
US-09-938-703-6
Sequence 6, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: 1linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

Query Match 100.0%; Score 190; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36
1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

Db 1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

RESULT 10
US-09-725-285-2
Sequence 2, Application US/09725285
Patent No. US20010000241A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGFR10
FILE REFERENCE: 1488.115003
CURRENT APPLICATION NUMBER: US/09/725,285
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
FEATURE:
OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 190; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36
1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

Db 1 MDYVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

RESULT 11
US-09-759-841-2
Sequence 2, Application US/09759841
Patent No. US20010039026A1
GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Dobbs, Susan
APPLICANT: Petros, Manousos
TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348APMR
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000659.3
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 100.0%; Score 190; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 12

US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match 100.0%; Score 190; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 13

US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 190; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 14

US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehlt, Christina
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 190; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 15

US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehlt, Christina
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 190; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

Db 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36

Search completed: May 13, 2004, 15:43:29
Job time : 6.3301 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 1.62524 Seconds
(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-8

Perfect score: 190

Sequence: 1 MDYGVSSPIYDINYTTSEPCQKINVKQIARLLPLP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	190	100.0	352	2	A43113	chemokine (C-C) re
2	75	39.5	360	2	UC2443	chemokine (C-C) re
3	75	39.5	374	2	I38450	chemokine (C-C) re
4	74.5	39.2	355	2	A45177	chemokine (C-C) re
5	65	34.2	355	2	I49339	macrophage inflamma
6	65	34.2	359	2	I49341	MIP-1 alpha recept
7	59	31.1	383	2	S55594	G protein-coupled
8	57	30.0	178	2	T20317	hypothetical protei
9	57	30.0	242	2	F84788	hypothetical protei
10	56.5	29.7	360	2	A57160	chemokine (C-C) re
11	56	29.5	211	2	B86864	uracil phosphoribo
12	55.5	29.2	818	2	T40491	hypothetical protei
13	55	28.9	54	2	PT0189	protein-tyrosine k
14	55	28.9	194	2	D87648	conserved hypotet
15	55	28.9	503	2	T29870	hypothetical protei
16	54.5	28.7	130	2	T47540	actin depolymerizi
17	54	28.4	617	2	AF1284	5-methyltetrahydro
18	54	28.4	617	2	AF1284	5-methyltetrahydro
19	53.5	28.2	132	2	A11655	actin depolymerizi
20	53	27.9	516	2	T40181	conserved hypotet
21	53	27.9	1130	2	T29089	alpha-mannosidase
22	53	27.9	2039	2	S64540	probable calicium c
23	52.5	27.6	809	2	E71660	hypothetical protei
24	52	27.4	1162	1	VG1HAK	E2 glycoprotein pr
25	51	26.8	191	2	H70209	decorin binding pr
26	51	26.8	364	2	AE0169	probable exported
27	51	26.8	520	2	S14599	E2 glycoprotein -
28	51	26.8	520	2	S14600	E2 glycoprotein pr
29	51	26.8	520	2	S14598	E2 glycoprotein -

30	51	26.8	528	2	T33464	hypothetical prote
31	51	26.8	544	2	S41626	spike protein chat
32	51	26.8	550	1	VG1HDE	E2 glycoprotein pr
33	51	26.8	1154	1	VG1HIB	E2 glycoprotein pr
34	51	26.8	1162	2	S14939	E2 glycoprotein pr
35	51	26.8	1162	2	S14940	E2 glycoprotein pr
36	51	26.8	1790	1	MMFEB1	laminin beta-1 cha
37	50.5	26.6	1505	2	T31418	synactonemal compl
38	50	26.3	849	2	T04242	abdominal segment
39	49.5	26.1	268	2	T50523	hypothetical prote
40	49.5	26.1	477	2	S16383	carboxypeptidase B
41	49.5	26.1	1039	2	T22982	hypothetical prote
42	49.5	26.1	1192	2	H88293	protein F59B10.1 l
43	49	25.8	1487	2	AG2560	hypothetical prote
44	48.5	25.5	126	2	S10934	actin-depolymerizi
45	48.5	25.5	130	2	T05788	actin-depolymerizi

ALIGNMENTS

RESULT 1
A43113
Chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #ext change 20-Jun-2000
C:Accession: A43113; S11808; A58834; A58832; G02553; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:G1262810; PIDN:CA62796.1; PID:G1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Lienard, C.; Farber, C.M.; Saragost
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles c
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184 'IKDHLGAGPAAACHGHLGPNPNSASVSK' <SAM3>
A:Cross-references: GB:X9393; NID:G1524062; PIDN:CA67767.1; PID:G1524063
A>Note: this frameshift mutation results in a non-functional receptor but confers a degr
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:9629570; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:G1502408; PIDN:AA817071.1; PID:G1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Comadere, C.
Submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314

A/Accession: A58833
A/Molecule type: mRNA
A/Residues: 1-352 <RAP>
A/Cross-references: GB:U5494; NID:G1457945; PIDN:AA05098.1; PID:G1457946
C/Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-beta (see PIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine (see PIR:A30574).
A/Status: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A/Map position: 3p21-3p21
C/Function:
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-beta and RANTES
C/Superfamily: Vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F/103-124/Domain: transmembrane #status predicted <TM1>
F/167-87/Domain: transmembrane #status predicted <TM2>
F/132-56/Domain: transmembrane #status predicted <TM3>
F/193-218/Domain: transmembrane #status predicted <TM4>
F/236-257/Domain: transmembrane #status predicted <TM5>
F/285-300/Domain: transmembrane #status predicted <TM6>
F/20-269/Domain: transmembrane #status predicted <TM7>
F/268/Binding site: disulfide bonds: #status predicted
F/336/337/342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340/343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match
Best Local Similarity 100.0%; Score 190; DB 2; Length 352;
Matches 36; Conservative 0; Pred. No. 7.1e-19;
Mismatches 0; Indels 0; Gaps 0;
DB 1 MDYQVSSPIYDINVTSEPCCKINVKQIARLPL 36
1 MDYQVSSPIYDINVTSEPCCKINVKQIARLPL 36

RESULT 2
JC2443
Chemokine (C-C) receptor 2, splice form B - human
N/Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C/Species: Homo sapiens (man)
C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
A/Accession: JC2443; J38463
A/Status: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A/Map position: 3p21-3p21
C/Function:
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-beta and RANTES
C/Superfamily: Vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F/103-124/Domain: transmembrane #status predicted <TM1>
F/167-87/Domain: transmembrane #status predicted <TM2>
F/132-56/Domain: transmembrane #status predicted <TM3>
F/193-218/Domain: transmembrane #status predicted <TM4>
F/236-257/Domain: transmembrane #status predicted <TM5>
F/285-300/Domain: transmembrane #status predicted <TM6>
F/20-269/Domain: transmembrane #status predicted <TM7>
F/268/Binding site: disulfide bonds: #status predicted
F/336/337/342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340/343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match
Best Local Similarity 100.0%; Score 190; DB 2; Length 352;
Matches 36; Conservative 0; Pred. No. 7.1e-19;
Mismatches 0; Indels 0; Gaps 0;
DB 1 MDYQVSSPIYDINVTSEPCCKINVKQIARLPL 36
1 MDYQVSSPIYDINVTSEPCCKINVKQIARLPL 36

RESULT 3
JC2443
Chemokine (C-C) receptor 2, splice form A - human
N/Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
A/Accession: JC2443; J38450
A/Status: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A/Map position: 3p21-3p21
C/Function:
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-beta and RANTES
C/Superfamily: Vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F/103-124/Domain: transmembrane #status predicted <TM1>
F/167-87/Domain: transmembrane #status predicted <TM2>
F/132-56/Domain: transmembrane #status predicted <TM3>
F/193-218/Domain: transmembrane #status predicted <TM4>
F/236-257/Domain: transmembrane #status predicted <TM5>
F/285-300/Domain: transmembrane #status predicted <TM6>
F/20-269/Domain: transmembrane #status predicted <TM7>
F/268/Binding site: disulfide bonds: #status predicted
F/336/337/342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340/343/Binding site: phosphate (Thr) (covalent) #status predicted

F/114/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/113-190/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 39.5%; Score 75; DB 2; Length 360;
Matches 15; Conservative 4; Mismatches 6; Indels 2; Gaps 1;
DB 10 YDINVTSEPCCKINVKQIARLPL 36
24 FDYDY--GAPCHKPDVQIQAGQLPL 48

RESULT 4
JC2443
Chemokine (C-C) receptor 1 - human
N/Alternate names: C-C CR-1; macrophage inflammatory protein-1-alpha receptor
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
A/Accession: JC2443; J38450
A/Status: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A/Map position: 3p21-3p21
C/Function:
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-beta and RANTES
C/Superfamily: Vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F/103-124/Domain: transmembrane #status predicted <TM1>
F/167-87/Domain: transmembrane #status predicted <TM2>
F/132-56/Domain: transmembrane #status predicted <TM3>
F/193-218/Domain: transmembrane #status predicted <TM4>
F/236-257/Domain: transmembrane #status predicted <TM5>
F/285-300/Domain: transmembrane #status predicted <TM6>
F/20-269/Domain: transmembrane #status predicted <TM7>
F/268/Binding site: disulfide bonds: #status predicted
F/336/337/342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340/343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match
Best Local Similarity 39.5%; Score 75; DB 2; Length 374;
Matches 15; Conservative 4; Mismatches 6; Indels 2; Gaps 1;
DB 10 YDINVTSEPCCKINVKQIARLPL 36
24 FDYDY--GAPCHKPDVQIQAGQLPL 48

RESULT 4
JC2443
Chemokine (C-C) receptor 1 - human
N/Alternate names: C-C CR-1; macrophage inflammatory protein-1-alpha receptor
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
A/Accession: JC2443; J38450
A/Status: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A/Map position: 3p21-3p21
C/Function:
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-beta and RANTES
C/Superfamily: Vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F/103-124/Domain: transmembrane #status predicted <TM1>
F/167-87/Domain: transmembrane #status predicted <TM2>
F/132-56/Domain: transmembrane #status predicted <TM3>
F/193-218/Domain: transmembrane #status predicted <TM4>
F/236-257/Domain: transmembrane #status predicted <TM5>
F/285-300/Domain: transmembrane #status predicted <TM6>
F/20-269/Domain: transmembrane #status predicted <TM7>
F/268/Binding site: disulfide bonds: #status predicted
F/336/337/342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340/343/Binding site: phosphate (Thr) (covalent) #status predicted

A>Title: Structure and functional expression of the human macrophage inflammatory 1 alpha

A|Title: Reference number: 155671; MUID:93240122; PMID:7683036

A|Accession: 155671

A|Status: preliminary; translated from GB/EMBL/DDBJ

A|Molecule type: mRNA

A|Residues: 1-355 <RES>

A|Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C|Genetics:

A|Gene: GDB:CMKBR1, CMKR-1

A|Cross-references: GDB:138446; OMIM:601159

A|Map position: 3p21-3p21

C|Superfamily: vertebrate rhodopsin

C|Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane

F|336-61/Domain: transmembrane #status predicted <TM1>

F|71-91/Domain: transmembrane #status predicted <TM2>

F|108-139/Domain: transmembrane #status predicted <TM3>

F|147-171/Domain: transmembrane #status predicted <TM4>

F|205-223/Domain: transmembrane #status predicted <TM5>

F|240-264/Domain: transmembrane #status predicted <TM6>

F|288-305/Domain: transmembrane #status predicted <TM7>

F|5/Binding site: carbohydrate (Asn) (covalent) #status predicted

F|24-273,106-183/disulfide bonds: #status predicted

F|345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 39.2%; Score 74.5; DB 2; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.012;
Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Oy 2 DYGVSPFYDINYYTSEPCQKINVKQIARLRPL 36
|| | : | : ||| : | : |||
Db 9 DYDTTT---EPDYGDATPCQKNRARAQAQLRPL 40

RESULT 5

I49339

macrophage inflammatory protein-1 alpha receptor - mouse

C|Species: Mus musculus (house mouse)

C|Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C|Accession: I49339

R|Gao, J.L.; Murphy, P.M.

J Biol. Chem. 270, 17494-17501, 1995

A|Title: Cloning and differential tissue-specific expression of three mouse beta chemokins

A|Reference numbers: I49339; MUID:95340546; PMID:7542241

A|Accession: I49339

A|Status: preliminary; translated from GB/EMBL/DDBJ

A|Molecule type: DNA

A|Residues: 1-355 <RES>

A|Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548

C|Superfamily: vertebrate rhodopsin

Query Match 34.2%; Score 65; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 0.27;
Matches 13; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Oy 11 DINYTSBPCQKINVKQIARLRPL 36
: | | | | : | | | |
Db 15 EPDYGDSTPCCQKTAVRAFGAGLRPL 40

RESULT 6

I49341

MIP-1 alpha receptor like-2 - mouse

C|Species: Mus musculus (house mouse)

C|Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998

C|Accession: I49341

R|Gao, J.L.; Murphy, P.M.

J Biol. Chem. 270, 17494-17501, 1995

A|Title: Cloning and differential tissue-specific expression of three mouse beta chemokins

A|Reference numbers: I49339; MUID:95340546; PMID:7542241

A|Accession: I49341

A|Status: preliminary; translated from GB/EMBL/DDBJ

A|Molecule type: DNA

A|Residues: 1-359 <RES>

```

C:\cross-references: EMBL:U28406; NID:9881551; PID:9881552
C:\superfamily: vertebrate rhodopsin

Query Match          34.2%; Score 65; DB 2; Length 359;
Best Local Similarity 43.5%; Pred. No. 0.27;
Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY      14  YTTSEPCOKINVKQIARLAPPL 36
      |::|::|::|::|::|::|
Db       22  YEMAPCEKVKIKELGSLAPPL 44

RESULT 7
G protein-coupled receptor E1 - equine herpesvirus 2
C:\Species: equine herpesvirus 2
C:\Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
R:\Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:\Title: The DNA sequence of equine herpesvirus 2.
A:\Reference number: S55594; MUID:95302501; PMID:7783207
A:\Accession: S55594
A:\Status: preliminary; nucleic acid sequence not shown
A:\Molecule type: DNA
A:\Residues: 1-383 <TEL>
A:\Cross-references: GB:U20824; NID:9695172; PIDN:AA13788.1; PID:9695173
C:\Superfamily: vertebrate rhodopsin
C:\Keywords: G protein-coupled receptor

Query Match          31.1%; Score 59; DB 2; Length 383;
Best Local Similarity 38.5%; Pred. No. 2;
Matches 10; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY      11  DINYTSEPCOKINVKQIARLAPPL 36
      |::|::|::|::|::|::|
Db       53  DVDYBSAPCTKSDTTRLAQVPEAL 78

RESULT 8
T20317
hypothetical protein D1081.6 - Caenorhabditis elegans
C:\Species: Caenorhabditis elegans
C:\Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:\Accession: T20317
R:\Dobson, R.
submitted to the EMBL Data Library, July 1996
A:\Reference number: Z19256
A:\Accession: T20317
A:\Status: preliminary; translated from GB/EMBL/DBJ
A:\Molecule type: DNA
A:\Residues: 1-178 <WIL>
A:\Cross-references: EMBL:Z75710; PIDN:CA80027.1; GSPDB:GN00019; CESP: D1081.6
C:\Genetic8:
A:\Gene: CESP:D1081.6
A:\Map position: 1
A:\Introns: 95/3; 114/3

Query Match          30.0%; Score 57; DB 2; Length 178;
Best Local Similarity 52.9%; Pred. No. 1.7;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      3  YQVSSPIYDINYTSEP 19
      |::|::|::|::|::|
Db       47  FQVQIPLYDINITYAEP 63

RESULT 9
F84788
hypothetical protein At2g37110 [imported] - Arabidopsis thaliana
C:\Species: Arabidopsis thaliana (mouse-ear cress)
C:\Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

```

C/Accession: F84788
 R./Lin, X./Kaul, S./Rounalev, S.D./Shea, T.P./Benito, M.I./Town, C.D./Pujil, C.Y./
 M./Koo, H./Moffat, K.S./Cronin, L.A./Shen, M./Vanaken, S.E./Umayam, L./Tailon, L./
 Natures, D./Nierman, W.C./White, O./Eisen, J.A./Salzberg, S.L./Fraser, C.M./Venter, J.
 Nature 402, 761-766, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: F84788
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-242 <STO>
 A/Cross-references: GB:A8002093; NID:94371290; PIDN:AAD18148.1; GSPDB:GN00139
 A/Gene: At2g37110
 A/Map position: 2

Query Match 30.0%; Score 57; DB 2; Length 242;
 Best Local Similarity 38.2%; Pred. No. 2.3;
 Matches 13; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 2 DYQVSPYDINYYTSPCKQKINVKQIARLPP 35
 DB 14 EYESSPLKYNENDGKICKRDAK--AAPVLP 45

RESULT 10

A57160
 Chemokine (C-C) receptor 4 - human
 N/Alternate names: C-C CKR-4
 C/Species: Homo sapiens (man)
 C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 R/Accession: A57160
 R/Power, C.A./Meyer, A./Nemeth, K./Bacon, K.B./Hoogewerf, A.J./Proudfoot, A.E.I./
 J. Biol. Chem. 270, 19495-19500, 1995
 A/Title: Molecular cloning and functional expression of a novel CC chemokine receptor cD
 A/Reference number: A57160; MUID:95370289; PMID:7642634
 A/Accession: A57160
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-360 <POW>
 A/Cross-references: GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:9971452
 A/Note: source clone KS-5
 A/Gene: GDB:CMKBR4
 A/Cross-references: GDB:677463
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F/40-65/Domain: transmembrane #status predicted <TM1>
 F/76-97/Domain: transmembrane #status predicted <TM2>
 F/112-133/Domain: transmembrane #status predicted <TM3>
 F/151-175/Domain: transmembrane #status predicted <TM4>
 F/208-226/Domain: transmembrane #status predicted <TM5>
 F/243-264/Domain: transmembrane #status predicted <TM6>
 F/291-308/Domain: transmembrane #status predicted <TM7>
 F/329-276,110-187/Diulfide bonds: #status predicted
 F/145/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F/183/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F/321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 29.7%; Score 56.5; DB 2; Length 360;
 Best Local Similarity 38.5%; Pred. No. 4.3;
 Matches 15; Conservative 2; Mismatches 17; Indels 5; Gaps 2;

QY 2 DYQVSSPIYDINYYTSPCKQKINVKQIARLPP 36
 DB 8 DTTLDSEIYS-NYLYESIPPECTKEGKAGGELFPLPL 45

RESULT 11

B86864
 uracil phosphoribosyltransferase (EC 2.4.2.9) [imported] - Lactococcus lactis subsp. lad

C/Species: Lactococcus lactis subsp. lactis
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C/Accession: B86864
 R/Bolotin, A./Wincker, P./Mauger, S./Tailon, O./Malarme, K./Weissenbach, J./En
 Genome Res. 11, 731-753, 2001
 A/Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis*
 A/Reference number: A86825; MUID:21235186; PMID:11337471
 A/Accession: B86864
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-211 <STO>
 A/Cross-references: GB:A8005176; PID:912724952; PIDN:AAK06012.1; GSPDB:GN00146
 A/Experimental source: strain IT1403
 C/Genetics:
 A/Gene: upp
 C/Superfamily: uracil phosphoribosyltransferase upp
 C/Keywords: glycosyltransferase; pentosyltransferase

Query Match 29.5%; Score 56; DB 2; Length 211;
 Best Local Similarity 45.7%; Pred. No. 2.8;
 Matches 16; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

QY 1 MDYQVS--PIYDINYYTSPCKQKINVKQIARL 33
 DB 40 MAYEVSRLPLEDVEIET--PVQKTVKQIAGKKL 72

RESULT 12

T40491
 Hypothetical protein SPBC4C3.06 - fission yeast (*Schizosaccharomyces pombe*)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 R/Accession: T40491
 R/Wood, V./Rajandream, M.A./Barrell, B.G./Lauber, J./Hilbert, H./Duesterhoeft, A.
 submitted to the EMBL Data Library, February 1998
 A/Reference number: Z21910
 A/Accession: T40491
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-818 <MO>
 A/Cross-references: EMBL:AL021730; PIDN:CAA16828.1; GSPDB:GN00067; SPDB:SPBC4C3.06
 A/Experimental source: strain 972h-; cosmid c4C3
 C/Genetics:
 A/Gene: SPDB:SPBC4C3.06
 A/Map position: 2
 A/Introns: 14/3

Query Match 29.2%; Score 55.5; DB 2; Length 818;
 Best Local Similarity 41.9%; Pred. No. 15;
 Matches 13; Conservative 8; Mismatches 7; Indels 3; Gaps 2;

QY 4 QVSSPIYD--INYYTSPCKQKINVKQIARL 32
 DB 99 QIAGVYPLIDYITSP-QTATLRRLAERL 128

RESULT 13

PT0189
 protein-tyrosine kinase (EC 2.7.1.112) tyro-7 - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 04-Feb-2000
 C/Accession: PT0189
 R/Isai, C./Lemke, G.
 Neuron 6, 691-704, 1991
 A/Title: An extended family of protein-tyrosine kinase genes differentially expressed in
 A/Reference number: PT0189; MUID:91222560; PMID:2025425
 A/Accession: PT0189
 A/Molecule type: mRNA
 A/Residues: 1-54 <LAI>
 A/Experimental source: sciatic nerve
 C/Genetics:
 A/Gene: tyro-7
 C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 1.01359 Seconds

(without alignments)
1849.388 Million cell updates/sec

Title: US-10-072-301-8

Perfect score: 190

Sequence: 1 MDYGVSPIDYINYYTSPCKINVKQIAARLPL 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	100.0	352	1	CRK5_HUMAN
2	185	97.4	352	1	CRK5_HUMAN
3	180	94.7	352	1	CRK5_CERY
4	180	94.7	352	1	CRK5_CERY
5	180	94.7	352	1	CRK5_HYLY
6	180	94.7	352	1	CRK5_PACMU
7	180	94.7	352	1	CRK5_PACMU
8	180	94.7	352	1	CRK5_PACMU
9	179	94.2	352	1	CRK5_PACMU
10	179	94.2	352	1	CRK5_PACMU
11	179	94.2	352	1	CRK5_PACMU
12	179	94.2	352	1	CRK5_PACMU
13	175	92.1	352	1	CRK5_GORGO
14	173	91.1	352	1	CRK5_HYLY
15	171	90.0	352	1	CRK5_CERAR
16	170	89.5	352	1	CRK5_HYLY
17	131	68.9	354	1	CRK5_MOUSE
18	131	68.9	354	1	CRK5_MOUSE
19	76.5	40.3	373	1	CRK2_MOUSE
20	76.5	40.3	373	1	CRK2_MOUSE
21	75	39.5	360	1	CRK2_MOUSE
22	75	39.5	360	1	CRK2_MOUSE
23	74.5	37.2	355	1	CRK1_MOUSE
24	74.5	37.2	355	1	CRK1_MOUSE
25	65	34.2	359	1	CRK3_MOUSE
26	65	34.2	359	1	CRK3_MOUSE
27	63	33.2	359	1	CRK3_MOUSE
28	61	33.1	357	1	CRK9_MOUSE
29	57	30.0	369	1	CRK9_MOUSE
30	56.5	28.7	360	1	CRK4_MOUSE
31	56	28.5	211	1	UPP_LACTA
32	56	28.5	211	1	UPP_LACTA
33	54.5	28.7	137	1	ADP2_ARATH

34	54.5	28.7	139	1	ADP4_ARATH	Q92sk3 arabidopsis
35	53.5	28.2	139	1	ADP1_PETRY	Q9fvl2 pecunia hyb
36	53.5	28.2	146	1	ADP6_ARATH	Q92sk2 arabidopsis
37	53	27.9	143	1	ADP_VITVI	Q8esg3 vicia vinif.
38	53	27.9	358	1	CRK3_CAVRO	Q92z13 cavia porce
39	53	27.9	516	1	YB4F_SCHPO	Q14360 schizosach
40	53	27.9	721	1	THIC_SHEON	Q8eed7 shewanella
41	53	27.9	2039	1	CCH1_YEAST	P50077 saccharomyc
42	52	27.4	1162	1	VGL2_IBVK	P12650 avian infec
43	52	27.4	1790	1	IL2B_DROME	P11045 drosophila
44	51.5	27.1	537	1	IL2B_RAT	P26896 rattus norv
45	51	26.8	139	1	ADP1_ARATH	Q39250 arabidopsis

ALIGNMENTS

RESULT 1	CRK5_HUMAN	STANDARD;	PRT;	352 AA.
ID	CRK5_HUMAN	014692; 014693; 014695; 014696; 014697; 014698; 014699;		
AC	P51681; 014700; 014701; 014702; 014703; 014704; 014705; 014706; 014707;			
AC	014708; 015538; 09UPA4;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	C-C chemokine receptor type 5 (C-C-CCR-5) (CCR-5) (CCR5)			
DE	(HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).			
GN	CCR5 OR CCR5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96241590; PubMed=8639485;			
RA	Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;			
RT	"Molecular cloning and functional expression of a new human			
RT	CC-chemokine receptor gene.";			
RL	Biochemistry 35:3362-3367(1996).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=96291862; PubMed=8663114;			
RA	Rapport C.J., Gosling J., Schweilhart V.L., Gray P.W., Charo I.F.;			
RT	"Cloning and functional characterization of a novel human			
RT	CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";			
RL	J. Biol. Chem. 271:17161-17166(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96295970; PubMed=8659119;			
RA	Combadere C., Anuja S.K., Tiffany H.L., Murphy P.M.;			
RT	"Cloning and functional expression of CC CRK5, a human monocyte CC			
RT	chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and			
RT	RANTES.";			
RL	J. Leukoc. Biol. 60:147-152(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	McCombe W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,			
RA	Nham M., Parnell L., Dedhia N., Ansari A., Maris E., Schutz K.,			
RA	Gnot D., la Bastide M., Kaplan N., Greco T., Touchman J.,			
RA	Munz J., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,			
RA	Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,			
RA	Solinsky K.A., Desliva U., Diaz-Perez S., Zhou X., Yu Y.,			
RA	Watanabe M., Doggett N., Garcia D., Sagittanti J.L.;			
RL	Submitted (May-1997) to the EMBL/Genbank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96001387; PubMed=9343322;			
RA	Kuhmann S.B., Platt E.U., Kozak S.L., Kabat D.;			
RT	"Polymorphisms in the CCR5 genes of African green monkeys and mice			
RT	implicate specific amino acids in infections by simian and human			
RT	immunodeficiency viruses.";			
RL	J. Virol. 71:8642-8656(1997).			

RN [6]
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
 RX MEDLINE=98022612; PubMed=935954;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RT HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049523; PubMed=9388201;
 RA Mummid S., Ahuja S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 with 5'-end heterogeneity, dual promoter usage, and evidence for
 polymorphisms within the regulatory regions and noncoding exons."
 RL J. Biol. Chem. 272:30662-30671(1997).
 RN [8]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Isaacs H., Theodorou I.,
 RL Debrie P.;
 RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RP [9]
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guthrie cDNA resource center (www.cdna.org)."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260017; PubMed=8649511;
 RA Deng H., Liu R., Rilmeyer W., Choe S., Unutmaz D., Burkhardt M.,
 RA Balger S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 HIV-1."
 RL Nature 381:661-666(1996).
 RN [11]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260018; PubMed=8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 CC-CKR-5."
 RL Nature 381:667-673(1996).
 RN [12]
 RP SULFATION.
 RX MEDLINE=99189752; PubMed=10089882;
 RA Parzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 entry."
 RL Cell 96:667-676(1999).
 RN [13]
 RP FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation. Acts as co-receptor with CD4 for primary non-
 CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
 CC virus. It promotes Env-mediated fusion of the virus.
 CC [14]
 RP TISSUE SPECIFICITY: Found in promyelocytic cells.
 CC [15]
 RP SULFATION: Contributes to the efficiency of HIV-1 entry.
 CC [16]
 RP PTM: Modified by O-linked glycosylation, but not by N-linked
 CC glycosylation.
 RN [17]
 RP SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 DR EMBL: AF011819; AAB66019.1;
 DR EMBL: AF011820; AAB66020.1;
 DR EMBL: AF011821; AAB66021.1;
 DR EMBL: AF011822; AAB66022.1;
 DR EMBL: AF011823; AAB66023.1;
 DR EMBL: AF011824; AAB66024.1;
 DR EMBL: AF011825; AAB66025.1;
 DR EMBL: AF011826; AAB66026.1;
 DR EMBL: AF011827; AAB66027.1;
 DR EMBL: AF011828; AAB66028.1;
 DR EMBL: AF011829; AAB66029.1;
 DR EMBL: AF011830; AAB66030.1;
 DR EMBL: AF011831; AAB66031.1;
 DR EMBL: AF011832; AAB66032.1;
 DR EMBL: AF011833; AAB66033.1;
 DR EMBL: AF011834; AAB66034.1;
 DR EMBL: AF011835; AAB66035.1;
 DR EMBL: AF011836; AAB66036.1;
 DR EMBL: AF011837; AAB66037.1;
 DR EMBL: AF011838; AAB66038.1;
 DR EMBL: AF011839; AAB66039.1;
 DR EMBL: AF011840; AAB66040.1;
 DR EMBL: AF011841; AAB66041.1;
 DR EMBL: AF011842; AAB66042.1;
 DR EMBL: AF011843; AAB66043.1;
 DR EMBL: AF011844; AAB66044.1;
 DR EMBL: AF011845; AAB66045.1;
 DR EMBL: AF011846; AAB66046.1;
 DR EMBL: AF011847; AAB66047.1;
 DR EMBL: AF011848; AAB66048.1;
 DR EMBL: AF011849; AAB66049.1;
 DR EMBL: AF011850; AAB66050.1;
 DR EMBL: AF011851; AAB66051.1;
 DR EMBL: AF011852; AAB66052.1;
 DR EMBL: AF011853; AAB66053.1;
 DR EMBL: AF011854; AAB66054.1;
 DR EMBL: AF011855; AAB66055.1;
 DR EMBL: AF011856; AAB66056.1;
 DR EMBL: AF011857; AAB66057.1;
 DR EMBL: AF011858; AAB66058.1;
 DR EMBL: AF011859; AAB66059.1;
 DR EMBL: AF011860; AAB66060.1;
 DR EMBL: AF011861; AAB66061.1;
 DR EMBL: AF011862; AAB66062.1;
 DR EMBL: AF011863; AAB66063.1;
 DR EMBL: AF011864; AAB66064.1;
 DR EMBL: AF011865; AAB66065.1;
 DR EMBL: AF011866; AAB66066.1;
 DR EMBL: AF011867; AAB66067.1;
 DR EMBL: AF011868; AAB66068.1;
 DR EMBL: AF011869; AAB66069.1;
 DR EMBL: AF011870; AAB66070.1;
 DR EMBL: AF011871; AAB66071.1;
 DR EMBL: AF011872; AAB66072.1;
 DR EMBL: AF011873; AAB66073.1;
 DR EMBL: AF011874; AAB66074.1;
 DR EMBL: AF011875; AAB66075.1;
 DR EMBL: AF011876; AAB66076.1;
 DR EMBL: AF011877; AAB66077.1;
 DR EMBL: AF011878; AAB66078.1;
 DR EMBL: AF011879; AAB66079.1;
 DR EMBL: AF011880; AAB66080.1;
 DR EMBL: AF011881; AAB66081.1;
 DR EMBL: AF011882; AAB66082.1;
 DR EMBL: AF011883; AAB66083.1;
 DR EMBL: AF011884; AAB66084.1;
 DR EMBL: AF011885; AAB66085.1;
 DR EMBL: AF011886; AAB66086.1;
 DR EMBL: AF011887; AAB66087.1;
 DR EMBL: AF011888; AAB66088.1;
 DR EMBL: AF011889; AAB66089.1;
 DR EMBL: AF011890; AAB66090.1;
 DR EMBL: AF011891; AAB66091.1;
 DR EMBL: AF011892; AAB66092.1;
 DR EMBL: AF011893; AAB66093.1;
 DR EMBL: AF011894; AAB66094.1;
 DR EMBL: AF011

Query Match 100.0%; Score 190; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.9e-19;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSPCKINVKQIARLLPPL 36
 DB 1 MDYQVSSPIYDINYYTSPCKINVKQIARLLPPL 36

RESULT 2
 ID CCR5 PANTR STANDARD; PRT; 352 AA.
 AC P56440; 002778;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OC NCBI_TaxID=9598;
 OK [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97426118; PubMed=9282822;
 RA Zacharova V., Zachar V., Goustein A.S.;
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 RT HIV type 1 host.";
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98090115; PubMed=9430250;
 RA Perret J.-L., Zerbib A., Girard M., Guillet J.-G., Buroc C.;
 RT "Chimpanzee CCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 or send an email to license@sib.ch).

DR EMBL; AF005663; AAB62557.1; -
 DR EMBL; U94329; AAB58446.1; -
 DR EMBL; AF011542; AAB65742.1; -
 DR EMBL; U97666; AAC51670.1; -
 DR EMBL; AF011540; AAB65740.1; -
 DR EMBL; U89797; AAC03717.1; -
 DR EMBL; AF177894; AAK43377.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
 DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFD 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 123 123
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 97.4%; Score 185; DB 1; Length 352;
 Best Local Similarity 97.2%; Pred. No. 2.5e-18;
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSPCKINVKQIARLLPPL 36
 DB 1 MDYQVSSPIYDINYYTSPCKINVKQIARLLPPL 36

RESULT 3
 ID CCR5 CERPY STANDARD; PRT; 352 AA.
 AC O9TV42;
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Cercopithecus pygerythrus (Vervet monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OK NCBI_TaxID=60710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=100; PubMed=10408730;
 RX MEDLINE=99335215; PubMed=10408730;
 RA Muller-Trutwin M.C., Corbet S., Hansen J., Fomsgaard A.;
 RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
 RT "Mutations in CCR5-coding sequences are not associated with HIV
 RT carrier status in African nonhuman primates.";

```

RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF051902; AAC39830.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 31 58
FT TRANSMEM 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 235
FT DOMAIN 236 260
FT TRANSMEM 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 15 15
FT MOD_RES 15 15
FT SEQUENCE 352 AA; 40558 MW; E117D67CBCC3DB0 CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 1.2e-17;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPYDIDYNTSPCKINVKQIAARLLPPL 36
DB 1 MDYQVSSPYDIDYNTSPCKINVKQIAARLLPPL 36

RESULT 4
CKRS CERTO STANDARD; PRT; 352 AA.
AC 062743; 062744; 062745; 062746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C-CCR-5) (CC-CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5R5.
OS Cereococcus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cercopitheciinae; Cercopithecidae; Catarrhini; Cercopithecidae;
OC NCBI_TaxID=9531;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=I isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettle A., Ho D.D., Marx P.A.;

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RT "Primary SIVem isolates use the CKRS coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of Primary SIVem, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF051902; AAC39830.1; -
DR EMBL; AF051903; AAC39831.1; -
DR EMBL; AF051904; AAC39832.1; -
DR EMBL; AF051905; AAC39833.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 31 58
FT TRANSMEM 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 235
FT TRANSMEM 236 260
FT TRANSMEM 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT MOD_RES 15 15
FT MOD_RES 15 15
FT SEQUENCE 352 AA; 40489 MW; 20A196E2D47E9CA CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 1.2e-17;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPYDIDYNTSPCKINVKQIAARLLPPL 36
DB 1 MDYQVSSPYDIDYNTSPCKINVKQIAARLLPPL 36

RESULT 5
CKRS HYLSY STANDARD; PRT; 352 AA.
AC 095NC5;
ID CKRS HYLSY
RA

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DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5B5.
 OS Hylobates syndactylus (Simang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 NCBI_Taxid=9590;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL: AF177884; AAK43367.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;
 Query Match 94.7%; Score 180; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 1.2e-17;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5B5.
 OS Macaca mulatta (Rhesus macaque).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_Taxid=9544, 9541, 9545;
 [1]
 RP SEQUENCE FROM N.A.
 RA SPECIES=M.mulatta;
 RC MEDLINE=97184592; PubMed=9032394;
 RA Maron L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
 RA Newman W., Gerard N., Gerard C., Sodroski J.;
 "Utilization of C-C chemokine receptor 5 by the envelope
 RT glycoproteins of a pathogenic simian immunodeficiency virus,
 RT SIVmac239.";
 RT J. Virol. 71:2522-2527(1997).
 RL [2].
 RN SEQUENCE FROM N.A.
 RP SPECIES=M.mulatta; STRAIN=Indian macaque;
 RC MEDLINE=97213934; PubMed=9060623;
 RX Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
 RA "Genetically divergent strains of simian immunodeficiency virus use
 RT CCR5 as a coreceptor for entry.";
 RL J. Virol. 71:2705-2714(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta;
 RX MEDLINE=21354176; PubMed=11461684;
 RA Marquies B.U., Haer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL Aids Res. Hum. Retroviruses 17:981-986(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amodee A., Miller K., Doranz B.U., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL: U77672; AAC51109.1; -
 DR EMBL; U73739; AAC51158.1; -
 DR EMBL; U96762; AAC34132.1; -
 DR EMBL; AF005660; AAB62554.1; -
 DR EMBL; AF005661; AAB62555.1; -
 DR EMBL; AF005662; AAB62556.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.

DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSSEM 31 58
 FT TRANSSEM 59 68
 FT TRANSSEM 69 89
 FT TRANSSEM 90 102
 FT TRANSSEM 103 124
 FT TRANSSEM 125 141
 FT TRANSSEM 142 166
 FT TRANSSEM 167 198
 FT TRANSSEM 199 218
 FT TRANSSEM 219 235
 FT TRANSSEM 236 260
 FT TRANSSEM 261 277
 FT TRANSSEM 278 301
 FT TRANSSEM 302 352
 FT TRANSSEM 101 178
 FT TRANSSEM 3 3
 FT TRANSSEM 10 10
 FT TRANSSEM 14 14
 FT TRANSSEM 15 15
 FT TRANSSEM 268 268
 FT TRANSSEM 241 241
 FT TRANSSEM 292 292
 SQ SEQUENCE 352 AA; 40507 MW; 58896C85909FACB2 CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 1.2e-17;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQSSPTDYDNYTSPCKINVKQIAARLPL 36
 Db 1 MDYQSSPTDYDNYTSPCKINVKQIAARLPL 36

RESULT 7
 ID CCR5_PAPHA STANDARD; PRT; 352 AA.
 AC P56441;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9557, 9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=9726867; PubMed=9108095;
 RA Edinger A.L., Amodeo A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.B., Murphy-Corb M.,
 RA Piller S.C., Parmentier M., Broder C.C., Doms R.W.,
 RA "Differential utilization of CCR5 by macrophage and T cell tropic
 RT "Human immunodeficiency virus strains".
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=9921033; PubMed=10195758;
 RA Sakeena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lai R.B.,
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RL nonhuman primates".
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.anubis;
 RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;

RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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DR EMBL; AF005658; AAB2552.1;
 DR EMBL; AF105287; AAD20556.1;
 DR EMBL; AF105288; AAD20557.1;
 DR EMBL; AF105289; AAD20558.1;
 DR EMBL; AF105290; AAD20559.1;
 DR EMBL; AF023452; AAC63830.1;
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSSEM 31 58
 FT TRANSSEM 59 68
 FT TRANSSEM 69 89
 FT TRANSSEM 90 102
 FT TRANSSEM 103 124
 FT TRANSSEM 125 141
 FT TRANSSEM 142 166
 FT TRANSSEM 167 198
 FT TRANSSEM 199 218
 FT TRANSSEM 219 235
 FT TRANSSEM 236 260
 FT TRANSSEM 261 277
 FT TRANSSEM 278 301
 FT TRANSSEM 302 352
 FT TRANSSEM 101 178
 FT TRANSSEM 3 3
 FT TRANSSEM 10 10
 FT TRANSSEM 14 14
 FT TRANSSEM 15 15
 FT TRANSSEM 268 268
 FT TRANSSEM 241 241
 FT TRANSSEM 292 292
 SQ SEQUENCE 352 AA; 40489 MW; 5E15049BA1FEB82 CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 1.2e-17;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQSSPTDYDNYTSPCKINVKQIAARLPL 36
 Db 1 MDYQSSPTDYDNYTSPCKINVKQIAARLPL 36
 RESULT 8
 ID CCR5_PONPY STANDARD; PRT; 352 AA.
 AC O97861;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.

NCBI_TaxID=9600;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=99416438; PubMed=10486970;
 Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 Mol. Biol. Evol. 16:1145-1154(1999).
 -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC EMBL: AF075446; AAD19858.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7cm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 1 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;
 Query Match 94.4%; Score 180; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 1.2e-17;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQVSSPTDYIDYITSEPCCKINVKQIAARLLPPL 36
 Db 1 MDYQVSSPTDYIDYITSEPCCKINVKQIAARLLPPL 36
 RESULT 9
 CCR5_PYGBI STANDARD; PRT; 352 AA.
 ID CCR5_PYGBI
 AC 097880;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCRS).
 GN CCR5 OR CCR5.
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinohiphus bieti).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;

Pygathrix.
 NCBI_TaxID=61621;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=99416438; PubMed=10486970;
 Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 Mol. Biol. Evol. 16:1145-1154(1999).
 -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC EMBL: AF075445; AAD19857.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7cm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;
 Query Match 94.2%; Score 179; DB 1; Length 352;
 Best Local Similarity 91.7%; Pred. No. 1.7e-17;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQVSSPTDYIDYITSEPCCKINVKQIAARLLPPL 36
 Db 1 MDYQVSSPTDYIDYITSEPCCKINVKQIAARLLPPL 36
 RESULT 10
 CCR5_PYGNE STANDARD; PRT; 352 AA.
 ID CCR5_PYGNE
 AC 097882;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCRS).
 GN CCR5 OR CCR5.
 OS Pygathrix nemaeus (Dove langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_Taxid=54133;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=99416438; PubMed=10486970;
RT Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RL "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RM Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AF075448; AAD19860.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1.1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT TRANSMEM 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT TRANSMEM 125 141
FT TRANSMEM 142 166
FT TRANSMEM 167 198
FT TRANSMEM 199 218
FT TRANSMEM 219 235
FT TRANSMEM 236 260
FT TRANSMEM 261 277
FT TRANSMEM 278 301
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40532 MW; FE4P9D8D3B3861 CRC64;

Query Match 94.2%; Score 179; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 1.7e-17;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPTIDYNTYSEPCQKINVKQIARLLPPL 36
DB 1 MDYVSSPTIDYNTYSEPCQKINVKQIARLLPPL 36

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_Taxid=54180;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=99416438; PubMed=10486970;
RT Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RL "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RM Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AF075442; AAD19854.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1.1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT TRANSMEM 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT TRANSMEM 125 141
FT TRANSMEM 142 166
FT TRANSMEM 167 198
FT TRANSMEM 199 218
FT TRANSMEM 219 235
FT TRANSMEM 236 260
FT TRANSMEM 261 277
FT TRANSMEM 278 301
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C25938F CRC64;

Query Match 94.2%; Score 179; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 1.7e-17;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPTIDYNTYSEPCQKINVKQIARLLPPL 36
DB 1 MDYVSSPTIDYNTYSEPCQKINVKQIARLLPPL 36

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OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_Taxid=61618;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL AF075443; AAD19855.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7cm 1; 1.
DR PRINTS; PR00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 82
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A538F CRC64;
Query Match 94.2%; Score 179; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 1.7e-17;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYGVSSPTDYIDYTTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYGVSSPTDYIDYTTSEPCQKINVKQIAARLLPPL 36
RESULT 13
ID CCR5 GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DR C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCR5).

GN CCR5 OR CCRKRS.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_Taxid=9595;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amdebe A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peeper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL AF005659; AAB62553.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7cm 1; 1.
DR PRINTS; PR00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 82
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40515 MW; D0B6FCB9E5EAC84 CRC64;
Query Match 92.1%; Score 175; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 6.1e-17;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDYGVSSPTDYIDYTTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYGVSSPTDYIDYTTSEPCQKINVKQIAARLLPPL 36
RESULT 14
ID CCR5 HYLMU STANDARD; PRT; 352 AA.
AC Q95NC0;
DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)
DB C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
GN CCR5 OR CCR5
OS Hylobates moloch (Silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9941638; PubMed=10486970;
RX Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: A177899; AAK4382.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT TRANSMEM 1 30
FT DOMAIN 31 58
FT TRANSMEM 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340C274 CRC64;
Query Match 91.1%; Score 173; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 1.2e-16;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDYQVSSPYIDYNTSSPCOKINVKQIAARLLPPL 36
DB 1 MDYQVSSPYIDYNTSSPCOKINVKQIAARLLPPL 36
RESULT 15
ID CKR5 CERAR STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
GN CCR5 OR CCR5
OS Cercopithecus aethiops (Green monkey) (Givett).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RT Kuhnmann S.E., Platt B.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U83324; AAC51795.1; -
CC EMBL: U83325; AAC51796.1; -
CC EMBL: AB015944; BAA1328.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KM Polymorphism.
FT TRANSMEM 1 30
FT DOMAIN 31 58
FT TRANSMEM 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 15 15
FT MOD_RES 14 14
FT VARIANT 352 352
SQ SEQUENCE 352 AA; 40561 MW; 7F52E6990C72EC29A CRC64;
Query Match 90.0%; Score 171; DB 1; Length 352;

Mon May 17 11:04:01 2004

us-10-072-301-8.rap

Page 11

Best Local Similarity 91.7%; Pred. No. 2,2e-16;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY      1 MDQVSSPPIYDINNTYTSPPCQKINVKQIARLLPPL 36
        |||||:|||||
DB      1 MDYQVSSPYDIDINTSEPCQKINVKQIARLLPPL 36

```

Search completed: May 13, 2004, 15:02:03
Job time : 2.01359 secs

USE BLANK (USPTO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 4.84078 Seconds
(without alignments)
2346.453 Million cell updates/sec

Title: US-10-072-301-8
Perfect score: 190
Sequence: 1 MDQVSPHYDINYTSEPCQKINVKQIAARLLPPL 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeal: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	100.0	215	4	075303 homo sapien
2	185	97.4	352	6	095NCS3
3	185	97.4	352	6	095NCS3
4	185	97.4	352	6	018771
5	185	97.4	352	6	018772
6	180	94.7	344	6	097QX0
7	180	94.7	344	6	097QX0
8	180	94.7	352	6	097QX0
9	180	94.7	352	6	095NCS5
10	180	94.7	352	6	095NCS5
11	180	94.7	352	6	097V49
12	180	94.7	352	6	097V49
13	180	94.7	352	6	018770
14	180	94.7	352	6	097V44
15	180	94.7	352	6	097V45
16	180	94.7	352	6	09X12

17	180	94.7	352	6	097V42	097V42 cercopithec
18	180	94.7	352	6	09X13	09X13 papio anubi
19	180	94.7	352	6	095NCS2	095NCS2 mandrillus
20	180	94.7	352	6	077776	077776 cercocobus
21	180	94.7	352	6	097V46	097V46 cercopithec
22	180	94.7	352	6	097V46	097V46 cercopithec
23	180	94.7	352	6	097V50	097V50 pan troglod
24	180	94.7	352	6	095NCS1	095NCS1 cercocobus
25	180	94.7	352	6	095NCS0	095NCS0 erythrocebu
26	180	94.7	352	6	095NCS8	095NCS8 cercopithec
27	179	94.2	352	6	09X114	09X114 colobus que
28	179	94.2	352	6	095NCS6	095NCS6 trachypithec
29	179	94.2	352	6	095NCS6	095NCS6 colobus pol
30	179	94.2	352	6	095NCS7	095NCS7 naealia lar
31	179	94.2	352	6	097V62	097V62 pygathrix a
32	176	92.6	352	6	095NCS1	095NCS1 theropithec
33	175	92.1	352	6	09XK35	09XK35 macaca neme
34	175	92.1	352	6	097V93	097V93 macaca arct
35	175	92.1	352	6	095NCS1	095NCS1 mandrillus
36	175	92.1	352	6	09XK99	09XK99 gorilla gor
37	174	91.6	352	6	097V43	097V43 cercopithec
38	173	91.1	352	6	095NCS0	095NCS0 hylobates m
39	173	91.1	352	6	09XK23	09XK23 hylobates a
40	171	90.0	352	6	095NCS5	095NCS5 cercopithec
41	171	90.0	352	6	095NCS6	095NCS6 cercopithec
42	170	89.5	352	6	097V07	097V07 cercopithec
43	170	89.5	352	6	097V45	097V45 cercopithec
44	161	84.7	352	6	097V47	097V47 cercopithec
45	155	81.6	339	4	09UN26	09UN26 homo sapien

ALIGNMENTS

RESULT 1	ID	075303	PRELIMINARY;	PRT;	215 AA.
AC	075303				
DT	01-NOV-1998	(TRENBLREL. 08, Created)			
DT	01-NOV-1998	(TRENBLREL. 08, Last sequence update)			
DT	01-JUN-2003	(TRENBLREL. 24, Last annotation update)			
DE	CC-chemokine receptor.				
GN	CCR-5.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Tse L., Ehrenberg P.K., Chang G., Michael N.L.;				
RT	"Genomic Organization and Functional Characterization of the Complete				
RT	Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-				
RT	Receptor for HIV-1."				
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF009962; AAC23944.1; -.				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.				
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.				
DR	InterPro; IPR00276; GPCR_Rhodopsn.				
DR	Pfam; PF00001; 7tm.1; 1.				
DR	PRINTS; PR00237; GPCR_RHODOPSIN.				
DR	PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.				
DR	PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.				
DR	Receptor.				
SQ	SEQUENCE	215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;			
Qy	Query Match	100.0%; Score 190; DB 4; Length 215;			
	Best Local Similarity	100.0%; Pred. No. 1.3e-19;			
	Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
		1 MDQVSPHYDINYTSEPCQKINVKQIAARLLPPL 36			

Db 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

RESULT 2

OS 095NC3 PRELIMINARY; PRT; 352 AA.

AC 095NC3

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE C-C chemokine receptor 5.

GN CCR5.

OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC NCBI_TaxID=36231;

OK NCBI_TaxID=36231;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang Y., Ryder O.A., Zhang Y.,

RT "Sequence comparison of the CCR5 gene in primates and primate

RT phylogeny."

RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF177886; AAK43369.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.

KW RECEPTOR.

SQ SEQUENCE 352 AA; 40546 MW; 64641523F3E566A5 CRC64;

Query Match 97.4%; Score 185; DB 6; Length 352;

Best Local Similarity 97.2%; Pred. No. 1.2e-18;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

Db 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

RESULT 3

OS 018771 PRELIMINARY; PRT; 352 AA.

AC 018771

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE CCR5 receptor (Fragment).

GN CCR5.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

OC NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang L., Carnuthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

RA Ho D.D.,

RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."

RL AIDS Res. Hum. Retroviruses 0:0-0(1997).

DR EMBL; AF011539; AAB65739.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.

KW RECEPTOR.

SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match 97.4%; Score 185; DB 6; Length 352;

Best Local Similarity 97.2%; Pred. No. 1.2e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

Db 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

RESULT 5

OS 097OXO PRELIMINARY; PRT; 352 AA.

AC 097OXO

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE CC chemokine receptor 5.

GN CCR5.

OS Cercopithecus aethiops (Green monkey) (Givet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC NCBI_TaxID=9534;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang L., Carnuthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

RA Ho D.D.,

RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."

RL AIDS Res. Hum. Retroviruses 0:0-0(1997).

DR EMBL; AF011541; AAB65741.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.

KW RECEPTOR.

SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match 97.4%; Score 185; DB 6; Length 352;

Best Local Similarity 97.2%; Pred. No. 1.2e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

Db 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

RESULT 4

OS 018772 PRELIMINARY; PRT; 352 AA.

AC 018772

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE CCR5 receptor (Fragment).

GN CCR5.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

OC NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang L., Carnuthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

RA Ho D.D.,

RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."

RL AIDS Res. Hum. Retroviruses 0:0-0(1997).

DR EMBL; AF011541; AAB65741.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.

KW RECEPTOR.

SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match 97.4%; Score 185; DB 6; Length 352;

Best Local Similarity 97.2%; Pred. No. 1.2e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

Db 1 MDYOVSSPIYDINYTSEPCCKINVKQIARLPL 36

RP SEQUENCE FROM N.A.
 RC STRAIN=AGM-8CCRS5, AGM-3CCRS5, and AGM-5CCRS5;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Sakeena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.,
 RT "Species-specific changes in the CCR5 gene from African and Asian
 nonhuman primates.";
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 DR EMBL, AF105286; AAD20555.1; -;
 DR EMBL, AF105284; AAD20553.1; -;
 DR EMBL, AF105285; AAD20554.1; -;
 DR GO, GO:0016021, C:integral to membrane; IEA.
 DR GO, GO:0004872, F:receptor activity; IEA.
 DR GO, GO:0001584, F:rhodopsin-like receptor activity; IEA.
 DR GO, GO:0007186, P:G-protein coupled receptor protein signaln. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40588 MW; 0A4B4119FAC8EC75 CRC64;

Query Match 97.4%; Score 185; DB 6; Length 352;
 Best Local Similarity 97.2%; Pred. No. 1.2e-18;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYVSSPTDYDINTYTSPPCKINVKQIAARLLPPL 36
 DB 1 MDYVSSPTDYDINTYTSPPCKINVKQIAARLLPPL 36

RESULT 6

ID 09T0R8 PRELIMINARY; PRT; 344 AA.

AC 09T0R8; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Chemokine receptor CCR5.
 GN CCR5.
 OS Cercocobus torquatus torquatus, and
 OS Cercocobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercocobus.
 OC NCBI_TaxID=81944, 9531;
 OX 11
 RN SEQUENCE FROM N.A.
 RP SPECIES=C.torquatus torquatus; STRAIN=1049, and 997;
 RC Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
 RA Aguilari R., Ho D.D., Marx P.A.;
 RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
 with a R2b-tropic simian immunodeficiency virus.";
 RL J. Exp. Med. 0:0-0(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RP SPECIES=C.torquatus atys;
 RC Palacios E., Digilio L., McClure H.M., Chen Z., Marx P.A.,
 RA Goldsmith M.A., Grant R.M.;
 RT "Parallel evolution of CCR5-null phenotypes in humans and in a natural
 host of simian immunodeficiency virus.";
 RL Curr. Biol. 0:0-0(1998).
 [3]
 RN SEQUENCE FROM N.A.
 RC SPECIES=C.torquatus torquatus; STRAIN=RCM411;
 RA Beer B.E., Kuiken C.L., Toole Z., Foley B.T., Goeken R.M., Brown C.R.,
 RT St. Claire M., Hirsch V.M.;
 RT "Characterization of novel simian immunodeficiency viruses from
 RT red-capped mangabey from Nigeria (SIVcmgm411 and Ng0409).";
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBD databases.
 DR EMBL, AF079473; AAC62474.1; -;
 DR EMBL, AF079473; AAC62474.1; -;
 DR EMBL, AF084003; AAC62471.1; -;

DR EMBL, AF349683; AAK69685.1; -;
 DR GO, GO:0016021, C:integral to membrane; IEA.
 DR GO, GO:0004872, F:receptor activity; IEA.
 DR GO, GO:0001584, F:rhodopsin-like receptor activity; IEA.
 DR GO, GO:0007186, P:G-protein coupled receptor protein signaln. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 344 AA; 39592 MW; E15F5F601191A4D1 CRC64;

Query Match 94.7%; Score 180; DB 6; Length 344;
 Best Local Similarity 94.4%; Pred. No. 6.3e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPTDYDINTYTSPPCKINVKQIAARLLPPL 36
 DB 1 MDYVSSPTDYDINTYTSPPCKINVKQIAARLLPPL 36

RESULT 7

ID 077833 PRELIMINARY; PRT; 344 AA.

AC 077833; 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Chemokine receptor CCR5.
 GN CCR5.
 OS Cercocobus torquatus torquatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercocobus.
 OC NCBI_TaxID=81944;
 OX 11
 RN SEQUENCE FROM N.A.
 RP STRAIN=1208, and 009;
 RC Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
 RA Aguilari R., Ho D.D., Marx P.A.;
 RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
 with a R2b-tropic simian immunodeficiency virus.";
 RL J. Exp. Med. 0:0-0(1998).
 DR EMBL, AF094752; AAC62473.1; -;
 DR EMBL, AF084002; AAC62470.1; -;
 DR GO, GO:0016021, C:integral to membrane; IEA.
 DR GO, GO:0001584, F:rhodopsin-like receptor activity; IEA.
 DR GO, GO:0007186, P:G-protein coupled receptor protein signaln. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 SQ SEQUENCE 344 AA; 39578 MW; 0CE05B47C2FED6 CRC64;

Query Match 94.7%; Score 180; DB 6; Length 344;
 Best Local Similarity 94.4%; Pred. No. 6.3e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPTDYDINTYTSPPCKINVKQIAARLLPPL 36
 DB 1 MDYVSSPTDYDINTYTSPPCKINVKQIAARLLPPL 36

RESULT 8

ID 09TSK1 PRELIMINARY; PRT; 352 AA.

AC 09TSK1; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE G-protein coupled chemokine receptor.

OS Cercopithecus aethiops (Green monkey) (Griwet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Holtkamp N., Baler M., Werner A.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF019379; AAD01639.1.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPRO00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40588 MW; 0F1869DA6668DB CRC64;

Query Match 94.7%; Score 180; DB 6; Length 352;
 Best Local Similarity 94.4%; Pred. No. 6.4e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPL 36
 Db 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPL 36

RESULT 9
 OS NCNS
 ID 095NC5 PRELIMINARY; PRT; 352 AA.
 AC 095NC5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE C-C chemokine receptor 5.
 GN CCR5.
 OS Hylobates syndactylus (Siawang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RL "Sequence comparison of the CCR5 gene in primates and primate phylogeny."
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF177884; AAK43367.1.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPRO00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 94.7%; Score 180; DB 6; Length 352;
 Best Local Similarity 94.4%; Pred. No. 6.4e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPL 36
 Db 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPL 36

RESULT 10
 Q9TV48

ID 09TV48 PRELIMINARY; PRT; 352 AA.
 AC 09TV48;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CC chemokine receptor type 5.
 GN CCR5.
 OS Cercopithecus aethiops (Black-cheeked white-nosed monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Holtkamp N., Baler M., Werner A.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF019379; AAD01639.1.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPRO00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40650 MW; 7906256AA3945266 CRC64;

Query Match 94.7%; Score 180; DB 6; Length 352;
 Best Local Similarity 94.4%; Pred. No. 6.4e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPL 36
 Db 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPL 36

RESULT 11
 OS Cercopithecus aethiops (Agile mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Holtkamp N., Baler M., Werner A.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF019379; AAD01639.1.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPRO00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40650 MW; 7906256AA3945266 CRC64;

Q9TV48 94.7%; Score 180; DB 6; Length 352;
 Best Local Similarity 94.4%; Pred. No. 6.4e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RP SEQUENCE FROM N.A.
RC STRAIN=4;
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.,
RN Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
(3)
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF035215; AAD44008.1; -
DR EMBL; AF177898; AAK43381.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPT_F1_2; 1.
DR Receptor.
SQ SEQUENCE 352 AA; 40479 MW; 5E1504A9B87278B2 CRC64;
Query Match 94.7%; Score 180; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 6.4e-18;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPTDYIDYTSBPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPTDYIDYTSBPCQKINVKQIAARLLPPL 36
RESULT 12
Q9XT76 PRELIMINARY; PRT; 352 AA.
ID 09XT76
AC 09XT76;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Cercopithecus lhoesti (L'Hoest's monkey), and
OC Cercopithecus preussi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC NCBI_TaxId=100224; 147649;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=C.lhoesti;
RX MEDLINE=9335215; PubMed=10408730;
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
RT carrier status in African nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [12]
RP SEQUENCE FROM N.A.
RC SPECIES=C.preussi;
RA Beer B.E., Kuiken C.L., Bailes E., Korber B., Sharp P.M., Hirsch V.M.;
RT "Phylogeny and cross-species transmission of simian and human
RT immunodeficiency viruses.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF081579; AAD45497.1; -
DR EMBL; AF212102; AAG53467.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPT_F1_2; 1.
RW Receptor.
SQ SEQUENCE 352 AA; 40408 MW; 2D354B5128C779B0 CRC64;
Query Match 94.7%; Score 180; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 6.4e-18;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPTDYIDYTSBPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPTDYIDYTSBPCQKINVKQIAARLLPPL 36
RESULT 13
O18770 PRELIMINARY; PRT; 352 AA.
ID 018770
AC 018770;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OC NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MacCR5-140a;
RA Zhang L., Caruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011538; AAB65738.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPT_F1_2; 1.
RW Receptor.
FT NON_TER
KW Receptor.
SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;
Query Match 94.7%; Score 180; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 6.4e-18;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPTDYIDYTSBPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPTDYIDYTSBPCQKINVKQIAARLLPPL 36
RESULT 14
O9TV44 PRELIMINARY; PRT; 352 AA.
ID 09TV44
AC 09TV44;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Cercopithecus patas.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxId=27677;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=04;
 RX MEDLINE=9335215; PubMed-10408730;
 RA Miller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
 RA Diop O., Rigoulet J., Baire-Sinoussi F., Fomsgaard A.;
 RT "Mutations in CCR5-coding sequences are not associated with SIV
 RT carrier status in African nonhuman primates";
 RU AIDS Res. Hum. Retroviruses 15:931-939(1999).
 RN [2]
 RP SEQUENCE FROM N.A.

RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
 RA Georges-Courbot M.C., Baire-Sinoussi F., Fomsgaard A.;
 RU Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035220; AAD44013.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECPT_F2_1; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40747 MW; 3A56E90D3528D94C CRC64;

Query Match 94.7%; Score 180; DB 6; Length 352;
 Best Local Similarity 94.4%; Pred. No. 6.4e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQSSPIYDINYYTSPCKINVKQIAARLLPPL 36
 DB 1 MDYQSSPTDYDIDYTSPPCKINVKQIAARLLPPL 36

RESULT 15

ID 097975 PRELIMINARY; PRT; 352 AA.
 AC 097975;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE C-C chemokine receptor type 5.
 GN CCR5.
 OS Macaca arctoides (Stump-tailed macaque), and
 OS Macaca assamensis (Assam's macaque) (Assam's monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_taxonomy:9540, 9551;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y.-W., Zhang Y.-P.;
 RT "Sequence evolution of chemokine receptor CCR5 gene in primates";
 RU Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF075450; AAD19862.1; -
 DR EMBL; AF075449; AAD19861.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECPT_F2_1; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40521 MW; 5F276C85909FACB2 CRC64;

Query Match 94.7%; Score 180; DB 6; Length 352;
 Best Local Similarity 94.4%; Pred. No. 6.4e-18;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQSSPIYDINYYTSPCKINVKQIAARLLPPL 36
 DB 1 MDYQSSPTDYDIDYTSPPCKINVKQIAARLLPPL 36

Search completed: May 13, 2004, 15:06:53
 Job time : 5.84078 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 52.0738 Seconds
(without alignments)
1372.754 Million cell updates/sec

Title: US-10-072-301-17

Perfect score: 1351

Sequence: 1 QVTLKESGFLVVKPTQTTLT.....CQAMDSTAVFGNGTKLTVL 253

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	788.5	58.4	245	4	ABP67620 Human Bly
2	783	58.0	250	5	ABP45537 Human Bly
3	779.5	57.7	247	5	ABP45640 Human Bly
4	771.5	57.1	249	6	AAE36257 TRAIL rec
5	756.5	56.0	245	4	AAE36257 Human Bly
6	753.5	55.8	245	4	AAE36257 Human Bly
7	753	55.7	237	6	ABP67621 Human Bly
8	752.5	55.7	245	4	ABP67622 Human Bly
9	752.5	55.7	245	4	ABP67623 Human Bly
10	751.5	55.6	245	4	ABP67624 Human Bly
11	747	55.3	245	5	ABP45955 Human Bly
12	742	54.9	250	5	ABP45956 Human Bly
13	736	54.5	256	5	ABP45957 Human Bly
14	734.5	54.3	252	5	ABP45958 Human Bly
15	733	54.2	245	4	ABP45959 Human Bly
16	732.5	54.1	245	4	ABP45960 Human Bly
17	731	54.0	252	6	ABP45961 Human Bly
18	730	54.0	252	6	ABP45962 Human Bly
19	729.5	53.9	247	5	ABP45963 Human Bly
20	728.5	53.6	251	5	ABP45964 Human Bly
21	723.5	53.6	251	5	ABP45965 Human Bly
22	723.5	53.6	251	5	ABP45966 Human Bly
23	722.5	53.5	251	5	ABP45967 Human Bly
24	721.5	53.4	255	5	ABP45968 Human Bly
25	721	53.4	248	5	ABP45969 Human Bly

ALIGNMENTS

26	719.5	53.3	249	5	ABP45714 Human Bly
27	718.5	53.2	249	5	ABP45713 Human Bly
28	718.5	53.2	251	5	ABP45527 Human Bly
29	718	53.1	244	5	ABP45831 Human Bly
30	717	53.1	244	2	AAI06718 Human Bly
31	717	53.1	266	5	ABG97835 Human Bly
32	717	53.1	266	5	ABG97835 Human Bly
33	716.5	53.0	253	5	ABP45491 Human Bly
34	716	53.0	254	5	ABP45491 Human Bly
35	715.5	53.0	249	5	ABP45104 Human Bly
36	715.5	53.0	249	5	ABP45991 Human Bly
37	715.5	53.0	251	5	ABP44971 Human Bly
38	715	52.9	234	6	ABP45333 Human Bly
39	714.5	52.9	247	5	ABP45459 Human Bly
40	714.5	52.9	247	5	ABP45195 Human Bly
41	714.5	52.9	253	5	ABP44927 Human Bly
42	712.5	52.7	247	5	ABP45311 Human Bly
43	712.5	52.6	250	5	ABP44982 Human Bly
44	710.5	52.6	249	5	ABP44946 Human Bly
45	710	52.6	246	3	AAV15126 Anti-muri

RESULT 1	ABP67620	standard; protein; 245 AA.
AC	ABP67620;	
XX	29-MAY-2001 (first entry)	
XX	Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_4.	
XX	Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;	
XX	miscarriage; abortion; preeclampsia; antibody; HLA phenotyping; ss.	
OS	Homo sapiens.	
XX	WO200114558-A1.	
XX	01-MAR-2001.	
XX	28-AUG-2000; 2000WO-EP008388.	
XX	26-AUG-1999; 99BP-00116691.	
XX	(MORP-) MORPHOSYS AG.	
XX	Kretschmar T, Tesar M, Marget M, Kroenke M;	
XX	WPI; 2001-218451/22.	
XX	Novel isolated human immunoglobulin or functional immunoglobulin fragment	
XX	specific for human leukocyte antigen Cw6, useful for treatment of humans	
XX	and for human leukocyte antigen phenotyping.	
XX	Claim 3; Fig 1; 23p; English.	
XX	ABP67617-23 represent single chain antibody (scFv) fragments which are	
XX	specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived	
XX	from a synthetic human combinatorial antibody library based on molecular	
XX	consensus frameworks and CDRs randomised with trinucleotides. The	
XX	specificity of the fragments is considered highly relevant in studies of	
XX	Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of	
XX	natural killer cell silencing in some recurrent abortions. Preeclampsia may	
XX	also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are	
XX	useful for the preparation of a pharmaceutical for the treatment of	
XX	humans. They are also useful for HLA phenotyping	
XX	Sequence 245 AA;	

```

Query Match      58.4%; Score 788.5; DB 4; Length 245;
Best Local Similarity 62.4%; Pred. No. 2,9e-45;
Matches 159; Conservative 30; Mismatches 53; Indels 13; Gaps 4;

QY 1 QVTLKSGPTLVKPTQTLTLTCTLSGFSLSSTGVSVGIRQPPKALEMTASIMNDKC 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSYAMS--WKQAPFKGLEWVSAISGGSGST 58
QY 61 -YSPSLKSRLLTTTKTPKNQVVLAMSNMPPADLTATYSCALDMPHDSGPOSFASDVMGP 119
DB 59 YVADSVKGRFTISRNNSKNTIYLQNNSLRADTAVYYCA-----RVSFQWPDVWQ 109
QY 120 GTMTVVSQGGSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPQGTASITCSGNLGDKYA 179
DB 110 GTLVTVSSAGGGSGGGSGGGSGGGSDIELQPPSVAPQQTAKRISCGDALGDKYA 169
QY 180 CMYQOKPGRSPVLVIYGDNRKPSGIPRFGSGNSGNTATLTISGTQAMDEADYCOAMD 239
DB 170 SMYQOKPQGAFLVLIYDSDRPSGIPRFGSGNSGNTATLTISGTQAMDEADYCOASYDN 229
QY 240 -STAVFGTGTGLTVL 253
DB 230 FDSFVFGGTGLTVL 244

RESULT 2
ABP45537
ID ABP45537 standard; protein; 250 AA.
AC ABP45537;
DE 19-AUG-2002 (first entry)
XX Human BlyS binding scFv SEQ ID 1548.
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,
XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2250-2251; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX tumour necrosis factor (TNF) superfamily and induces B cell
XX proliferation and differentiation. The antibodies of the invention have

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CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders end
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
SQ Sequence 250 AA;

```

```

Query Match      58.0%; Score 783; DB 5; Length 250;
Best Local Similarity 63.5%; Pred. No. 6,8e-45;
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

```

```

QY 1 QVTLKSGPTLVKPTQTLTLTCTLSGFSLSSTGVSVGIRQPPKALEMTASIMNDKC 60
DB 1 QVQLQSGEPGLVPSSTLSLTCVAVSVIS--SGYWGWIQPPKGLWMTGSIYHSGSTY 59
QY 61 YSPSLKSRLLTTTKTPKNQVVLAMSNMPPADLTATYSCALDMPHDSGPOSFASDVMGP 120
DB 60 YNPSLKSRVTVISVDPSKQPSLKSVAADTAVYYCA--RVHYDILTVGLMAFDIWQGG 117
QY 121 TMVTVSSGGSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPQGTASITCSGNLGDKYA 180
DB 118 TMVTVSSGGSGGGSGGGSGGGSGGGSS--ALSSSLTQDPVAVSVALGQTVITQGSLSRSTYAS 174
QY 181 WYQOKPGRSPVLVIYGDNRKPSGIPRFGSGNSGNTATLTISGTQAMDEADYCOAMD 240
DB 175 WYQOKPQGAFLVLIYGNKRPSPGIPRFGSSSGNTATLTISGTQAMDEADYCNRSRDS 234
QY 241 --TAVFGTGTGLTVL 253
DB 235 GNVHVFQGGTGLTVL 249

```

```

RESULT 3
ABP45640
ID ABP45640 standard; protein; 247 AA.
XX
XX ABP45640;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human BlyS binding scFv SEQ ID 1651.
XX
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.

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PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1, Page 2373-2374; 3148bp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumor necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineoplastic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 247 AA;
 XX
 Query Match 57.7%; Score 779.5; DB 5; Length 247;
 Best Local Similarity 60.5%; Pred. No. 1.2e-44;
 Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;
 QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSISTGVSVMIRPGKALMLASINMDDKC 60
 1 QVQLQESGPGVLPSTTSLTCTVSNYSIS-SGYTGMIRPGKLEMTIGSYIGSGTRY 59
 DB 61 YSPSLKSLTLITKDPKNOVLAMSNMDDPATRYTSCA-----LDMPHDGSPQ 109
 60 YNPSTLSRYTISVDTSKQFSLKLSVTADTFVYVCARFRYDILTYGYDM----- 111
 QY 110 STDASVMPGCTMYTSSGSGGSGGSGGSGGSGGSSSELMQLSVSVSPGQTASITC 169
 112 ----DWGRGTLVTVSSGGSGGSGGSGGSGS-----ELTQDPAVSVALGQTVRTIC 160
 DB 170 SGNLDGDKTACWYQOKRGRSPVVIYGDNRPEGIPERFSGNSGNTATLTISGTCAMD 229
 161 QGDSLSRYSYASWYQOKRGPAPVLYIGKNNRPSGIDRFSGSSGNTATLTIGQAQDE 220
 QY 230 ADYYCOAMDTS--TAVFGTGKTLTVL 253
 221 ADYYCNSRDSGSHNVFVGSGTKTLTVL 246
 DB
 RESULT 4
 AAE36257 standard; protein; 249 AA.
 XX
 AC AAE36257;
 XX
 XX 26-JUN-2003 (first entry)
 DT
 DE TRAIL receptor protein binding scfv protein, T1006F07.
 XX
 XX TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;
 KM hyperproliferative disorder; neurodegenerative disorder; immune disorder;
 KM Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KM retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;
 KM rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;
 KM biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;
 KM glomerulonephritis; immune deficiency syndrome; myasthenia gravis;

KM polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;
 KM infectious disease; acquired immunodeficiency syndrome; viral infection;
 KM AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anemia;
 KM ischaemic injury; myocardial infarction; reperfusion injury; cachexia;
 KM anorexia; stroke; cardiovascular disorder; peripheral artery disease;
 KM limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;
 KM ocular disorder; wound healing; angiogenesis; transplantation.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Domain 1..125
 FT /note= "VH domain"
 FT Region 26..35
 FT /note= "VH domain complementarity determining region 1
 FT (CDR1)"
 FT Region 50..66
 FT /note= "VH domain complementarity determining region 2
 FT (CDR2)"
 FT Region 99..114
 FT /note= "VH domain complementarity determining region 3
 FT (CDR3)"
 FT Domain 142..249
 FT /note= "VL domain"
 FT Region 164..174
 FT /note= "VL domain complementarity determining region 1
 FT (CDR1)"
 FT Region 190..196
 FT /note= "VL domain complementarity determining region 2
 FT (CDR2)"
 FT Region 229..238
 FT /note= "VL domain complementarity determining region 3
 FT (CDR3)"
 XX
 PN WO200297033-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 07-MAY-2002; 2002WO-US014268.
 XX
 XX 25-MAY-2001; 2001US-0293473P.
 PR 04-JUN-2001; 2001US-0294981P.
 PR 02-AUG-2001; 2001US-0309176P.
 PR 21-SEP-2001; 2001US-0323807P.
 PR 09-OCT-2001; 2001US-0327364P.
 PR 07-NOV-2001; 2001US-0331044P.
 PR 14-NOV-2001; 2001US-0341237P.
 PR 20-DEC-2001; 2001US-0349860P.
 PR 05-APR-2002; 2002US-0369860P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;
 PI WPI; 2003-140454/13.
 XX
 DR N-PSDB; AAD54858.
 XX
 PT Novel antibody useful for treating cancers and other hyperproliferative
 PT disorders, immunospecifically binds to TRAIL receptor and comprises
 PT variable heavy or light chain complementarity determining regions.
 XX
 PS Claim 1, Page 294-295; 301pp; English.
 XX
 XX The present invention relates to novel antibodies that immunospecifically
 CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for
 CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,
 CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.
 CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in
 CC human. They are useful for detecting expression of TR4 polypeptide and
 CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-
 CC proliferative disorders. Antibodies of the invention are useful for
 CC treating, preventing or ameliorating neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,

CC reinititis pigmentosa, cerebellar degeneration and Huntington's disease),
 CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,
 CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,
 CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,
 CC Hashimoto's thyroiditis and immune deficiency syndrome),
 CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),
 CC herpes viral infections and other viral infections) and proliferative
 CC disorders. They are also useful for treating myelodysplastic syndromes
 CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,
 CC myocardial infarction and reperfusion injury), septic shock, cachexia,
 CC anorexia and toxin-induced liver diseases (such as alcohol). They are
 CC also useful for treating cardiovascular disorders including peripheral
 CC artery diseases such as limb ischaemia, arrhythmia, congestive heart
 CC failure and cardiovascular tuberculosis, diseases or disorders associated
 CC with neovascularisation and ocular disorders, for wound healing, for
 CC promoting angiogenesis and as adjuvants to enhance immune responsiveness
 CC to specific antigen e.g. viral antigen. They are also useful in the
 CC preparation or recovery from surgery, trauma, radiation therapy and
 CC transplantation. The present sequence is T106F07 single chain Fv (scFv)
 CC antibody that immunospecifically bind to TR4 protein. This sequence is
 CC used in the invention

SO Sequence 249 AA;

Query Match 57.1%; Score 771.5; DB 6; Length 249;
 Best Local Similarity 62.4%; Pred. No. 46-44;
 Matches 159; Conservative 26; Mismatches 59; Indels 9; Gaps 5;

```

QY 1 QVTLKESGPTLVKPTOTLTCTLSGFSLSSTGSVSGWIRPPGKALMLASINWDDK 60
DB 1 EVQLVDSGGGLVQPGGSLRLSCAASGFTFSYAMS--WRQAPGKGLMFWVAISGSGST 58
QY 61 -YSLSLSRLTITKDTPPKQVNLAMSNMPPADTATYSCALMPPHDSQPSFDSVWGP 119
DB 59 YVADSVKGRFTISRDKSNKLTLYQMNSLRAEDTAVYICARHPSFQGMHWYX--GMDVWQ 117
QY 120 GTVAVTVSSGGSGSGGGSGGGSGGSSYEIMQLPSVSVSPQGTASTSGDNLGDKYA 179
DB 118 GTVAVTVSSGGSGSGGGSGGGSGGSS---AOSVLTQPPSVSPGQAALITCSGKLDKXA 173
QY 180 CWYQOKPGRSPVLYVYGDNKRPSGIPERFSGNSGNTATLTISGTOAMDADYYCOAMD 239
DB 174 SWYQOKPGRSPVLYVYQDNKRPSGIPERFSGNSGNTATLTISGTOAMDADYYCLAMDS 233
QY 240 STA-VFGTGTXTLV 253
DB 234 SADWVFGGCTKTVL 248

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RESULT 5

AAB67621
 ID AAB67621 standard; protein; 245 AA.
 AC AAB67621;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_5.
 XX
 KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
 XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
 OS Homo sapiens.
 XX
 PN WO200114558-A1.
 PD
 XX
 XX 01-MAR-2001.
 PF 28-AUG-2000; 2000WO-EP008388.
 XX
 PR 26-AUG-1999; 99EP-00116691.
 XX

PA (MORP-) MORPHOSYS AG.
 XX
 PI Kretschmar T, Tesar M, Marget M, Kroenke M;
 XX
 DR WPI; 2001-218451/22.
 XX
 PT Novel isolated human immunoglobulin or functional immunoglobulin fragment
 PT specific for human leukocyte antigen Cw6, useful for treatment of humans
 PT and for human leukocyte antigen phenotyping.
 XX
 PS Claim 3; Fig 1; 23pp; English.

CC AAB67617-23 represent single chain antibody (scFv) fragments which are
 CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
 CC from a synthetic human combinatorial antibody library based on molecular
 CC consensus frameworks and CDRs randomised with trinucleotides. The
 CC Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
 CC natural killer cell silencing as well as miscarriages. HLA-Cw6
 CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may
 CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
 CC useful for the preparation of a pharmaceutical for the treatment of
 CC humans. They are also useful for HLA phenotyping

SO Sequence 245 AA;

Query Match 56.0%; Score 756.5; DB 4; Length 245;
 Best Local Similarity 60.2%; Pred. No. 46-43;
 Matches 154; Conservative 32; Mismatches 55; Indels 15; Gaps 5;

```

QY 1 QVTLKESGPTLVKPTOTLTCTLSGFSLSSTGSVSGWIRPPGKALMLASINWDDK 59
DB 1 EVQLVDSGGGLVQPGGSLRLSCAASGFTFSYAMS--WRQAPGKGLMFWVAISGSGST 58
QY 60 CYSPLSKSLRTITKDTPPKQVNLAMSNMPPADTATYSCALMPPHDSQPSFDSVWGP 118
DB 59 RYSPRSFGQVTLISADSLSTAVYLQWSLKAADTATYCA-----NSWDVDFDWG 108
QY 119 PGTAVTVSSGGSGSGGGSGGGSGGSSYEIMQLPSVSVSPQGTASTSGDNLGDKYA 178
DB 109 OGTLVTVSSAGGSGGGSGGGSGGGSDIELTPPSVSVAPQGTARISGSDALGDKY 168
QY 179 ACWYQOKPGRSPVLYVYGDNKRPSGIPERFSGNSGNTATLTISGTOAMDADYYCOAMD 238
DB 169 ASWYQOKPGRSPVLYVYQDNKRPSGIPERFSGNSGNTATLTISGTOAMDADYYCOAMD 228
QY 239 T-STAVFGTGTXTLV 253
DB 229 DHDRTVFGGCTKTVL 244

```

RESULT 6

AAB67622
 ID AAB67622 standard; protein; 245 AA.
 AC AAB67622;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_6.
 XX
 KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
 XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
 OS Homo sapiens.
 XX
 PN WO200114558-A1.
 PD
 XX
 XX 01-MAR-2001.
 PF 28-AUG-2000; 2000WO-EP008388.
 XX
 PR 26-AUG-1999; 99EP-00116691.
 XX

XX (MORP-) MORPHOSYS AG.
 PA Kretzschmar T, Tesar M, Marget M, Kroenke M;
 XX WPI; 2001-218451/22.
 DR
 XX Novel isolated human immunoglobulin or functional immunoglobulin fragment
 PT specific for human leukocyte antigen Cw6, useful for treatment of humans
 PT and for human leukocyte antigen phenotyping.
 XX
 XX Claim 3; Fig 1; 23pp; English.
 PS
 XX AAB67617-23 represent single chain antibody (scFv) fragments which are
 CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
 CC from a synthetic human combinatorial antibody library based on molecular
 CC consensus frameworks and CDRe randomized with trinucleotides. The
 CC specification describes a human immunoglobulin fragments specific for HLA
 CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
 CC natural killer cell silencing as well as miscarriages. HLA-Cw6
 CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may
 CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
 CC useful for the preparation of a pharmaceutical for the treatment of
 CC humans. They are also useful for HLA phenotyping
 CC
 SQ Sequence 245 AA;
 Query Match 55.8%; Score 753.5; DB 4; Length 245;
 Best Local Similarity 60.3%; Pred. No. 6.3e-43;
 Matches 155; Conservative 29; Mismatches 56; Indels 17; Gaps 5;
 QY 1 QVTLKESGPTLVPTOTLTCTLSGFSLSGSVGMIRPPKXLEWLASINMND-DK 59
 Db 1 EVOLVSGAEVKKPPGSLKISCKSGSYFTS--YWGVAQMPGKLEMGITTPGSDTR 58
 QY 60 CVSPSLKSRLLTKDPTKQOVVLAMSNMPPADATATYSCALDMPHDSGPOSFD--ASDVW 117
 Db 59 RVSFSPFOGVTITADKISITAVYLQWMSLKASDTAMTYCA-----RFDWPNIDW 107
 QY 118 GPEITMTVTVSSGGGSGGGSGGGSGGGSSYELMOLPSVSVSPGQTASTGCGNLGDK 177
 Db 108 GGGTLVTVSSAGGSGGGSGGGSGGGSGGSDIELTQPPSVVAPQGTARISCGDALGDK 167
 QY 178 YACWYQOKPGRSPVLVIYGNKRPSPGIPERFSGNSGNATLTITSGQAMDEADYVCOAM 237
 Db 168 YASWYQOKPQQAQVLAVIDSDRPPSGIPERFSGNSGNATLTITSGQAMDEADYVCOAM 227
 QY 238 DTST-AVFGTGTGTLTVL 253
 Db 228 DSDSDVLPFGGTLTVL 244

RESULT 7
 ABR62332
 ID ABR62332 standard; protein; 237 AA.
 XX
 AC ABR62332;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE Anti-EBV latent membrane protein scFv antibody FG-1.
 XX
 KW Latent membrane protein; LMP; antibody; scFv; Epstein-Barr virus; EBV;
 KM lymphoma; lymphoproliferative disease; carcinoma; malignancy.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 1..29
 FT /label= VH_FRI
 FT Region 31..35
 FT /label= VH_CDR1
 FT Region 36..48

FT /label= VH_FR2
 FT Region 50..65
 FT /label= VH_CDR2
 FT Region 67..97
 FT /label= VH_FR3
 FT Region 98..104
 FT /label= VH_CDR3
 FT Region 106..116
 FT /label= VH_FR4
 FT Region 117..131
 FT /label= Linker
 FT Region 132..152
 FT /label= VL_FRI
 FT Region 154..164
 FT /label= VL_CDR1
 FT Region 165..178
 FT /label= VL_FR2
 FT Region 180..186
 FT /label= VL_CDR2
 FT Region 187..218
 FT /label= VL_FR3
 FT Misc-difference 209
 FT /note= "Encoded by ACG"
 FT Region 219..226
 FT /label= VL_CDR3
 FT Region 228..237
 FT /label= VL_FR4
 FT Misc-difference 234
 FT /note= "Encoded by GTC"
 FT
 PN WO2003048337-A2.
 PD 12-JUN-2003.
 XX
 PF 04-DEC-2002; 2002WO-US038849.
 XX
 PR 04-DEC-2001; 2001US-0337294P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX Marasco WA, Gennari F;
 PI WPI; 2003-482710/45.
 DR N-PDB; ACC84103.
 XX
 XX Novel antibody to extracellular epitopes of Epstein Barr virus latent
 PT membrane protein, useful for prevention and treatment of diseases caused
 PT by Epstein-Barr Virus, e.g. malignancies and lymphoproliferative
 PT diseases.
 XX
 PS Disclosure; Page 20; 52pp; English.
 XX
 XX The present sequence is the protein sequence of anti-Epstein-Barr virus
 CC (EBV) latent membrane protein (LMP) scFv FG-1. The scFv was isolated from
 CC a human antibody phage display library. It comprises a DP-88/hv1051K VH
 CC germline and 3r.9C5/DP123 VL germline. It is an example of antibodies of
 CC the invention directed against EBV LMP proteins (LMP1, LMP2A or LMP2B).
 CC Claimed methods of generating an immune reaction comprise administering
 CC an antibody with specificity for EBV LMP, or an immune cell endowed with
 CC antibody specificity for an EBV LMP by transformation, to an individual
 CC having an EBV-associated disease such as malignancy, Hodgkin's disease,
 CC chronic EBV syndrome or oral hairy cell leukoplakia. The malignancy is
 CC especially Burkitt's lymphoma, lymphoproliferative disease, B
 CC lymphoproliferative disease, non-Hodgkin's lymphoma (NHL), T-NHL, NK-NHL,
 CC lymphonodopharyngeal carcinoma or gastric carcinoma. Alternatively, the
 CC lymphocytes of an individual having an EBV associated malignancy are
 CC transformed with a chimeric gene encoding e.g. a single chain antibody as
 CC a means of treatment
 CC
 SQ Sequence 237 AA;
 Query Match 55.7%; Score 753; DB 6; Length 237;
 Best Local Similarity 59.2%; Pred. No. 6.6e-43;

XX The invention relates to antibodies specific to pectin, such as PAM1 and
CC PAM2 scFv (single chain variable region). These antibodies are derived
CC from a native phage display library known as the synthetic scFv library
CC (#1). PAM1 and PAM2 antibodies are capable of binding to de-esterified
CC and un-substituted homogalacturonan (HG), useful for identifying a pectin
CC motif. PAM antibody is useful for identifying a pectin functional group
CC and in assays to determine if a particular pectin composition has the
CC pectin motif or can be used to prepare a food for human and animal
CC consumption, such as jams, yogurts or gels. The PAM antibodies are
CC further useful for quantifying the amount of pectin in a sample or for
CC extracting pectin from a sample. PAM antibodies are also used to identify
CC de-esterified homogalacturonan PAM2 scFv antibody specific to pectin.
CC plants. The present sequence is located in the primary cell walls of
CC Note: This sequence is stated as being the same as that shown as SEQ ID
CC No: 3 in the sequence listing of the specification, however the sequence
CC has 2 extra residues at the C-terminal end
XX
XX Sequence 280 AA;

Query Match	Score	DB	Length
55.78	752.5	4	280

Matches 154; Conservative 31; Mismatches 51; Indels 19; Gaps 5;

Matches 154; Conservative 31; Mismatches 51; Indels 19; Gaps 5;

Matches 154; Conservative 31; Mismatches 51; Indels 19; Gaps 5;

Qy	1	QVTLKESAPTLVYKPPQTLTLCTLSGFSLSSTGVSIVGMTRPPGKALEWLASINMMDDK	60
Db	23	QVQLQESPGELVKPESDLSLTCAVSGYSLSSSN-WKGMTRPPGKLEWITGITYYGSTY	81
Qy	61	YSPSLKSLRLITTKDTPKKNQVVLAMSNMDPADTATYSCALDMRPHDSPOSFSDADVGRQ	120
Db	82	YNPSLKSRLVMTSDVTSKNQFSKLTSVTRAVDTAVVYCA-----RPHPRVYD---WGQ	131
Qy	121	TMVTVSSGGSGSGSGSGSGSGSGSSTEIMQLPSVTSPPQTASITCSGDLGNKYAC	180
Db	132	TLVTVSSRGSGSGSGSGSGSGSS-----ELIQDPAVSVALTQYVITIQGSLRSYVAS	185
Qy	181	WYQOKPGRSPVLVIYGNKRPFGIPIERFSGNSNGVATLTISGQAMDEADYYCQAMDPS	240
Db	186	WYQKPGQAPVLVIYGNKRRPFGIDRFSGSSSGMTASLTITGAQMEDADYYCNSRDS	245
Qy	241	--TAVFGTGTKLTVL	253
Db	246	GNHVFVGGTKLTVL	260

RESULT 10

ID AAB67619 standard; protein; 245 AA.

AC AAB67619;

DT 29-MAY-2001 (first entry)

Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_3.

KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing; miscarriage; abortion; chorionic anti-body; HLA phenotyping; KIR

XX
XX
HOMO varians

XX WO200114558-A
PN

AA
PD 01-MAR-2001.

PF 28-AUG-2000

PR 26-AUG-1999; 99EP-00116691.

PA (MORP-) MORPHOSYS AG.

PI Kretzschmar T, Tesar

DR WPI; 2001-218451/22.

DR WPI; 2001-218451/22.

XX Novel isolated human immunoglobulin or functional immunoglobulin fragment
PT specific for human leukocyte antigen Cw6, useful for treatment of humans
PT and for human leukocyte antigen phenotyping.
XX
PS Claim 3, Fig 1, 23pp; English.

PS Claim 3; Fig 1; 23pp; English.

CC AA6B67617-23 represent single chain antibody (scFv) fragments which are
CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
CC from a synthetic human combinatorial antibody library based on molecular
CC consensus frameworks and CDRs randomised with tryptocleotides. The
CC specification describes a human immunoglobulin fragments specific for HLA-
CC Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
CC natural killer cell balancing as well as miscarriages. HLA-Cw6
CC demonstrates a disequilibrium in some recurrent abortions. Abortus may
CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
CC useful for the preparation of a pharmaceutical for the treatment of
CC humans. They are also useful for HLA phenotyping

SQ Sequence 245 AA;

Query Match	Score	DB 4;	Length
55.6%	751.5;		245;

Query Match	Score	DB 4;	Length
55.6%	751.5;		245;

Query Match	Score	DB 4;	Length
55.6%	751.5;		245;

Qy	1	QVTLKESQSPVLVKRPROTLITCTLSGFSLSISGVSVMGIRPPGKALEWLASINMNDKIC	60
Db	1	QVQLVQSGAEVKKPKQASVKVSCAKSGYFTFS--YYMHVWRQA.PGQGLEMMGMINPNSGGT	58
Qy	61	-YSPSLKSRLLITTKDTPKQVVLVLAISNMNDPADTATYSCLMDP.PPHDSGQSPDASVWGP	119
Db	59	NYAKPFGQRYVMTRITRSTISITAYMEI.SLSRSEPTAYYYCARG-----SFDPMNNWQ	109
Qy	120	GTMTVTS.SGGGSGGGGSGGGGSGGGSSYELMOL.PSVSPSPQGTASITRCSDNLDGKYA	179
Db	110	GTILTVTS.SAGGSGGGGSGGGGSGGGGSDILTQPPSVVA.PGQNRKISCSGDALDGKYA	169
Qy	180	CMYQOKPGRSEFVLYIYGDNKKRPSGILPERPFGSNGSNTATLTIISGTOAMD.EADYVQCAW-D	238
Db	170	SMYQOKPQQA.PVLVIYDDSDRPSGILPERPFGSGNSGNTATLTIISGTOA.EADYVQCSYND	229
Qy	239	TSTAVFGTGTLTYL	253
Db	230	TDLIVFGGTYLTYL	244

RESULT 11

ID ABP45955 standard; protein; 254 AA.

AC ABP45955;

DT 19-AUG-2002 (first entry)

Human BLYs binding scFv SEQ ID 1966.

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; KW

KW antiaids: vaccine; cancer: immune disorder: immunodeficiency

KW common variable immunodeficiency: acquired immunodeficiency syndrome.

aa
os Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001;

PR 16-JUN-2000; 20

16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC.
(CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,
WPI; 2002-114799/15.

Antibodies against B lymphocyte Stimulating polypeptides, useful for the
diagnosis and treatment of cancers and immune disorders.

Claim 1, Page 2746-2747; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to
B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
tumour necrosis factor (TNF) super family and induces B cell
proliferation and differentiation. The antibodies of the invention have
cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
anti-rheumatic and anti-AIDS activity and can be used in vaccines to
inhibit the expression and activity of Blys. The antibodies bind to Blys
and so may be used to detect and quantitate the presence of Blys in
biological samples and may be used in this way to diagnose disease
associated with aberrant expression of Blys. They may also be
administered to treat diseases associated with aberrant Blys expression
diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
immunodeficiency (e.g. common variable immunodeficiency (CVID) and
acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
the antibodies and fragments of the antibodies described in the method of
the invention

Sequence 254 AA;

Query Match 55.3%; Score 747; DB 5; Length 254;
Best Local Similarity 59.8%; Pred. No. 1.8e-42;
Matches 155; Conservative 34; Mismatches 58; Indels 12; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSSTGVSVMQIPPKALEWLASINMNDK 60
DB 1 QVQLDSGPGFLVEPSGTLSTLCANVSGASISSNNI-WKSVVQPPKGLIEWGEIYHSGSTS 59
QY 61 YSPSLKSRLLTITKQPKQVNLAMSNMPPADTATYSCALDMPHDSGPOS---FNASV 116
DB 60 YNPSLRGAVTISVDKSTNQFSLKLTSTYDADTVYYCARDY--YDSSYSVSGDYITMDV 117
QY 117 WPGGTMTVSSGGGSGGGSGGGSGGGSGGGSYELMQLPSVSVSPQQTASITCSGDNIGD 176
DB 118 WGGGTTVTVSSGGGSGGGSGGGSGGGSGGG---ALSTYELTQPPSVSVSPQQTATITCSGDALPK 174
QY 177 KYACMYOQKGRSPVLYIYGDNKRPSGIPRFGSGNSGNTATLTISGTQAMDEADYCOA 236
DB 175 QNAYWYQKRGQAFVLYIYDSSRRSGIPRFGSGSSGTTATLTISGTQAMDEADYCOA 234
QY 237 WDTSTA--VFGTGTKLTVL 253
DB 235 ADSTVSYVFGGKTATVL 253

RESULT 12
ABP45469
ID ABP45469 standard; protein; 250 AA.

XX ABP45469;

XX 19-AUG-2002 (first entry)

XX Human Blys binding scfv SEQ ID 1480.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
KW

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-MAR-2001; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,

WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

diagnosis and treatment of cancers and immune disorders.

Claim 1, Page 2169-2170; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to
B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
tumour necrosis factor (TNF) super family and induces B cell
proliferation and differentiation. The antibodies of the invention have
cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
anti-rheumatic and anti-AIDS activity and can be used in vaccines to
inhibit the expression and activity of Blys. The antibodies bind to Blys
and so may be used to detect and quantitate the presence of Blys in
biological samples and may be used in this way to diagnose disease
associated with aberrant expression of Blys. They may also be
administered to treat diseases associated with aberrant Blys expression
diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
immunodeficiency (e.g. common variable immunodeficiency (CVID) and
acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
the antibodies and fragments of the antibodies described in the method of
the invention

Sequence 250 AA;

Query Match 54.9%; Score 742; DB 5; Length 250;
Best Local Similarity 56.9%; Pred. No. 3.8e-42;
Matches 152; Conservative 30; Mismatches 53; Indels 32; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSSTGVSVMQIPPKALEWLASINMNDK 59
DB 1 QVQLDSGPGFLVEPSGTLSTLCANVSGASISSNNI-WKSVVQPPKGLIEWGEIYHSGSTS 58
QY 60 YSPSLKSRLLTITKQPKQVNLAMSNMPPADTATYSCALDMPHDSGPOSFADSV--- 116
DB 59 YNPSLRGAVTISVDKSTNQFSLKLTSTYDADTVYYCARDY--YDSSYSVSGDYITMDV 116
QY 117 WPGGTMTVSSGGGSGGGSGGGSGGGSGGGSYELMQLPSVSVSPQQTASIT 162
DB 107 WYLFQHMKGKGLTVSSGGGSGGGSGGGSGGG---AQSVLTQPPSVSVSPQQTASIT 162
QY 169 CSGDNIGDKYACMYOQKGRSPVLYIYGDNKRPSGIPRFGSGNSGNTATLTISGTQAMD 228
DB 163 CSGDNIGDKYACMYOQKGRSPVLYIYDTRKPSGIPRFGSGNSGNTATLTISGTQAMD 222
QY 229 EADYTCOAMD--TSTAIVFGTGTKLTVL 253

Db 223 EADYSCQTMDSSTSVFVGSGTTLTVL 249

RESULT 13

ABP45596

ID ABP45596 standard; protein; 256 AA.

XX

AC ABP45596;

DT 19-AUG-2002 (first entry)

XX

DE Human BlyS binding scFv SEQ ID 1607.

XX

KM BlyS; B lymphocyte stimulator; TNF superfamily; human; cytosolic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 2320-2321; 3148pp; English.

XX

XX This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS

CC and so may be used to detect and quantitate the presence of BlyS in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BlyS. They may also be

CC administered to treat diseases associated with aberrant BlyS expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of

CC the invention

XX

XX

SQ Sequence 256 AA;

XX

Query Match 54.5%; Score 736; DB 5; Length 256;

Best Local Similarity 58.5%; Pred. No. 9.8e-42;

Matches 152; Conservative 33; Mismatches 63; Indels 12; Gaps 5;

Db 1 QVTLKSGPTLVKPTQTLLTCTLSGSLTSGVSGVMIRQPKALEWLASINMNDKDC 60

1 QVQLQSSGSLVKSPTLSLTCAVSGSGSISSGYSWVRQPKGLEWIGYIHSGSTY 60

QY 61 YSPSLKRLTLITKDTKPNQVILAMSNMDDPATATYSCA-LDMPPHD--SGPQSFADSDVW 117

Db 61 YNPSLSKRVTLISVDRKKNQPSLKLSSVTAAADTVYCAKQRQDDYILITGYQUGYAFDIW 120

QY 118 GPCTWTVTSSGGGGSGGGSGGGSGGGSSYLEMQLPSVSVSPGQTASTTSCG--DNIG 175

Db 121 GRCTPTVTS----SGGGSGGGGGSGGGSGSVLTQPPSVSAPPGQKVTISCGSTSNIG 175

QY 176 DKYACWYQOKPGRSPVLVLYGDKNRPSTGIPERRSGNSGNTATLTISGQAMEADYTCQ 235

Db 176 NNTVSWYQQHPGKAPPLMTYDVSKRPSGVDRPSGSGNSASLDISGLQSEADYCA 235

QY 236 AMDTSTA--VFGTGTTLTVL 253

Db 236 AMDDSLSEFLFGTGTTLTVL 255

RESULT 14

ABP44979

ID ABP44979 standard; protein; 251 AA.

XX

AC ABP44979;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human BlyS binding scFv SEQ ID 990.

XX

KM BlyS; B lymphocyte stimulator; TNF superfamily; human; cytosolic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 1583-1584; 3148pp; English.

XX

XX This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS

CC and so may be used to detect and quantitate the presence of BlyS in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BlyS. They may also be

CC administered to treat diseases associated with aberrant BlyS expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 251 AA;

Query Match 54.4%; Score 734.5; DB 5; Length 251;
Best Local Similarity 59.9%; Pred. No. 1.2e-41; Mismatches 62; Indels 11; Gaps 4;
Matches 154; Conservative 30; Mismatches 62; Indels 11; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSVMIRPGKALEWLASINMDDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYVMGMINRPGKLEWIGSIYSGSTY 60
QY 61 YSPSLKSRLLTTKTPTKQVVLAMSNMPPADTATYSCALDMPHDSGPGSFPASDVWPG 120
DB 61 YNPSLKSRLVITISVDTSKNQFSLKLSVTADTAVYCARFR--YDILTSYYGMVWGRG 118
QY 121 TMVTVSSGGGSGGGGSGGGGSGGGGSGGYELMQLPVSVSPPQTASITGSG--DNLDK 177
DB 119 TMVTVSS--SGGGSGGGGSGGGGSGGSLVLTQPAVSQSPQGSITISCTGSDVGGYN 173
QY 178 YACMYQOKPGRSPVLVIYGDNRKPSGIPRFGSGNSGNTATLTISGTQAMDEADYCCQAW 237
DB 174 YVSMYQOHPGKAPKLMITYGSKRPSGVSNRFGSKSGNTASLTISGLQAEDEADYCCSY 233
QY 238 DT-STAVFGTGTLTVL 253
DB 234 TTNSIRVFQGGTKLTVL 250

RESULT 15
ABP45318
ID ABP45318 standard; protein; 252 AA.
XX

AC ABP45318;
XX
DT 19-AUG-2002 (first entry)
XX

DE Human Blys binding scFv SEQ ID 1329.
XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
FN WO200202641-A1.
XX
PD 10-JAN-2002.
XX

PF 15-JUN-2001; 2001WO-US019110.
XX

PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR MPI; 2002-114799/15.
XX

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
diagnosis and treatment of cancers and immune disorders.

XX
PS Claim 1; Page 1989-1990; 3148bp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantify the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX

SQ Sequence 252 AA;

Query Match 54.3%; Score 733; DB 5; Length 252;
Best Local Similarity 58.0%; Pred. No. 1.5e-41; Mismatches 56; Indels 24; Gaps 5;
Matches 153; Conservative 31; Mismatches 56; Indels 24; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSVMIRPGKALEWLASINMDDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYVMGMINRPGKLEWIGSIYSGSTY 60
QY 61 YSPSLKSRLLTTKTPTKQVVLAMSNMPPADTATYSCA-----DMPHDSGPGSFP 113
DB 61 YNPSLKSRLVITISVDTSKNQFSLKLSVTADTAVYCARGDVYDILGYELH-----A 112
QY 114 SDVWPGTMTVSSGGGSGGGGSGGGGSGGGGSGGYELMQLPVSVSPPQTASITGSGDN 173
DB 113 FDIWKGITLVTS-----SGGGSGGGGSGGGGSGGSLVLTQPAVSQSPQGSITISCTGTS 167
QY 174 L--GDKYACMYQOKPGRSPVLVIYGDNRKPSGIPRFGSGNSGNTATLTISGTQAMDEA 230
DB 168 SAVGGINVYSWYQOHPGKAPKLMITYGSKRPSGVSNRFGSKSGNTASLTISGLQAEDEA 227
QY 231 DYCCQAMDT-STAVFGTGTLTVL 253
DB 228 DYCCSYTTRISIRVFQGGTKLTVL 251

Search completed: May 13, 2004, 15:00:55
Job time : 54.0738 secs

US-09-260-527-3
Sequence 3, Application US/09260527A
Patent No. 6328599

```

1  GENERAL INFORMATION:
2  APPLICANT: Kiox, J.P.
3  APPLICANT: Mikkelsen, J.D.
4  APPLICANT: Willats, W.G.
5  TITLE OF INVENTION: ANTIBODY
6  FILE REFERENCE: DYOUL9.001AUS
7  CURRENT APPLICATION NUMBER: US/09/260,527A
8  CURRENT FILING DATE: 1999-02-26
9  NUMBER OF SEQ ID NOS: 7
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 3
12 LENGTH: 278
13 TYPE: PRT
14 ORGANISM: UNKNOWN
15 FEATURE:
16 OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
17 OTHER INFORMATION: from a naive phage display library known as the
18 OTHER INFORMATION: Synthetic scfv Library (#1) from the Centre for
19 US-09-260,527-3 Protein Engineering, MRC Centre, Cambridge, UK

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Best Local Similarity	DB 3	Length
60.4%; Pred. No. 3.4e-49;		278;
Matches 154; Conservative 31. Mismatch		

QY 1 QVTLKESGPTLVKPKPQTLTLTLCTLSGFSLSSTGVSVMGIRPOCKALEWMLASINMMDDKC 60
Db 23 QVQLDSGSGGLVAKPSGLTSLTCAVSGYSISSN--MMGIRQPOCKGLEWIGIYYIGSTY 81
QY 61 YSPSLKSLRLTLTKDTPKNQVYLAMSNMDDPATATYSCALMDPHDGGPQSFDAADVMGPG 120
Db 82 YNPSLKSRLTMSVDPSTSKQPSLKLSTSYAVDTATYYTA-----RHPHYVD----WGQ 131
QY 121 TMVTVSSGGGSGGGGSGGGSGGGSSYLEMQLPSVYSFGQTASITGSGDMLGDKYAC 180
Db 132 TLVTVSRGGGSGGGGSGGGGSS-----ELTDDPAVSVALQVYVITCGGSLSTSYAS 185
QY 181 MYQQKPGGSPVLVLYGDNKRPSGICPERFSGNSNGNTATLLTSGTAMDEADYYCOAMDT 240
Db 186 MYQQKPGQAPVLVLYGNNRPSGIPRFSGSSSGNTASTLTITGAQAEADYYCNSRDS 245
QY 241 --TAVRGCTKLTLYL 253
Db 246 GNVHYVGGGKTLTLYL 260

Sequence 79, Application US/08918148A
Patent No. 6342220

GENERAL INFORMATION:
 APPLICANT: Adams, Camellia
 APPLICANT: W.
 APPLICANT: Carter, Paul J.
 APPLICANT: Fendly, Brian M.

```

/ APPLICANT: Gurney, August L.
/ TITLE OF INVENTION: Agonist Antibodies
/ FILE REFERENCE: P0979
/ CURRENT APPLICATION NUMBER: US/08/918,148#
/ CURRENT FILING DATE: 1997-08-25
/ NUMBER OF SEQ ID NOS: 73
/ SEQ ID NO 79
/ LENGTH: 244
/ TYPE: PRT
/ ORGANISM: artificial
US-08-918-148-79

```

Best Local Similarity 59.1%; Pred. NO. 1.3e-46; Length 244
Matches 152; Conservative 30; Mismatches 53; Indels

Qy	1	QVTLKEGGPPLVYPTOTLTLTCTLSGFSLSTSGVSGVMIPGPKALEMLASLNKNDKC	60
Db	3	QVQLQSGGPEELVPSSETLSLTCTVSGDLSISYSVM--NIQPGPKGLEIMIGIYIYSGSTN	60
Qy	61	YSPSLKSLRLTIKTQTEPKQNVFLAMSNMDPATATATYSCALMPPHDSGPOSFSDASVDMGPG	120
Db	61	YNPSLKSRLVTIYSDTISKSGFSLKLSSTVADTAVITCARGR-----YFDVMGRG	109
Qy	121	TMTVTSGGGGSGGGSGGGSGGGSGGSSYELMQLPSVSVSPGQTASITCSG---DNIGDK	177
Db	110	TMTVTS-----SGGGSGSGGGSGGGSGSYLVLPSPVSGSPQGSITISCTGTSDDVGQIN	164
Qy	178	YACWYQOKRGRSPVLVIYGNDKRPSGIPERFSGSNSGNATLITIGTQAMDEADYYCOAW	237
Db	165	YISWYQOQHGRGAPKLMITYEGSKRPSGVSNRFSGSSKSGNTASLTISGLQADEADYYCSY	224
Qy	238	DT--STAVEFGTQKLTVL	253
Db	225	TRSTRVFGGSTKLTVL	241

US-10-039-785-50
Sequence 50, Application US/10039785

```

/ Patent No. 6538938
/ GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ FILE REFERENCE: PPS50
/ CURRENT APPLICATION NUMBER: US/10/039,785
/ CURRENT FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 60/369,860
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/331,310
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/331,044
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: 60/327,364
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/323,807
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/309,176
/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/294,981
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/293,473
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 250
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:

```

OTHER INFORMATION: T1015A02 scfv
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (250)
 OTHER INFORMATION: Xaa equals either Gly or Ser
 US-10-039-785-50

Query Match 51.4%; Score 694; DB 4; Length 250;
 Best local similarity 54.5%; Pred. No. 7, 3e-45;
 Matches 140; Conservative 36; Mismatches 69; Indels 12; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPKALEWLASINWDDKC 60
 1 QVQLQSGPGGLVPSGQTLTKKCNVSGSGSISGTDYMSWIRQPGKLEWIGYIHSQSTY 60
 QY 61 YSPSLKSLRTITKTPKQNVLAAMNMDPADTATYSCALDMPHDSGQSPDASDVWGP 120
 61 YKPSLSRLTVSMDSIRNQSLSLTSVTADTALYYCVREMANGD---HMSAFDLMGQ 116
 QY 121 TWVTSSGGGSGGGSGGGSGGSSYELMQLPSVSPGQTASITCSG--DNLGDKY 178
 117 TLVTVSSGGGSGGGSGGGSGGSS---AQAVLTQPSASGTPGQRTTTPCGSSSNIGANT 172
 DB 179 ACWYQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCQAM 238
 173 VMWYQQLPGTAPKLLYGNDRPSGVPRFSGSKGTSALITGLQSEADYCCAM 232
 QY 239 TSTA--VFETGKLTVL 253
 DB 233 DSLIGVFGTGTQLTVL 249

RESULT 5

US-09-079-029-9
 Sequence 9, Application US/09079029
 Patent No. 6342369
 GENERAL INFORMATION:
 APPLICANT: Adams, Camilla W.
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Chuntarapai, Anan
 APPLICANT: Kim, Kyung J.
 TITLE OF INVENTION: Apo-2 Receptor
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/079,029
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5416
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-079-029-9

Query Match 51.2%; Score 692; DB 4; Length 309;
 Best local similarity 55.9%; Pred. No. 1, 3e-44;
 Matches 143; Conservative 33; Mismatches 64; Indels 16; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPKALEWLASINWDDKC 60
 40 EVQLVQSGGGLVPSGQTLTKKCNVSGSGSISGTDYMSWIRQPGKLEWIGYIHSQSTY 97
 DB 61 YSPSLKSLRTITKTPKQNVLAAMNMDPADTATYSCALDMPHDSGQSPDASDVWGP 119
 98 GYADSVKGVNITSRDAKNSLYLQNMSLRAEDTAYYCKIL---GAGRCMYFDLWGR 152
 QY 120 GTWTVSSGGGSGGGSGGGSGGSSYELMQLPSVSPGQTASITCSGDNLCDKYA 179
 153 GTTVTVSSGGGSGGGSGGGSGGSS---ELTQDPVAVALGQYRITCGDSLSRYA 206
 DB 180 CWYQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCQAM 239
 207 SWYQKPGQAPVLVIYGNKRPSPGIPDRFSGSSGNTALITGLQSEADYCCNSRDS 266
 QY 240 S--TAVFGTGTQLTVL 253
 DB 267 SGNHVVFEGGTQLTVL 282

RESULT 6

US-09-079-029-10
 Sequence 10, Application US/09079029
 Patent No. 6342369
 GENERAL INFORMATION:
 APPLICANT: Adams, Camilla W.
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Chuntarapai, Anan
 APPLICANT: Kim, Kyung J.
 TITLE OF INVENTION: Apo-2 Receptor
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/079,029
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5416
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 312 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-079-029-10

Query Match 51.0%; Score 688.5; DB 4; Length 312;
 Best local similarity 56.9%; Pred. No. 2, 4e-44;
 Matches 145; Conservative 31; Mismatches 66; Indels 13; Gaps 5;

QY 2 VTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPKALEWLASINWDDKC 60
 DB 41 VQLVQSGGGLVPSGQTLTKKCNVSGSGSISGTDYMSWIRQPGKLEWIGYIHSQSTY 98

Query Match	50.6%	Score 684	DB 4	Length 244
Best Local Similarity	55.6%	Pred. NO.	4e-44	
Matches 143	Conservation			

```

QY      1 QVTLKSGPVLVLPQTLTLTCTLSGFSLTSGVSVGMIPQPKALEWIASINMDDKC 60
Db      1 QVQLDSGGGLVLPSETLSTLTCTVSGSISDYVMS--WASQSGKLEWIGSIDVAGSTN 58
QY      61 YSPSLKSRLLTKDTPPKQVVLAMSNDDPADTATYSCALDMPHDGSPGSFASVMPGP 120
Db      59 YNPSLKSRVLTMTIDKSKQFPLKIDSTVADTMYCA-----RLGRIISDYWGQ 109
QY      121 TMTVTSGGGGSGGGSGGGSGGGSSGYELMQLPSVSVSPQGLASITSG--DNLGRT 178
Db      110 TLVTVSSGGGGSGGGSGGGGGSS--ALSYVLTPPSPASGIPGQRTITICAGSSSNGT 166

```

QY 179 ACRYOOKPGRSPVLVYDGNKRPSGI PERFGSGNSGNATATLTISGTAMDEADYYCOAMD 238
Db 167 VNNYQDLPTAFAPLTLTYSNNORPSGVPRFGSKSGTASIALISGLSBEADYYCATWD 226
QY 239 TSTPA--VRGTGKLTLYL 253
Db 227 DSRGGWVFGGTHLTLYL 243

```

RESULT 8
US-09-260-527-1
/ Sequence 1, Application US/09260527A
/ Patent No. 6228599
/ GENERAL INFORMATION:
/ APPLICANT: Knox, J.P.
/ APPLICANT: Mikelsen, J.D.
/ APPLICANT: Willats, W. G.
/ TITLE OF INVENTION: ANTI-BODY
/ FILE REFERENCE: DY0U19.001AUS
/ CURRENT APPLICATION NUMBER: US/09/260.527A
/ CURRENT FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 280
/ TYPE: PROT
/ ORGANISM: UNKNOWN
/ FEATURE:
/ OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
/ OTHER INFORMATION: phase display library known as the Synthetic scFv
/ OTHER INFORMATION: library (#1) from the Centre for Protein
US-09-260-527-1
Engineering, MRC Centre, Cambridge, UK.

```

Query Match	49.5%	Score 668.5;	DB 3;	Length 280;
Best Local Similarity	54.7%	Pred. No. 6,8e-43;		
Matches 141;	Conservative 31;	Mismatches 63;	Indels 23;	Gaps 5
QY	1	QVTLKESGPTLVKPTOTLTLTCTGSGFLSTNSGVSVGKIQPPGKALEWLASINWDD--	58	
Db	23	EVOLVESGGGLVYKPGSLSRLSCAASGFTFSNAMS--WVQAQKGKLEWGVIKKRTDGG	80	
QY	59	-KCPSPKLSRLITITDPTKKNQVVLASNNMDPADTATYSALMDPMDGSGPQSFASDVW	117	
Db	61	TTVYAPVYKGRFTISDSSKNTLYLQNMSLTETDTAVYYCA-----RKKKKLRW	130	
QY	118	GFPTMVTWSSGGGSSGGGSGGGSGGGSSYEELMDLPSVSYFQGTASITCSGDNIDDK	177	
Db	131	GGQTLVYTSRRGGSGGGSGGGSS-----ELTDDPAVSVALQVTRITTCQDPSLRSY	184	
QY	178	YACWYQOKRGSRPVLVIYGDNKRPSGIPERFGSNGSGNTATLTITSGTQAMDEADYCGAW	237	
Db	185	YASWYQOKRGQAPVLVIYGNKNRPSGILPDRFGSSSGNTASTLTITGAQAEADYCNCSR	244	
QY	238	PTS--TAFTGCTGLTTL	253	
Db	245	DSSGNHVFGGGTLTTL	262	

RESULT 9
 US-09-079-029-11
 : Sequence 11, Application US/090790225
 : Patent No. 6342369
 : GENERAL INFORMATION:
 : APPLICANT: Adams, Camilla W.
 : APPLICANT: Ashkenazi, Avi J.
 : APPLICANT: Chuntharapai, Anan
 : APPLICANT: Kim, Kyung J.
 : TITLE OF INVENTION: Apo-2 Recept
 : NUMBER OF SEQUENCES: 14
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Genentech, Inc.
 : STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11

Query Match 46.7%; Score 630.5; DB 4; Length 310;
Best Local Similarity 51.4%; Pred. No. 5,4e-40;
Matches 133; Conservative 42; Mismatches 63; Indels 21; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSVMIRPPKALEWLASINMN-DDK 59
DB 40 QVQLVDSGGGVQPGKSLSLSCASCFITSSYGM--WVQAPGKLEWVAGIFTYGK 97
QY 60 CYSPLSKSLRTITTKTPKNQVVLAMSNMADPATIATYSCALDMPHDSGQSPDSDVWCP 119
DB 98 YYADVSKGFTISRDNSKNTLVLTQWNSLAEDTAVYYCARD-----RGYYMDVWVK 149
QY 120 GIMVTVSSGGGSGGGGSGGGGSSYEIMQLPVSVSFQQTASITCSG--DNLGDK 177
DB 150 GTTLTVS-----SGGGSGGGGSGGGGSGSVLTQPPSVSGAPGQRTVITISCTGSSNIGAG 204
QY 178 Y-ACWYQOKRSPVLYIGDNKRPSGIPERFSGNSGNTATLTISGTOAMDEADYYCA 236
DB 205 HGVHWYQQLPGTAPKLLIYDSDNSRPSGVDPFRSGSKSGTSASLAIITGLQAEDEADYYCOS 264
QY 237 WDTST--AVFGTGTKLTVL 253
DB 265 YDSLSRGVFGGKTVTL 283

RESULT 10

US-08-665-202-5
Sequence 5, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-202-5

Query Match 45.7%; Score 617.5; DB 2; Length 258;
Best Local Similarity 49.3%; Pred. No. 4.1e-39;
Matches 132; Conservative 39; Mismatches 68; Indels 29; Gaps 8;

QY 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSVMIRPPKALEWLASINMN-DDK 59
DB 1 QVQLVDSGAEKLPKESLKSCKSGSYFTSYWIA--WVQAPGKLEWVAGIFTYGK 58
QY 60 CYSPLSKSLRTITTKTPKNQVVLAMSNMADPATIATYSCALDMPHDSG-----PQ 109
DB 59 KYSFSGQGVITISVSKSVSTAVLTQWNSLSKPSDSAVYFCA-----RDVGYCSSSNCAKWP 114
QY 110 SPDASDWGPGTMTVSSGGGSGGGGSGGGGSSYEIMQLPVSVSFQQTASITC 169
DB 115 YQD--WQGTLLTVS-----SGGGSGGGGSGGGGSGSVLTQPPSVSAAPGQRTVITIS 166
QY 170 SG--DNLGDKYACWTQOKRSPVLYIGDNKRPSGIPERFSGNSGNTATLTISGTOAM 227
DB 167 SSSSNIGNNVSWYQQLPGTAPKLLIYGTNRPAQVDPFRSGSKSGTSASLAIISFRSE 226
QY 228 DEADYYCAAMDYSTA--VFGTGTKLTVL 253
DB 227 DEADYYCAAMDLSLGGWVFGGKTVTL 254

RESULT 11

US-09-315-574-5
Sequence 5, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-315-574-5
```

```

Query Match      45.7%; Score 617.5; DB 4; Length 258;
Best Local Similarity 49.3%; Pred. No. 4,1e-39;
Matches 132; Conservative 39; Mismatches 68; Indels 29; Gaps 8;
```

```

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTGVSVGNIRPPKALMLASINMND-DK 59
DB 1 QVQLQSGALELKPESLTKSCSGSYFTSYWIA--WVRQMPGKLEWGLIYPSGSDT 58
QY 60 CTSPLSKRLTTTKDTPKNQVVLAMSNMPPADTAATYSCALDMPHDGS-----PQ 109
DB 59 KTSPLFQCVITISVVKSTAYLQWSSLSKPSDSAVTCA-----RHDVGYCSSNCAKWE 114
QY 110 SFDADWVGPGMTLVSSGGGSGGGSGGGSGGGSSVELMQLPSVSVSPQQTASITC 169
DB 115 YFGH---WGQGLTVVS-----SGGGSGGGSGGGSGGGSVLTPPSVSAAPQKXTISC 166
QY 170 SG--DNIGDKYACAYQOKPGRSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQM 227
DB 167 SGSSSNIGNNYVSWYQQLPGTAPRLILYGHTRNPAVGVPDRFSSKSGTASALISGFRSE 226
QY 228 DEADYYCOAMDSTA--VFEGTGLTVL 253
DB 227 DEADYYCAMDDSLSGWVFGGGLTVL 254
```

```

RESULT 12
US-08-190-199A-61
Sequence 61, Application US/08190199A
Patent No. 5830663
GENERAL INFORMATION:
APPLICANT: EMBLETON, Michael J.
APPLICANT: GOROKHOV, Guy
APPLICANT: JONES, Peter T.
APPLICANT: WINTER, Gregory P.
TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSER: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,199A
FILING DATE: 13-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01483
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9212419.7
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9117352.6
FILING DATE: 10-AUG-1991
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-190-199A-61
```

```

Query Match      45.0%; Score 607.5; DB 2; Length 235;
Best Local Similarity 51.0%; Pred. No. 2,1e-38;
Matches 128; Conservative 31; Mismatches 71; Indels 21; Gaps 5;
```

```

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTGVSVGNIRPPKALMLASINMNDKC 60
DB 1 QVQLQSGALELKPESLTKSCSGSYFTSYWIA--WVRQMPGKLEWGLIYPSGSDT 58
QY 61 YSPSLKRLTTTKDTPKNQVVLAMSNMPPADTAATYSCALDMPHDGSPPQSFDAADWGP 120
DB 59 YNSALMSRLISLXKNSLSQVFLKNSLQTDITMYCARDRAV-----WGQG 106
QY 121 TMTLVSSGGGSGGGSGGGSGGGSGGGSSVELMQLPSV-SVSPQQTASITCGDNIGDKYA 179
DB 107 TLTVVS-----AGGGSGGGSGGGSGGGSVLTPPSVSAAPQKXTISC 166
QY 180 CWYQOKPGRSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYYCOAMD 239
DB 161 HWYQOKSGSPKRWITDTSLKASGVAPRPSGSGATSYSLTISMEADDAATYYCOQSS 220
QY 240 STAVFGTGL 250
DB 221 NPLTFAGTGL 231
```

```

RESULT 13
US-08-918-148-74
Sequence 74, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camella
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 74
LENGTH: 249
TYPE: PRT
ORGANISM: artificial
US-08-918-148-74
```

```

Query Match      44.9%; Score 606.5; DB 4; Length 249;
Best Local Similarity 49.6%; Pred. No. 2,6e-38;
Matches 128; Conservative 41; Mismatches 70; Indels 19; Gaps 6;
```

```

OY 1 VYTLKESGGTLLKVPOTLLTCTLLSGPFLSTSGVSGMTRQPGKALLEMLASTI--NNMDDK 59
Db 3 QVQLDPSGGEMMKPGPESLKISCKGYISFATSW--IGWAKQMGKGLLEMLALYPPGSDT 60
OY 60 CYSPELSKRLITTKDTPKNQVVLVLAWSNMDDPATIATYSCALDMPHDSQPSDFASDVWGP 119
Db 61 RHNPFFEDDVTWISADTISINTAYLQWISLKASTDPMATYCA-----RAGVAGGAFDLMGK 113
OY 120 GMMTVVSSGGGGSGGGGGSGGGGSSGYELMQLSVSVSPQGTASITCSGNL---GD 176
Db 114 GTMTVVS-----SGGGGSGGGGSGGGGSGSVLQPPASVSGSPQOSTITSTGYSGGVGY 168
OY 177 KYACWYQOKPGASPVYLVLYGDNKRPGSIPERFSGNSGNATATLTISGQAMDDADYVCOA 236
Db 169 NVSVSWYQHGPAGKAPKLLIYGNNSRPGVDPDRFGASKSGNTASLTISGLQMEDADYFCST 228
OY 237 W--DTSTAVRGCTGYTLVL 253
Db 229 YAPPGIIMFGGCTGYTLVL 246

```

```

01  RESULT 14
02  US-08-752-844-66
03  ; Sequence 66, Application US/08752844
04  ; Patent No. 5935821
05  ; GENERAL INFORMATION:
06  ; APPLICANT: Chatterjee, Malaya
07  ; APPLICANT: Foon, Kenneth A.
08  ; APPLICANT: Chatterjee, Sunil K.
09  ; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
10  ; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
11  ; NUMBER OF SEQUENCES: 66
12  ; CORRESPONDENCE ADDRESS:
13  ; ADDRESSEE: MORRISON & FOERSTER
14  ; STREET: 755 PAGE MILL ROAD
15  ; CITY: PALO ALTO
16  ; STATE: CA
17  ; COUNTRY: USA
18  ; ZIP: 94304-1018
19  ; COMPUTER READABLE FORM:
20  ; MEDIUM TYPE: Floppy disk
21  ; COMPUTER: IBM PC compatible
22  ; OPERATING SYSTEM: PC-DOS/MS-DOS
23  ; SOFTWARE: PatentIn Release #1.0, Version #1.30
24  ; CURRENT APPLICATION DATA:
25  ; APPLICATION NUMBER: US/08/752,844
26  ; FILING DATE:
27  ; CLASSIFICATION: 424
28  ; ATTORNEY/AGENT INFORMATION:
29  ; NAME: Schief, J. Michael
30  ; REGISTRATION NUMBER: 40, 253
31  ; REFERENCE/DOCKET NUMBER: 30414-20002.21
32  ; TELECOMMUNICATION INFORMATION:
33  ; TELEPHONE: (415) 813-5600
34  ; TELEFAX: (415) 494-0792
35  ; TELEX: 706141
36  ; INFORMATION FOR SEQ ID NO: 66:
37  ; SEQUENCE CHARACTERISTICS:
38  ; LENGTH: 263 amino acids
39  ; TYPE: amino acid
40  ; TOPOLOGY: linear
41  ; MOLECULE TYPE: protein
42  ; US-08-752-844-66
43
44  Query Match 43.9%; Score 592.5; DB 2; Length 263;
45  Best Local Similarity 51.7%; Pred. No. 3, 1e-37;
46  Matches 134; Conservative 30; Mismatches 72; Indels 23; Gaps 7
47
48  1  QVTLKESPTLVKPPQTLTLTCTLSGFSSTGSGVSGVIRPQGRKLTWLASINRWDDKC 60
49  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50  20  QVQVSEGPFLVPPQSISITLVGFSFLTYGVV--WLRPQGRKLEWLAGL-WEDGTT 76

```

```

Oy      61  -YSPSKSLRTLTQTPKQVVLASNMDDPADTATYSCALDMPHDSGPOSFLDASDVWGP 119
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      77  NYSALISLHLSISKDMSQVFLKANSIQTDITATYCA-----KLGNYDADLYWQ 128
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy      120  GIMVTVSSGGGSGGGGSGGGSGGGSGSSYELMQLP-SVSVSPGQTASITGSGD-----N 173
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      129  GTSVTVS-----SGGGSGGGGSGGGSGGGSDVLMTQPLSLPLVSLDQASISRSQSIVHS 183
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy      174  LGDKTCMTQQRKGRSPVLVIYGNKRPSSGILPERFSGNSGNTLTLTISTGQAMDEADYY 233
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      184  NGNTVYLEWVILQKPGQSPNLLIFVSNRFSGVDPDRSGSGSTDEFTLKISRYVEADLGYY 243
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy      234  QQAMDITSTAVFGNGTFLTV 252
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      244  CFQGSHPVPTFGGTLLEI 262
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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1      RESULT 15
2      US-09-293-533-66
3      : Sequence 66, Application US/09293533
4      : Patent No. 6509016
5      : GENERAL INFORMATION:
6      :   APPLICANT: Chatterjee, Malaya
7      :   APPLICANT: Foon, Kenneth A.
8      :   APPLICANT: Chatterjee, Sunil K.
9      :   TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
10     :   TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
11     :   NUMBER OF SEQUENCES: 66
12     :   CORRESPONDENCE ADDRESS:
13     :     ADDRESSEE: MORRISON & FOERSTER
14     :     STREET: 755 PAGE MILL ROAD
15     :     CITY: PALO ALTO
16     :     STATE: CA
17     :     COUNTRY: USA
18     :     ZIP: 94304-1018
19     : COMPUTER READABLE FORM:
20     :   MEDIUM TYPE: Floppy disk
21     :   COMPUTER: IBM PC compatible
22     :   OPERATING SYSTEM: PC-DOS/MS-DOS
23     :   SOFTWARE: PatentIn Release #1.0, Version #1.30
24     :   CURRENT APPLICATION DATA:
25     :     APPLICATION NUMBER: US/09/293,533
26     :     FILING DATE:
27     :     CLASSIFICATION:
28     :     PRIOR APPLICATION DATA:
29     :       APPLICATION NUMBER: US/08/752,844
30     :     FILING DATE:
31     :     ATTORNEY/AGENT INFORMATION:
32     :       NAME: Schiff, J. Michael
33     :       REGISTRATION NUMBER: 40,253
34     :       REFERENCE/DOCKET NUMBER: 30414-20002.21
35     :     TELECOMMUNICATION INFORMATION:
36     :       TELEPHONE: (415) 813-5600
37     :       TELEFAX: (415) 494-0792
38     :       TELEX: 706141
39     :     INFORMATION FOR SEQ ID NO: 66:
40     :       SEQUENCE CHARACTERISTICS:
41     :         LENGTH: 263 amino acids
42     :         TYPE: amino acid
43     :         TOPOLOGY: linear
44     :       MOLECULE TYPE: protein
45     :       US-09-293-533-66

```

Query Match	43.9%	Score 592.5;	DB 4;	Length 263;
Best Local Similarity	51.7%	Pred. No. 3.1e-37;		
Matches 134;	Conservative 30;	Mismatches 72;	Indels 23;	Gaps 7
QY	1	QVTLKESGFTLVKPTQTLITLTCTLSGFSLSSTSGVSMKIRPGKALEWLASINWDDKC	60	
DQ	20	QVQVKESSGFLVLPSPQSLSTICTVSGFSFLTYGVSS--WIRPGPKGLEWLGAI--WGDGTT	76	
QY	61	-YSPSLKSLKLTITKTQTPKNOVVLAMSNNDPDTTYSICALDMPHDSGPGSPFASDVWCF	119	

Mon May 17 11:03:30 2004

us-10-072-301-17.rai

Page 8

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Db      77  NYHSAISLRISISKDNKSGVFLKLNLSQTDPTATYYCA-----KLGNYADLADTWQ 128
QY      120  GTMTATVSSGGGGSGGGSGGGSGGGSSSEYLMQLP-SVSYSPQGTASITCSGD-----N 173
Db      129  GTSVTVS-----SGGGGSGGGGGSGGGGSLVMTQTPTPLPVSLDQASISGRSSQSIVHS 183
QY      174  LGDGYACWYQAKKGRSPVLVTYGDNRKPSGIRPERFGSSNSGNTATLTISGTQAMDEADYY 233
Db      184  NGNTYLEMYLQKPKQSPNLIIYFVSNRFGVDRISGSGSGTDTPLTKISREYEDDVGYY 243
QY      234  QAMADSTAVFGTGLTV 252
Db      244  CFQGSHPWTFGGGTYLEI 262

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Search completed: May 13, 2004, 15:10:45
Job time : 14.8782 secg

Qy 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240
Db 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240
Qy 241 TAVFGTGTCLTVL 253
Db 241 TAVFGTGTCLTVL 253

RESULT 2
US-10-072-301-25
; Sequence 25, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-072-301-25

Query Match 100.0%; Score 1351; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVTLKESGPTLVKPTOTLTITCTLSGFSLSGVSVMIRPPGKALEMLASINMNDKC 60
Db 1 QVTLKESGPTLVKPTOTLTITCTLSGFSLSGVSVMIRPPGKALEMLASINMNDKC 60
Qy 61 YSPSLKSRLLTIKDPKQVVLAMSNMPPADTATYSCALDMPPHDSGPGSFDAADVWGP 120
Db 61 YSPSLKSRLLTIKDPKQVVLAMSNMPPADTATYSCALDMPPHDSGPGSFDAADVWGP 120
Qy 121 TWTVTSSGGGSGGGGSGGGGSSYEIMOLPSVSPGQTASITCGDNLDGKTYAC 180
Db 121 TWTVTSSGGGSGGGGSGGGGSSYEIMOLPSVSPGQTASITCGDNLDGKTYAC 180
Qy 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240
Db 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240
Qy 241 TAVFGTGTCLTVL 253
Db 241 TAVFGTGTCLTVL 253

RESULT 3
US-10-071-866-17
; Sequence 17, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Clone 15.186.35
US-10-071-866-17

Query Match 100.0%; Score 1351; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVTLKESGPTLVKPTOTLTITCTLSGFSLSGVSVMIRPPGKALEMLASINMNDKC 60
Db 1 QVTLKESGPTLVKPTOTLTITCTLSGFSLSGVSVMIRPPGKALEMLASINMNDKC 60
Qy 61 YSPSLKSRLLTIKDPKQVVLAMSNMPPADTATYSCALDMPPHDSGPGSFDAADVWGP 120
Db 61 YSPSLKSRLLTIKDPKQVVLAMSNMPPADTATYSCALDMPPHDSGPGSFDAADVWGP 120
Qy 121 TWTVTSSGGGSGGGGSGGGGSSYEIMOLPSVSPGQTASITCGDNLDGKTYAC 180
Db 121 TWTVTSSGGGSGGGGSGGGGSSYEIMOLPSVSPGQTASITCGDNLDGKTYAC 180
Qy 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240
Db 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240
Qy 241 TAVFGTGTCLTVL 253
Db 241 TAVFGTGTCLTVL 253

RESULT 4
US-10-071-866-25
; Sequence 25, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-071-866-25

Query Match 100.0%; Score 1351; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVTLKESGPTLVKPTOTLTITCTLSGFSLSGVSVMIRPPGKALEMLASINMNDKC 60
Db 1 QVTLKESGPTLVKPTOTLTITCTLSGFSLSGVSVMIRPPGKALEMLASINMNDKC 60
Qy 61 YSPSLKSRLLTIKDPKQVVLAMSNMPPADTATYSCALDMPPHDSGPGSFDAADVWGP 120
Db 61 YSPSLKSRLLTIKDPKQVVLAMSNMPPADTATYSCALDMPPHDSGPGSFDAADVWGP 120
Qy 121 TWTVTSSGGGSGGGGSGGGGSSYEIMOLPSVSPGQTASITCGDNLDGKTYAC 180
Db 121 TWTVTSSGGGSGGGGSGGGGSSYEIMOLPSVSPGQTASITCGDNLDGKTYAC 180
Qy 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240
Db 181 MYOQKPGSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCAMDT 240

Db 181 WYQOKRGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVYCOAMDYS 240
QY 241 TAVFGTGTLTVL 253
Db 241 TAVFGTGTLTVL 253

RESULT 5

US-10-360-828-17
; Sequence 17, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Clone 15.186.35
US-10-360-828-17

Query Match 100.0%; Score 1351; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
QY 61 YSPSLKSRLLTIKDTFRKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFASDVWCGP 120
Db 61 YSPSLKSRLLTIKDTFRKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFASDVWCGP 120
QY 121 TWVTSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVPQGTASITCSGDNLDGKYAC 180
Db 121 TWVTSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVPQGTASITCSGDNLDGKYAC 180
QY 181 WYQOKRGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVYCOAMDYS 240
Db 181 WYQOKRGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVYCOAMDYS 240
QY 241 TAVFGTGTLTVL 253
Db 241 TAVFGTGTLTVL 253

RESULT 6

US-10-360-828-25
; Sequence 25, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-360-828-25

Query Match 100.0%; Score 1351; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
QY 61 YSPSLKSRLLTIKDTFRKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFASDVWCGP 120
Db 61 YSPSLKSRLLTIKDTFRKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFASDVWCGP 120
QY 121 TWVTSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVPQGTASITCSGDNLDGKYAC 180
Db 121 TWVTSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVPQGTASITCSGDNLDGKYAC 180
QY 181 WYQOKRGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVYCOAMDYS 240
Db 181 WYQOKRGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVYCOAMDYS 240
QY 241 TAVFGTGTLTVL 253
Db 241 TAVFGTGTLTVL 253

RESULT 7

US-10-072-301-23
; Sequence 23, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-072-301-23

Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 66; Indels 2; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLALIIYDDDDR 60
QY 61 YSPSLKSRLLTIKDTFRKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFASDVWCGP 120

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Db      61 YSPSLKSRLLTITDTSKQVVLMTNVDPADTATYCTHEQYYDTSGQPY-YFDPMGQG 119
Qy      121 TMTVSSGGGGGGGGGGGGGGGGGGSSYELMQLP-SVSVSPOQTASITCSGDNLGDKYA 179
        120 TLVTSSGGGGGGGGGGGGGGGGGGSSNIQVTSFSLASVGDRTVMTCRASQDIRKNL 179
Qy      180 CWYQOKRSPVLVIYDNRKPSGIPERFSGNSGNTALTITSGTQAMDEADYCCQAMDY 239
        180 NMWQOKRGPAPKVLIVDASDLRTGIPSRFSGSGSDTFLITSLQPEDIATYCCQSDY 239
Qy      240 STAVFGTGTCLTV 252
        240 LPLTFGGGTKVDI 252
Db

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RESULT 8
US-10-072-301-31
/ Sequence 31, Application US/10072301
/ Publication No. US20030152913A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
/ TITLE OF INVENTION: VIRUS
/ FILE REFERENCE: 25636-718
/ CURRENT APPLICATION NUMBER: US/10/072,301
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-31

```

```

Query Match      58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy      1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSVMIRPPGKALEMLASINMNDKC 60
Db      1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSRTTGEGVMVQPPGKALEMLALTYMDDDR 60
Qy      61 YSPSLKSRLLTITKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGPGSFDASDVWGP 120
Db      61 YSPSLKSRLLTITKDTSKQVVLMTNVDPADTATYCTHEQYYDTSGQPY-YFDPMGQG 119
Qy      121 TMTVSSGGGGGGGGGGGGGGGGGGSSYELMQLP-SVSVSPOQTASITCSGDNLGDKYA 179
Db      120 TLVTSSGGGGGGGGGGGGGGGGGGSSNIQVTSFSLASVGDRTVMTCRASQDIRKNL 179
Qy      180 CWYQOKRSPVLVIYDNRKPSGIPERFSGNSGNTALTITSGTQAMDEADYCCQAMDY 239
Db      180 NMWQOKRGPAPKVLIVDASDLRTGIPSRFSGSGSDTFLITSLQPEDIATYCCQSDY 239
Qy      240 STAVFGTGTCLTV 252
        240 LPLTFGGGTKVDI 252
Db

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RESULT 9
US-10-071-866-23
/ Sequence 23, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST H

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/ TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 23
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23

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```

Query Match      58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy      1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSVMIRPPGKALEMLASINMNDKC 60
Db      1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSRTTGEGVMVQPPGKALEMLALTYMDDDR 60
Qy      61 YSPSLKSRLLTITKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGPGSFDASDVWGP 120
Db      61 YSPSLKSRLLTITKDTSKQVVLMTNVDPADTATYCTHEQYYDTSGQPY-YFDPMGQG 119
Qy      121 TMTVSSGGGGGGGGGGGGGGGGGGSSYELMQLP-SVSVSPOQTASITCSGDNLGDKYA 179
Db      120 TLVTSSGGGGGGGGGGGGGGGGGGSSNIQVTSFSLASVGDRTVMTCRASQDIRKNL 179
Qy      180 CWYQOKRSPVLVIYDNRKPSGIPERFSGNSGNTALTITSGTQAMDEADYCCQAMDY 239
Db      180 NMWQOKRGPAPKVLIVDASDLRTGIPSRFSGSGSDTFLITSLQPEDIATYCCQSDY 239
Qy      240 STAVFGTGTCLTV 252
        240 LPLTFGGGTKVDI 252
Db

```

```

RESULT 10
US-10-071-866-31
/ Sequence 31, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST
/ TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.24 Variant
US-10-071-866-31

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```

Query Match      58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy      1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSVMIRPPGKALEMLASINMNDKC 60
Db      1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSRTTGEGVMVQPPGKALEMLALTYMDDDR 60
Qy      61 YSPSLKSRLLTITKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGPGSFDASDVWGP 120
Db      61 YSPSLKSRLLTITKDTSKQVVLMTNVDPADTATYCTHEQYYDTSGQPY-YFDPMGQG 119

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US-09-880-748-1548

Query Match 58.0%; Score 783; DB 10; Length 250;
Best Local Similarity 63.5%; Pred. No. 2e-47;
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFLSTSGVSVGIRPPKALEMLASINMDDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCAVSGYIS-SGYWGWIRQPPKGLGEMIGSIYHSGSTY 59
QY 61 YSPSLKSRLLTIKTPKQNVVLAMSNMPPADTATYSCALDMPHDSGPQSFSDVWGPG 120
DB 60 YNPSLSKSRVTISVDTSKNQFSLKLSVYAADTAVYYCA--RHVYDILITGYLMAFDIWGQ 117
QY 121 TMVTYSSGGGSGGGGSGGGGSGGGSSYELMQLPSVSVSPQQTASITSGDNLGDKYAC 180
DB 118 TMVTYSSGGGSGGGGSGGGGSGGGSSYELMQLPSVSVSPQQTASITSGDNLGDKYAC 174
QY 181 WYQKPKRSPVLVYGNKRPSCGIPERFGSGNSGNTATLTISGTOAMDEADYCOAMDTS 240
DB 175 WYQKPKRSPVLVYGNKRPSCGIPERFGSGNSGNTATLTISGTOAMDEADYCOAMDTS 234
QY 241 --TAVFGTGTKLTVL 253
DB 235 GNVHVFEGGTQTLTVL 249

RESULT 14

US-10-293-418-1548
Sequence 1548, Application US/10233418
Publication No. US2003023996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1548
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1548

Query Match 58.0%; Score 783; DB 12; Length 250;
Best Local Similarity 63.5%; Pred. No. 2e-47;
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFLSTSGVSVGIRPPKALEMLASINMDDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCAVSGYIS-SGYWGWIRQPPKGLGEMIGSIYHSGSTY 59
QY 61 YSPSLKSRLLTIKTPKQNVVLAMSNMPPADTATYSCALDMPHDSGPQSFSDVWGPG 120
DB 60 YNPSLSKSRVTISVDTSKNQFSLKLSVYAADTAVYYCA--RHVYDILITGYLMAFDIWGQ 117
QY 121 TMVTYSSGGGSGGGGSGGGGSGGGSSYELMQLPSVSVSPQQTASITSGDNLGDKYAC 180

DB 118 TMVTYSSGGGSGGGGSGGGGSGGGSSYELMQLPSVSVSPQQTASITSGDNLGDKYAC 174
QY 181 WYQKPKRSPVLVYGNKRPSCGIPERFGSGNSGNTATLTISGTOAMDEADYCOAMDTS 240
DB 175 WYQKPKRSPVLVYGNKRPSCGIPERFGSGNSGNTATLTISGTOAMDEADYCOAMDTS 234
QY 241 --TAVFGTGTKLTVL 253
DB 235 GNVHVFEGGTQTLTVL 249

RESULT 15

US-09-880-748-1651
Sequence 1651, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3249
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1651
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1651

Query Match 57.7%; Score 779.5; DB 10; Length 247;
Best Local Similarity 60.5%; Pred. No. 3.5e-47;
Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFLSTSGVSVGIRPPKALEMLASINMDDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSNYSIS-SGYWGWIRQPPKGLGEMIGSIYHSGSTY 59
QY 61 YSPSLKSRLLTIKTPKQNVVLAMSNMPPADTATYSCA-----LDMPPHDSGPQ 109
DB 60 YNPSLSKSRVTISVDTSKNQFSLKLSVYAADTAVYYCARFRYDILGYYYDM----- 111
QY 110 SFDASDVWGPQTMVTYSSGGGSGGGGSGGGGSGGGSSYELMQLPSVSVSPQQTASITC 169
DB 112 -----DVMGRGTLVTVSSGGGSGGGGSGGGGSGGGSS-----ELQDPVSVVAGQYTRITC 160
QY 170 SGNLIGRTYACMYQKRGSPVLVYGNKRPSCGIPERFGSGNSGNTATLTISGTOAMDE 229
DB 161 QGDSLSRYSYASMYQKRGQAPVLVYGNKRPSCGIPERFGSGNSGNTATLTISGTOAMDE 220
QY 230 ADYCOAMDTS--TAVFGTGTKLTVL 253
DB 221 ADYCNRSRDSGNHVFEGGTQTLTVL 246

Search completed: May 13, 2004, 15:43:30
Job time: 38.4587 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.4218 Seconds
(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-17

Perfect score: 1351

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....COAMDPTSTAVFGNGTKLTVL 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516	38.2	231	2	S25738 Ig lambda chain -
2	494.5	36.6	120	2	S30525 Ig lambda chain V
3	486.5	36.0	249	2	S41374 single chain Fv an
4	485	35.9	107	2	PC4283 anti-SS-A/Ro 60K p
5	483.5	35.8	124	2	A49002 Ig heavy chain V r
6	483	35.8	268	2	A56446 Ig heavy chain V r
7	479	35.5	151	2	S25739 Ig lambda chain -
8	478	35.4	231	2	S25751 Ig lambda chain -
9	474	35.1	106	1	L4HUBU Ig lambda chain V-
10	474	35.1	114	2	S16440 Ig lambda chain -
11	472	34.9	231	2	S25753 Ig lambda chain -
12	470	34.8	95	2	S36065 Ig lambda chain -
13	470	34.8	106	1	L4HUX Ig lambda chain V-
14	469	34.7	138	2	S31513 Ig heavy chain - h
15	466	34.5	374	2	S69339 Ig heavy chain V r
16	462.5	34.2	105	2	S44124 Ig lambda chain V-
17	457	33.8	125	1	MHHUMC Ig heavy chain V-I
18	455	33.7	119	2	S18555 Ig heavy chain V r
19	451	33.4	121	2	A36005 Ig heavy chain V r
20	441	32.6	106	1	L4HOML Ig lambda chain V-
21	436	32.3	121	1	G1H0HE Ig heavy chain V-I
22	427.5	31.6	233	2	JC5322 p53 specific singl
23	423.5	31.3	120	1	G1H0CO Ig heavy chain V-I
24	419.5	31.1	118	2	S18556 Ig heavy chain V r
25	418	30.9	107	1	L4H0HL Ig lambda chain V-
26	417	30.9	119	2	S30526 Ig lambda chain -
27	415.5	30.8	232	2	S25756 Ig lambda chain V
28	415	30.7	96	2	S26924 Ig heavy chain V r
29	412	30.5	120	2	S30527 Ig lambda chain V

30	411	30.4	96	2	S26923 Ig heavy chain V r
31	403.5	29.9	106	2	S38495 Ig lambda chain -
32	403	29.8	106	1	L4HUKN Ig lambda chain V-
33	400	29.6	132	2	S09713 Ig lambda chain V
34	398.5	29.5	143	2	PT0174 Ig heavy chain pre
35	398.5	29.5	147	1	G2HUCS Ig heavy chain pre
36	395	29.2	128	2	S24319 Ig lambda chain pr
37	393	29.1	108	1	L5HUDL Ig lambda chain V-
38	389	28.8	233	2	S25747 Ig lambda chain -
39	388	28.7	105	2	S49533 anti-Sm antibody V
40	386.5	28.6	122	2	S11740 Ig heavy chain pre
41	384	28.4	119	1	G1H0DW Ig heavy chain V-I
42	380	28.1	96	2	S26922 Ig heavy chain V r
43	378	28.0	127	2	S70444 Ig lambda chain pr
44	375	27.8	108	2	S47184 Ig lambda chain V
45	375	27.8	109	2	S19663 Ig lambda chain V

ALIGNMENTS

RESULT 1
S25738
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25738
R/Comptiaco, G./ Klobbeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25738
A/Status: preliminary; translation not shown
A/Residues: 1-231 (CDM>
A/Molecule type: mRNA
A/Cross-references: EMBL:X57802; NID:G33701; PIDN:CAA40940.1; PID:G33702
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:146-214/Domain: immunoglobulin homology <Imm>

Query Match 38.2%; Score 516; DB 2; Length 231;
Best Local Similarity 89.1%; Pred. No. 1.1e-27;
Matches 98; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 144 GGGSSYELMQLPSVSVSPQQTASITCSGDNLDKXACWYQOKRGSPTVYIGDKRPSG 203
DB 16 GGVASVELTPQPSVSVSPQQTASITCSGDTLDKXACWYQOKRGSPTVYIGDKRPSG 75

QY 204 IPERFGSGNSGNTATLTISGTQAMDEADYYCOAMDPTSTAVFGNGTKLTVL 253
DB 76 IPERFGSGNSGNTATLTISGTQAMDEADYYCOAMDPTSTAVFGNGTKLTVL 125

RESULT 2
S30525
Ig lambda chain V region - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S30525
R/Mariette, X.
submitted to the EMBL Data Library, October 1992
A/Reference number: S30520
A/Accession: S30525
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-120 (MAR>
A/Cross-references: EMBL:Z18331
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <Imm>

Query Match 36.6%; Score 494.5; DB 2; Length 120;
Best Local Similarity 88.8%; Pred. No. 1.6e-26;

Db 61 KYDPKFGKATLTADTSNTAYLQLSLTSEDTAVYYCA-----SYLTRENY 109
QY 117 WGGCMVTYVSSGGSGSGSGSGSGSGSGSYELMQLPSV-SVSPGQTASITCSGDLNIG 175
Db 110 WGGSTVTVTS-----SGGSGSGSGSGSGSGSDTLTQSPALMSASIGEKVYMSCRASS-S 163
QY 176 DKACVYQOKPGKRPVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCO 235
Db 164 VNFITYYQOKSDASPLKWTYYTSHLPVPVAPARFSGSGSGNSYLTISMEGDAATYYCO 223
QY 236 AMDSTAVFGTGTCLTV 252
Db 224 QFTSPFTFGSGTKLEI 240

RESULT 7
S25739
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25739
R/Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25739
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-151 <COM>
A/Cross-references: EMBL:X57803; NID:933703; PIDN:CAA40941.1; PID:933704
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 479; DB 2; Length 151;
Best Local Similarity 84.5%; Pred. No. 2.2e-25;
Matches 93; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 144 GGGSYELMQLPSVSVSPGQTASITCSGDLNIGDKYACWYQOKRSPVLYIGDNKRPSG 203
Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDLNIGDKYACWYQOKRSPVLYIGDNKRPSG 75

QY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCOAMDSTAVFGTGTCLTVL 253
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYYCOALGQHCVFGGTGTCLTVL 125

RESULT 8
S25751
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25751
R/Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25751
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-231 <COM>
A/Cross-references: EMBL:X57816; NID:933731; PIDN:CAA40953.1; PID:933732
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDLNIGDKYACWYQOKRSPVLYIGDNKRPSG 75
QY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCOAMDSTAVFGTGTCLTVL 253
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYYCOAMDSTAVFGGTTCLTVL 125

RESULT 9
L4HUBU
Ig lambda chain V-IV region (Bau) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
C/Accession: A01981
R/Bachko, K.; Braun, D.; Hillebrand, N.
Hoppe-Seyler's Z. Physiol. Chem. 355, 131-154, 1974
A/Title: Pattern of antibody structure. The primary structure of a monoclonal immunoglob
A/Reference number: A01981; MUID:75059189; PMID:4435717
A/Accession: A01981
A/Molecule type: protein
A/Residues: 1-106 <BAC>
C/Comment: This is a Bence Jones protein.
C/Genetics:
A/Gene: GDB:IGLV@
A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/14-88/Domain: immunoglobulin homology <IMM>
F/21-86/Disulfide bonds: #status predicted

Query Match 35.1%; Score 474; DB 1; Length 106;
Best Local Similarity 83.8%; Pred. No. 3.2e-25;
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 149 YELMQLPSVSVSPGQTASITCSGDLNIGDKYACWYQOKRSPVLYIGDNKRPSGIPERF 208
Db 1 YELTQPPSVSVSPGQTASITCSGDLNIGDKYACWYQOKRSPVLYIGDNKRPSGIPERF 60

QY 209 GSGNSGNTATLTISGTQAMDEADYYCOAMDSTAVFGTGTCLTVL 253
Db 61 GSGNSGNTATLTISGTQAMDEADYYCOAMDSTAVFGGTTCLTVL 105

RESULT 10
S16440
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S16440
R/Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S16440
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <COM>
A/Cross-references: EMBL:X57826
C/Genetics:
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.1%; Score 474; DB 2; Length 114;
Best Local Similarity 89.9%; Pred. No. 3.5e-25;
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 144 GGGSYELMQLPSVSVSPGQTASITCSGDLNIGDKYACWYQOKRSPVLYIGDNKRPSG 203
Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDLNIGDKYACWYQOKRSPVLYIGDNKRPSG 75

QY 204 IPRFSGNSGNTATLTISGTQAMDEADYVCOAMDSTSA 242
 Db 76 IPRFSGNSGNTATLTISGTQAMDEADYVCOAMDSTSA 114

RESULT 11

S25753
 Ig lambda chain - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S25753
 R/Combiatic, G.; Klobbeck, H.G.
 Eur. J. Immunol. 21: 1513-1522, 1991
 A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
 A/Accession: S25753
 A/Reference number: S16439; MUID:91257162; PMID:1904362
 A/Molecule type: mRNA
 A/Status: preliminary; translation not shown
 A/Residues: 1-231 <COM>
 A/Cross-references: EMBL:X57818; NID:G33735; PIDN:CAA40955.1; PID:G33736
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/146-214/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 34.9%; Score 472; DB 2; Length 231;
 Matches 89; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 144 GGGSYELMQLPSVSVSPQGTASITSGDNLGDKYACWYQKRGSPVLVYIGDNKRPSG 203
 Db 16 GSVASVYELTPSPSVSPQGTASITCFGDKLGDKXSMYQKRGSPVLVYIGDNKRPSG 75
 QY 204 IPRFSGNSGNTATLTISGTQAMDEADYVCOAMDSTSAVGTGKTTLVL 253
 Db 76 IPRFSGNSGNTATLTISGTQAMDEADYVCOAMDSTSAVGTGKTTLVL 125

RESULT 12

S36065
 Ig lambda chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
 C/Accession: S36065
 R/Williams, S.C.
 Submitted to the EMBL Data Library, April 1993
 A/Reference number: S36065
 A/Accession: S36065
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-95 <WIL>
 A/Cross-references: EMBL:Z22208; NID:G312871; PIDN:CAA80216.1; PID:G312872
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 34.8%; Score 470; DB 2; Length 95;
 Matches 86; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 148 SYELMQLPSVSVSPQGTASITSGDNLGDKYACWYQKRGSPVLVYIGDNKRPSG 207
 Db 1 SYELTOPPSVSVSPQGTASITSGDNLGDKYACWYQKRGSPVLVYIGDNKRPSG 60
 QY 208 FSGNSGNTATLTISGTQAMDEADYVCOAMDSTSA 242
 Db 61 FSGNSGNTATLTISGTQAMDEADYVCOAMDSTSA 95

RESULT 13

L4HUX
 Ig lambda chain V-IV region (X) - human
 C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
 C/Accession: A01982
 R/Milestein, C.; Clegg, J.B.; Jarvis, J.M.
 Biochem. J. 110: 631-652, 1968
 A/Title: Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jone

A/Reference number: A90243; MUID:6908380; PMID:4683841
 A/Accession: A01982
 A/Molecule type: protein
 A/Residues: 1-106 <MIL>
 C/Comment: This is a Bence Jones protein.
 C/Genetics:

A/Gene: GDB:IGLV6
 A/Cross-references: GDB:119342; OMIM:147240
 A/Map position: 22q11.2-22q11.2
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer
 F/14-86/Domain: immunoglobulin homology
 F/21-86/Disulfide bonds: #status predicted

Query Match
 Best Local Similarity 34.8%; Score 470; DB 1; Length 106;
 Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 149 YELMQLPSVSVSPQGTASITSGDNLGDKYACWYQKRGSPVLVYIGDNKRPSG 208
 Db 1 YELTOPPSVSVSPQGTASITSGDNLGDKYACWYQKRGSPVLVYIGDNKRPSG 60
 QY 209 GSGNSGNTATLTISGTQAMDEADYVCOAMDSTSAVGTGKTTLVL 253
 Db 61 GSGNSGNTATLTISGTQAMDEADYVCOAMDSTSAVGTGKTTLVL 105

RESULT 14

S31513
 Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C/Accession: S31513
 R/Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
 Submitted to the EMBL Data Library, December 1992
 A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
 A/Reference number: S31509
 A/Accession: S31513
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-138 <CHA>
 A/Cross-references: EMBL:X69861; NID:G33084; PIDN:CAA49495.1; PID:G33085
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/30-114/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 34.7%; Score 469; DB 2; Length 138;
 Matches 94; Conservative 7; Mismatches 20; Indels 6; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTCTLSGFSLSGSVSVGMTRQPGALWELASINNDKDC 60
 Db 16 QVTLKESGPTLVKPTQTLTCTLSGFSLSGSVSVGMTRQPGALWELASINNDKDC 75
 QY 61 YSPSLKSLRLTITOTPKNOVYLAAMSNMADPATATYSCALDMPPHDSGQSPDAS-DVWGP 119
 Db 76 YSPSLKSLRLTITOTPKNOVYLAAMSNMADPATATYSCALDMPPHDSGQSPDAS-DVWGP 119
 QY 120 GTLVTVS 126
 Db 131 GTLVTVS 137

RESULT 15

S69339
 Ig heavy chain V region precursor - human

```

C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A>Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilchi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology

Query Match          34.5%: Score 466; DB 2; Length 374;
Beet Local Similarity 71.7%: Pred. No. 4.1e-24;
Matches 91; Conservative 11; Mismatches 21; Indels 4; Gaps 1;

QY 1 QVTLKESGFTLVKPTQTLTLCTLSGFSSTSGSVSGWIRQPGKALEWTLASINWDDKC 60
DB 20 QITLKESGFTLVKPTQTLTLCTLSGFSSTSGSVSGWIRQPGKALEWTLALTFWDDKR 79
QY 61 YSPSLKSRLLTKDTPKNOVLTAMSNMDDPADLTATYSICALMDFHSGPQSFDSVWPG 120
DB 80 YSPSLRTRLLTKDTSKNOVLTMTNVDDADLTATYCGSVSGGYRPHS----WGQG 135
QY 121 TMTVTSS 127
DB 136 TLVTSS 142

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Job time : 12.4218 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.1233 Seconds

(without alignments)
1849.388 Million cell updates/sec

Title: US-10-072-301-17

Perfect score: 1351
Sequence: 1 QVTLKESGPTLVKPTQTLTL.....CQAMDSTAVFGTGTCLTVL 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_42.*
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	474	35.1	106	LV4A_HUMAN	P01715 homo sapien
2	470	34.8	106	LV4B_HUMAN	P01716 homo sapien
3	457	33.8	125	HV2D_HUMAN	P01817 homo sapien
4	441	32.6	106	LV4E_HUMAN	P06889 homo sapien
5	436	32.3	121	HV2E_HUMAN	P01818 homo sapien
6	423.5	31.3	120	HV2B_HUMAN	P01815 homo sapien
7	418	30.9	107	LV4C_HUMAN	P01717 homo sapien
8	403	29.8	106	LV4D_HUMAN	P04438 homo sapien
9	398.5	29.5	147	HV2H_HUMAN	P01719 homo sapien
10	393	29.1	108	LV5A_HUMAN	P80748 homo sapien
11	389	28.8	111	LV3B_HUMAN	P01816 homo sapien
12	384	28.4	119	HV2C_HUMAN	P01814 homo sapien
13	369.5	27.4	126	HV2A_HUMAN	P01714 homo sapien
14	351	26.0	108	LV3A_HUMAN	P01720 homo sapien
15	351	26.0	111	LV7A_HUMAN	P01702 homo sapien
16	337	24.9	111	LV1D_HUMAN	P06316 homo sapien
17	336	24.9	130	LV1G_HUMAN	P04208 homo sapien
18	325	24.1	109	LV1F_HUMAN	P01819 mus sapien
19	324	24.0	144	HV43_MOUSE	P06888 homo sapien
20	324	24.0	109	LV1I_HUMAN	P01710 homo sapien
21	320	23.7	109	LV1J_HUMAN	P01701 homo sapien
22	319	23.6	111	LV2G_HUMAN	P01708 homo sapien
23	317	23.5	111	LV1C_HUMAN	P01709 homo sapien
24	313.5	23.2	112	LV1B_HUMAN	P01706 homo sapien
25	312	23.1	111	LV2F_HUMAN	P04209 homo sapien
26	310	22.9	109	LV2E_HUMAN	P06887 homo sapien
27	309.5	22.9	110	LV2J_HUMAN	P01721 homo sapien
28	309	22.9	111	LV2C_HUMAN	P01712 homo sapien
29	308.5	22.8	112	LV2K_HUMAN	P01713 homo sapien
30	303.5	22.5	112	LV1H_HUMAN	P06317 homo sapien
31	303.5	22.5	112	LV6A_HUMAN	P01712 homo sapien
32	302	22.4	111	LV6C_HUMAN	P01712 homo sapien
33	301	22.3	111	LV2I_HUMAN	P01712 homo sapien

34	296.5	21.9	131	1	LV6E_HUMAN	P06319 homo sapien
35	294	21.8	111	1	LV2B_HUMAN	P01705 homo sapien
36	292.5	21.7	135	1	HV02_XENLA	P20957 xenopus lae
37	290	21.5	137	1	HV46_MOUSE	P01820 mus musculu
38	289	21.4	111	1	LV2A_HUMAN	P01704 homo sapien
39	283	20.9	111	1	LV1A_HUMAN	P01699 homo sapien
40	283	20.9	111	1	LV6D_HUMAN	P06318 homo sapien
41	280.5	20.8	116	1	HV61_MOUSE	P18532 mus musculu
42	279	20.7	115	1	HV44_MOUSE	P01820 mus musculu
43	277	20.5	111	1	LV2H_HUMAN	P01711 homo sapien
44	275.5	20.4	112	1	LV6B_HUMAN	P01722 homo sapien
45	274	20.3	111	1	LV2D_HUMAN	P01707 homo sapien

ALIGNMENTS

RESULT 1		ALIGNMENTS	
LV4A_HUMAN	STANDARD;	PRT;	106 AA.
ID	P01715;		
AC	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Ig lambda chain V-IV region Bau.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE.		
RA	MEDLINE=75059189; PubMed=4435717;		
RT	Pattern of antibody structure, the primary structure of monoclonal		
RT	immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones		
RT	protein Bau.)		
RL	Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).		
CC	-1- MISCELLANEOUS: This is a Bence-Jones protein.		
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.		
DR	PIR; A01981; LAHUB.		
DR	HSSP; P80748; ZLOT.		
DR	GO; GO:000576; C:extracellular; NAS.		
DR	GO; GO:0003823; P:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS00835; IG_LIKE; 1.		
KW	Immunoglobulin V region; Bence-Jones protein.		
FT	DOMAIN		
FT	NON TER		
FT	106		
FT	106		
SO	SEQUENCE		
SO	106 AA; 11305 MW; 4B6A688B0EC46571 CRC64;		
Query Match			
Best Local Similarity 35.1%; Score 474; DB 1; Length 106;			
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;			
QY 149 YELMQPVSVPSPGCTASITCSGDNIGDKYACWYQOKPGRSPVLVYGDNRKPSGIPERP 208			
Db 1 YGLTGPPLSVSPGCTASITCSGDKLGEQVYQOKPGRSPVLVYHDSKRSGIPERP 60			
QY 209 SSGNSGNTATLTISGTQAMDEADYYQAMDSTAVFGTGTCLTVL 253			
Db 61 SSGNSGNTATLTISGTQAMDEADYYQAMDSTAVFGTGTCLTVL 105			
RESULT 2			
LV4B_HUMAN	STANDARD;	PRT;	106 AA.
ID	P01716;		
AC	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-IV region X.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RP [1]
 SEQUENCE.
 RX MEDLINE=69088380; PubMed=4883841;
 RA Miletich C., Clegg J.B., Jarvis J.M.,
 RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
 RL Bence-Jones protein.".
 CC Biochem. J. 110:631-652(1966).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01982; L4HDX.
 DR HSSP; P80748; 21OI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 102 IG-LIKE.
 FT NON_TER 106
 SQ SEQUENCE 106 AA; 11334 MW; 24D04344AA812855 CRC64;
 Query Match 34.8%; Score 470; DB 1; Length 106;
 Best Local Similarity 83.8%; Pred. No. 1.4e-27;
 Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 QY 149 YELMQLPSVSPSGQTASITSGDNLGDKYACWQKGRSPVLYVIGDNKRSPGIPERF 208
 DB 1 YDLTGPSPVSVSGQVASTITSGDNLGDKYACWQKGRSPVLYVIGDNKRSPGIPERF 208
 QY 209 SSGNSGNTATLTITSGTQAMDEADYVCOAMDSTAVFGNGTTLTL 253
 DB 61 SSGNSGNTATLTITSGTQAMDEADYVCOAMDSTAVFGNGTTLTL 253
 RESULT 3
 ID HV2D HUMAN STANDARD; PRT; 125 AA.
 AC P01817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region MCE.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RP [1]
 SEQUENCE.
 RX MEDLINE=8118242; PubMed=6780622;
 RA Gerber-Jensen B., Kazin A., Kenoe J.M., Scheffell C., Erickson B.W.,
 RA Litman G.W.;
 RT "Molecular basis for the temperature-dependent insolubility of
 RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
 RL region of MCE.".
 CC Immunol. 126:1212-1216(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
 CC CRYOTIMONOCLOBULIN.
 DR PIR; A02092; MHDMC.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Pyrolydine carboxylic acid.
 FT DOMAIN 1 113
 FT MOD_RES 1 125
 FT NON_TER 125
 SQ SEQUENCE 125 AA; 13783 MW; 7A1ADFC40F47B5 CRC64;
 Query Match 33.8%; Score 457; DB 1; Length 125;
 Best Local Similarity 70.9%; Pred. No. 1.5e-26;
 Matches 90; Conservative 11; Mismatches 24; Indels 2; Gaps 1;
 QY 1 QVTLKSGPTLVKPTQTLTLCTLSGFSLSSTGVSVCWIRPPKALEWLASINMDDKC 60
 DB 1 QVTLKSGPTLVKPTETTLTLCTLSGFSLSSTGVSVCWIRPPKALEWLASINMDDNR 60
 QY 61 YSPSLKSRITTKQTPKQVVLANSNDPADATATYSCALDMPHDSGPGSFDVWPGG 120
 DB 61 YSPSLKSRITTKQTPKQVVLANSNDPADATATYSCALDMPHDSGPGSFDVWPGG 120
 QY 121 TWVTYVS 127
 DB 119 TLVTYVS 125
 RESULT 4
 ID LV4E HUMAN STANDARD; PRT; 106 AA.
 AC P06889;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-IV region MOL.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RP [1]
 SEQUENCE.
 RX MEDLINE=8715615; PubMed=3103603;
 RA Holm E., Sletten K., Hubby G.;
 RT "Structural studies of a carbohydrate-containing
 RT immunoglobulin-lambda-1 light-chain amyloid fibril protein (AL) of
 RL Biochem. J. 239:545-551(1986).
 CC -1- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
 CC HOMOLOGU.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A26019; L4HDM.
 DR HSSP; P80748; 21OI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Amyloid; Glycoprotein.
 FT DOMAIN 1 103
 FT DISULFID 21 103
 FT CARBOHYD 90 90
 FT NON_TER 106
 SQ SEQUENCE 106 AA; 11272 MW; D9B877D4797D2123 CRC64;
 Query Match 32.6%; Score 441; DB 1; Length 106;
 Best Local Similarity 77.1%; Pred. No. 1.7e-25;
 Matches 81; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
 QY 149 YELMQLPSVSPSGQTASITSGDNLGDKYACWQKGRSPVLYVIGDNKRSPGIPERF 208

DB 1 YELTOPSVSVSPGQTATISCSGDKLGESYYDWYQSPGSPULVIYEGDKRSPGIPZRF 60
 QY 209 SGSNSCNTATLTITSGTOAMDEADYCOAMDTSTAVGCTKTLTVL 253
 DB 61 SGSNSCNTATLTITSGTSMDEADYCOAMNSSLVLPFGGCTKTLTVL 105

RESULT 5
 ID HY2E HUMAN STANDARD; PRT; 121 AA.
 AC P01818;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region HE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE
 RP MEDLINE=70114712; PubMed=5264153;
 RA Cunningham B.A., Pelum M.N., Rutishauser U., Edelman G.M.;
 RT "Subgroups of amino acid sequences in the variable regions of
 immunoglobulin heavy chains";
 RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003 (1969).
 CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR; A02093; GIH0HE.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 DR SMART; PS50835; IG_Like; 1.
 DR PROSITE; PS0835; Pyroliidone carboxylic acid.
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 120
 FT MOD RES 1 120 PYRROLIDONE CARBOXYLIC ACID.
 FT NON TER 121 121
 SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 32.3%; Score 436; DB 1; Length 121;
 Best Local Similarity 68.8%; Pred. No. 4.6e-25;
 Matches 88; Conservative 13; Mismatches 19; Indels 8; Gaps 3;

QY 1 QVTLKSGPTLVKPTQTTLTCTLSGFSSTSGSVSGMTRQPGKALEWLA-SINNDK 59
 DB 1 QVTLKSGPTLVKPTQTTLTCTLSGFSSTSGSVSGMTRQPGKALEWLA-SINNDK 60
 QY 60 CYSPLSKSLRTITKPKQNVVLAMSNMPPADPATYSCALDMPHSGPSPASDVWGP 119
 DB 61 RRPSPSKSLRTITKPKQNVVLAMSNMPPADPATYSCALDMPHSGPSPASDVWGP 113

QY 120 GTMVTYSS 127
 DB 114 GTRKAVSS 121

RESULT 6
 ID HY2B HUMAN STANDARD; PRT; 120 AA.
 AC P01815;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region COR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 RT heavy chains";
 RL Biochem. J. 117:641-660 (1970).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR; A02089; GIH0CO.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 DR SMART; PS50835; IG_Like; 1.
 DR PROSITE; PS0835; Pyroliidone carboxylic acid.
 KW Immunoglobulin V region; Glycoprotein; Pyroliidone carboxylic acid.
 FT DOMAIN 1 110
 FT MOD RES 1 110 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 94
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).
 FT NON TER 120 120
 SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;

Query Match 31.3%; Score 423.5; DB 1; Length 120;
 Best Local Similarity 67.2%; Pred. No. 3.6e-24;
 Matches 86; Conservative 14; Mismatches 19; Indels 9; Gaps 3;

QY 1 QVTLKSGPTLVKPTQTTLTCTLSGFSSTSGSVSGMTRQPGKALEWLA-SINNDK 60
 DB 1 QVTLKSGPTLVKPTQTTLTCTLSGFSSTSGSVSGMTRQPGKALEWLA-SINNDK 60
 QY 61 YSPSLSKSLRTITKPKQNVVLAMSNMPPADPATYSCA-LDMPHSGPSPASDVWGP 119
 DB 61 YSPSLSKSLRTITKPKQNVVLAMSNMPPADPATYSCA-LDMPHSGPSPASDVWGP 112

QY 120 GTMVTYSS 127
 DB 113 GTPVTYSS 120

RESULT 7
 ID LV4C HUMAN STANDARD; PRT; 107 AA.
 AC P01717;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-IV region H11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE
 RP MEDLINE=78187276; PubMed=418804;
 RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
 RT "Amino acid sequence of the variable region of the light (lambda)
 RT chain from human myeloma cryoimmunoglobulin IgG H11.";
 RL Biochemistry 17:1718-1723 (1978).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
 CC IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
 CC 155-118 (H11 NUMBERING) INSTEAD OF VIL.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC PIR; A01983; L4H0HL.
 DR HSSP; P80748; 21OI.
 DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 97
 FT NON TER 107 107
 FT SEQUENCE 107 AA; 11517 MW; ASCBAFEDCC590A CRC64;

Query Match 30.9%; Score 418; DB 1; Length 107;
 Best Local Similarity 74.5%; Pred. No. 7.9e-24;
 Matches 79; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 148 SYELMQLPSVSVSPQQTASITCSGDLGDKACWYQKPRSPVLVYIGDNKRPSGIPER 207
 DB 1 SYELMQLPSVSVSPQQTARITCSANALPNOYAYVYQKPRAPVWYIKDTORPSGIPER 60
 QY 208 FSGNSGNTATLTITSGTQAMDEADYCOAMDSTAVFGTGTKLTVL 253
 DB 61 FSSSTIGTTLTITSGVAEDYCOAMDNSASIFGGTGTKLTVL 106

RESULT 8
 ID LV4D_HUMAN STANDARD; PRT; 106 AA.
 AC P01718;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-IV region Kern.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=71150336; PubMed=5549568;
 RA Ponsing H., Hese M., Hilschmann N.;
 RT "Structural rule of antibodies. Primary structure of a monoclonal
 RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
 RT protein Kern). V. The complete amino acid sequence and its genetic
 RT interpretation.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ MARKER.
 CC -1- SIMILARITY: This is a Bence-Jones protein.
 DR PIR; A01984; L4HUKN.
 DR HSSP; P80748; ZLOI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 102
 FT DISULFID 21 86
 FT NON TER 106 106
 FT SEQUENCE 106 AA; 11277 MW; CBB4A05B9CB43CB CRC64;

Query Match 29.8%; Score 403; DB 1; Length 106;
 Best Local Similarity 72.4%; Pred. No. 9.4e-23;
 Matches 76; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 149 YELMQLPSVSVSPQQTASITCSGDLGDKACWYQKPRSPVLVYIGDNKRPSGIPER 208
 DB 1 YALMQLPSVSVSPQQTAVITCSGDLGDKACWYQKPRSPVLVYIGDNKRPSGIPER 60

QY 209 SGNNSGNTATLTITSGTQAMDEADYCOAMDSTAVFGTGTKLTVL 253
 DB 61 SSSSGATATLTITSGAVDEADYCOAMDSTAVFGTGTKLTVL 105

RESULT 9
 ID HV2H_HUMAN STANDARD; PRT; 147 AA.
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region SESS precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=84298107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RT "Rearranged immunoglobulin heavy chain variable region (VH)
 RT pseudogene that deletes the second complementarity-determining
 RT region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 DR PIR; A02090; G2HUCS.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.

FT CHAIN 1 19
 FT SIGNAL 1 19
 FT FT 20 147
 FT DOMAIN 20 118
 FT DOMAIN 119 132
 FT DOMAIN 133 147
 FT NON TER 147 147
 FT SEQUENCE 147 AA; 16323 MW; FCB3D3D00F6666 CRC64;

Query Match 29.5%; Score 398.5; DB 1; Length 147;
 Best Local Similarity 63.9%; Pred. No. 2.8e-22;
 Matches 78; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLTCTISGFSLSGVSVMIRPGKALEWLASINWDDKC 60
 DB 20 QVTLKESGPTLVKPTQTLTCTISGFSLSGVSVMIRPGKALEWLASINWDDKC 79
 QY 61 YPSLSKSLTLTKTPKQVVLAMSNDDPATATYSCA-LDMPPHSGPQSPFASVWCP 119
 DB 80 YPSLSKSLTLTKTPKQVVLAMSNDDPATATYSCA-LDMPPHSGPQSPFASVWCP 139
 QY 120 GT 121
 DB 140 GT 141

RESULT 10
 ID LV5A_HUMAN STANDARD; PRT; 108 AA.
 AC P01719;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-V region DEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;


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RN [1]
RP MEDLINE=75112179; PubMed=4452363;
RX Eulitz M.;
RT "A new subgroup of human L-chains of the lambda-type. Primary
  structure of Bence-Jones protein DEL."
RL Eur. J. Biochem. 50:49-69(1974).
CC -1- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
  CHAIN SUBGROUP V.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01985; LSHUDL.
DR HSSP; P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE: 1.
KM Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 97
FT NON TER 108
SQ SEQUENCE 108 AA; 11342 MW; B8E8ED9C09CE451 CRC64;

Query Match 29.1%; Score 393; DB 1; Length 108;
Best Local Similarity 71.0%; Pred. No. 5e-22;
Matches 76; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

QY 149 YELMOLPSVSVSGPQTASITCGSDNIGDKYACWQOKPGRSPVLYVYGNKRPSSGIPERF 208
DB 1 YVLSQPPSVSVAGETARLTICGNDIGSGSVHMYQOKPQAPVLYVFPDRDRPSGIPERF 60

QY 209 SGNNSGNTATLTITSGTQAMDEADYYCQAMDST--AVFGTGTLYL 253
DB 61 SGNNSGNTATLTITSGTQAMDEADYYCEVDDRTAHVVFGGTLYL 107

RESULT 11
LV3B HUMAN STANDARD; PRT; 111 AA.
AC P80748;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-III region LOI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
RC TISSUE=urine;
RX MEDLINE=99441384; PubMed=10510403;
RT "Neprilysin, a membrane-associated metalloprotease, is a unique human
  minitautocatalytic lambda light chain dimer: a unique human
  J. Immunol. 163:4590-4596(1999).
CC -1- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
  TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
CC -1- SUBUNIT: Homodimer.
CC -1- DISEASE: The blocking of factor H by LOI protein leads to the
  development of membranoproliferative glomerulonephritis (MPGN).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PDB; 2LOI; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS50835; IG LIKE: 1.
KM Immunoglobulin V region; 3d-structure.
FT DOMAIN 1 97
FT BINDING 15 15 SCR3.
FT BINDING 25 25 SCR3.
FT BINDING 29 29 SCR3.
FT BINDING 48 51 SCR3.
FT BINDING 94 94 SCR3.
FT DISULFID 21 86 BY SIMILARITY.
FT STRAND 4 4
FT STRAND 8 8
FT TURN 13 14
FT STRAND 16 22
FT STRAND 32 37
FT TURN 38 40
FT STRAND 41 46
FT TURN 49 50
FT STRAND 54 54
FT TURN 55 55
FT TURN 58 59
FT STRAND 60 61
FT STRAND 64 65
FT TURN 66 67
FT STRAND 68 74
FT TURN 78 79
FT STRAND 82 88
FT TURN 91 93
FT STRAND 97 98
FT STRAND 102 104
FT TURN 107 108
FT NON TER 111
SQ SEQUENCE 111 AA; 11935 MW; 69498BEBFDE82053 CRC64;

Query Match 28.8%; Score 389; DB 1; Length 111;
Best Local Similarity 70.1%; Pred. No. 1e-21;
Matches 75; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 149 YELMOLPSVSVSGPQTASITCGSDNIGDKYACWQOKPGRSPVLYVYGNKRPSSGIPERF 208
DB 1 YVLSQPPSVSVAGETARLTICGNDIGSGSVHMYQOKPQAPVLYVFPDRDRPSGIPERF 60

QY 209 SGNNSGNTATLTITSGTQAMDEADYYCQAMDST--AVFGTGTLYL 253
DB 61 SGNNSGNTATLTITSGTQAMDEADYYCQAMDSEHVFPGGTLTYL 107

RESULT 12
HV2C HUMAN STANDARD; PRT; 119 AA.
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DAW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RT "The amino acid sequences of the Pd fragments of two human gamma-1
  heavy chains."
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
  SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02091; GIHDM.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

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DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Immunoglobulin V region; Pyrrilidone carboxylic acid.
 FT DOMAIN 1 113
 FT MOD_RES 1 113
 FT NON_TER 1 113
 FT SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 28.4%; Score 384; DB 1; Length 119;
 Best Local Similarity 62.2%; Pred. No. 2.5e-21;
 Matches 79; Conservative 12; Mismatches 28; Indels 8; Gaps 2;

QY 1 QVTLKSGPTLVKPTQTLTCTTSGFSLSTSGVSGVIRPPGKALEWLASINWDDKX 60
 DB 1 QVTLKSGPALVRPTQTLTCTTSGFSLSTSGVSGVIRPPGKALEWLASINWDDKX 60
 QY 61 YSPSLKSLRTITKDPKPKQVVLAMSNMPPADPATYSCALDMPHDSGQSFDSADVWGP 120
 DB 61 YGASLETRILAVSKDTSKNQVVLAMSNMVPQGDITATYCA-----RSCGSGQYF---DIWGGG 112
 QY 121 TMTVTSS 127
 DB 113 ILVTYSS 119

RESULT 13
 ID HV2A_HUMAN STANDARD; PRT; 126 AA.
 AC P01814;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region OU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP NCBI_TaxId=9606;
 RX MEDLINE=74005511; PubMed=4742735;
 RA Putnam F.W., Florent G., Paul C., Shioda T., Shliman A.;
 RT "Complete amino acid sequence of the mu heavy chain of a human Igm
 immunoglobulin.";
 RL Science 182:287-291(1973).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02088; MHUOU.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-LIKE.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Immunoglobulin V region; Pyrrilidone carboxylic acid.
 FT DOMAIN 1 113
 FT MOD_RES 1 113
 FT NON_TER 1 113
 FT SEQUENCE 126 AA; 14276 MW; A85C0B0DABC296F CRC64;

Query Match 27.4%; Score 369.5; DB 1; Length 126;
 Best Local Similarity 62.5%; Pred. No. 2.9e-20;
 Matches 80; Conservative 15; Mismatches 30; Indels 3; Gaps 3;

QY 1 QVTLKSGPTLVKPTQTLTCTTSGFSLSTSGVSGVIRPPGKALEWLASINWDDKX 60
 DB 1 QVTLKSGPALVRPTQTLTCTTSGFSLSTSGVSGVIRPPGKALEWLASINWDDKX 60

DB 1 QVTLKSGPALVRKQPTLTCTTSGFSLSTSGVSGVIRPPGKALEWLASIRB-BBDKF 59
 QY 61 Y-SPSLKSLRTITKDPKPKQVVLAMSNMPPADPATYSCALDMPHDSGQSFDSADVWGP 119
 DB 60 YWSTSLRLRLSISKDSKNQVVLAMSNMVPQGDITATYCAKAVNSWAG-YYYYYNDVWVK 118
 QY 120 GTMTVTSS 127
 DB 119 GTVTYSS 126

RESULT 14
 ID LV7A_HUMAN STANDARD; PRT; 108 AA.
 AC P01714;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-II region SH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP NCBI_TaxId=9606;
 RX MEDLINE=7016723; PubMed=4909564;
 RA Titani K., Wikler M., Shioda T., Putnam F.W.;
 RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
 complete amino acid sequence and the location of the disulfide
 bridges.";
 RL J. Biol. Chem. 245:2171-2176(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A01980; L3HUSH.
 DR HSSP; P80748; 2LOI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-LIKE.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 97
 FT DISULFID 21 97
 FT NON_TER 108
 FT SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 26.0%; Score 351; DB 1; Length 108;
 Best Local Similarity 66.0%; Pred. No. 5.2e-19;
 Matches 70; Conservative 14; Mismatches 20; Indels 2; Gaps 1;

QY 150 ELMOLPSYSVSPQGTASITSGNLDKRYACWYQKRGSPVLYVYGDNKRPSGIPERFS 209
 DB 2 ELTDPAVSVALGQTVARITCGDGLRGYDAWYQKRGAPLVLVYGRNNRPSGIPERFS 61
 QY 210 GSNSTATTLLISGTQAMDEADYVCOAMDT--TAVFGTGLTVL 253
 DB 62 GSSSGHTASLTITGAQADEADYVCSNRSGSHVLPFGGKTLTVL 107

RESULT 15
 ID LV7A_HUMAN STANDARD; PRT; 111 AA.
 AC P01720;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-VII region MOT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=61122740; PubMed=6780787;
 RA Kojima M., Odani S., Ikenaka T.;
 RT "Amino acid sequence of the lambda type light chain of a human IgG1
 myeloma protein (MOP) with unusual antigenicity: a possible new
 RT subgroup of lambda chain having a unique N-terminal sequence.";
 RL Mol. Immunol. 17:1407-1414(1980).
 CC -1- MISCELLANEOUS: THIS SEQUENCE REPRESENTS A NEW LAMBDA CHAIN
 SUBGROUP. IT HAS AN AMINO-TERMINAL EXTENSION OF THREE RESIDUES
 CC COMPARED WITH OTHER HUMAN LAMBDA CHAINS.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
 CC MARKERS.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC -1- SIMILARITY: Contains 1 Immunoglobulin-like domain.
 DR HSP; P80748; 2LOI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_V.
 DR DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PSS0835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1..105 IG-LIKE.
 FT NON_TER 111..111
 SQ SEQUENCE 111 AA; 11942 MW; 140A28A2F86A6911 CRC64;

Query Match 26.0%; Score 351; DB 1; Length 111;
 Best Local Similarity 61.7%; Pred. No. 5,4e-19;
 Matches 66; Conservative 17; Mismatches 22; Indels 2; Gaps 1;
 QY 149 YELMQLPSVSVSPGQTASITCSGDNLDKXYACWYQKPGSRPVLVIYGDNKRPSGIPEPF 208
 DB 4 YELTQPPSVSLAGQTMITCEGNDIGERSVHTYQKPGQAPVPIYDDADRPSSGVPAFP 63
 QY 209 SGNSSGNTATLTITSGTQAMDEADYCCQAMDST--AVFGTGTKLTVL 253
 DB 64 SGNSSGNSAILTINRVEAGDEADYFCQSDNGSYEVVFGTGTWTVL 110

Search completed: May 13, 2004, 15:02:03
 Job time : 7.133 secs

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SEQUENCE 243 AA; 25976 MW; BEFF64D2DC64F76 CRC64;
Query Match 33.6%; Score 454; DB 11; Length 243;
Best Local Similarity 40.5%; Pred. No. 6.5e-29;
Matches 106; Conservative 42; Mismatches 78; Indels 36; Gaps 10;
QY 1 QVTLKSGPTLVPTOTLTCTLSGFSLSGVSVMIRQPPKALEWLASI-----53
1 QVLOQSGSELVPGASVSKSCASGYTFTTMMH--WVQRRHGGLEWGNIPSGIT 58
QY 54 NNRDDKCYSPSLKRLTITKOTPRNOVVLAMSNMNPADTATYSCALDMPHDSGPOSFDA 113
59 N-----YDEKFNKXGLITVDITSSSTAYMHLSSLASBDSAIVYCA-----RGRG 102
QY 114 SDVWPGTWTVTSSGGSGSGSGSGSSSYELMO-LPSVSPGQTASITC-SG 171
103 LDVWAGATLTIVS-----SGSGSGSGSGSGSGSDIOMTQSSSFVSLGDRVLTTCAS 157
QY 172 DNLGDKYACWYQKPRSPVLVIYGNKRPSPGIPERFSGSGSGNTATLTISGTQAMDEAD 231
158 EDIYNRLA-WYQKPGNAPRLILSGATSLSTGYVPSRFSGSGSKDYTLSTSLQTDVAT 216
QY 232 YVCOA-WDTSTAVFGTGTLTIV 252
217 YVCOYWTSTRT--FGGGTKLEI 236
Db

RESULT 5

Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MKP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AKK43733.1; -.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
Query Match 31.1%; Score 419.5; DB 11; Length 218;
Best Local Similarity 41.9%; Pred. No. 3.5e-26;
Matches 95; Conservative 37; Mismatches 74; Indels 21; Gaps 7;
QY 1 QVTLKSGPTLVPTOTLTCTLSGFSLSGVSVMIRQPPKALEWLASIINMND-K 59
3 QVLOQSGSELVPGASVSKSCASGYTFTTMMH--WVQRRHGGLEWGNIPSGIT 60
Db

QY 60 CYSPLSKRLTITKOTPRKQVVLAMSNMNPADTATYSCALDMPHDSGPOSFADWGP 119
61 KVAEERKGFAPSLERISASTAVILQISLNKEDPATYFCM--RMDYGG-----PAYWQ 112
QY 120 GTMTVYSSGGSGSGSGSGSGSGSGSSSYELMQLP-SVSPGQTASITC---SGDL 174
113 GTTIVTS-----SGGGSGSGSGSGSGSDIVLTQSPASLAVSIAGQRTISCRASBSVDNI 167
QY 175 GPKYACWYQKPRSPVLVIYGNKRPSPGIPERFSGSGSGNTATLTIT 221
168 GISFMNWFQKPGQPKLITVAASKGSGVPAGLLASGSGTDFSLNI 214
Db

RESULT 6

Q8TBC9 PRELIMINARY; PRT; 233 AA.
AC Q8TBC9; 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1; -.
DR PIR; S12442; S12442.
DR PIR; S30526; S30526.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PSS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD64FD92 CRC64;
Query Match 30.9%; Score 417; DB 4; Length 233;
Best Local Similarity 75.0%; Pred. No. 6e-26;
Matches 84; Conservative 8; Mismatches 18; Indels 2; Gaps 1;
QY 144 GGGSYELMQLPVSVPSPGQTASITSGDNLDKVCWYQKPRSPVLVIYGNKRPSPG 203
16 GSEASVELTQPPSVSVSPGQTARITCSGDLAKQYAVWYQKPGCAPVLVIYGNKRPSPG 75
QY 204 IPRFSGSGSGNTATLTISGTQAMDEADYVCGAMDSTA--VFGTGTLTIVL 253
76 IPRFSGSGSGTTLTITISGVAEDBADYVCGASDSSGTWVFGGGTKLTIVL 127
Db

RESULT 7

Q8N355 PRELIMINARY; PRT; 234 AA.
AC Q8N355; 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
QY 1 QVTLKSGPTLVPTOTLTCTLSGFSLSGVSVMIRQPPKALEWLASIINMND-K 59
3 QVLOQSGSELVPGASVSKSCASGYTFTTMMH--WVQRRHGGLEWGNIPSGIT 60
Db

DR EMBL; BC028090; AAH28090.1; --
 DR PIR; S12441; S12441.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match 30.4%; Score 410.5; DB 4; Length 234;
 Best Local Similarity 70.8%; Pred. No. 2e-25;
 Matches 80; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 144 GGGSSYELMQLPSVSVSPQQTASITGSGDNLGDKYACMYOQKGRSPVLYIGDNKRPSG 203
 DB 16 GSVTVSLTPSPSVAVAGQTARITCGNNIGSKSVMYOQKFGQAPVLYVDDSDRPSG 75
 QY 204 IPRFSGNSGNTATLTITSGTQAMDEADYCCOAMDIST--AVFGTGTXTLTVL 253
 DB 76 IPRFSGNSGNTATLTITSRVADGDEADYCCOAMDSSDHPVFGGTXTLTVL 128

RESULT 8

OS11US PRELIMINARY; PRT; 118 AA.
 AC OS11US.
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Anti-human Fc gamma receptor III 368 gamma heavy chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Brumke J., Valerius T., Repp R., Fey G.H.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Receptor.
 KW Receptor.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 118 AA; 12979 MW; F57BB0703742E99 CRC64;

Query Match 28.9%; Score 390.5; DB 11; Length 118;
 Best Local Similarity 61.4%; Pred. No. 3.7e-24;
 Matches 78; Conservative 17; Mismatches 23; Indels 9; Gaps 2;

QY 1 QVTLKSGTTLVKTPTQTLTLCTLTGSLSTSGVSMINQPGKALEMTASINWDDKC 60
 DB 1 QVTLKSGGGLIQPQTLSTLCSPGSLRTSGMGVMIQPGKGLMTLMIHIMWDDDKR 60
 QY 61 YSPSLKSLITTKDPPKQVVLAMNMDPADTATYSCALMDPHDSGPOSFDASDWMGPG 120
 DB 61 YNPALKSLITISKDTSSNQVFLKIASVYDTADTATYCA-----QNPAMF---AYMGQG 111

QY 121 TWTVSS 127
 DB 112 TLTVSA 118

RESULT 9

OSN5F4 PRELIMINARY; PRT; 233 AA.
 AC OSN5F4.
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032452; AAH32452.1; --
 DR PIR; S12441; S12441.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 233 AA; 24961 MW; F092CFB6AA6E3A9A CRC64;

Query Match 28.8%; Score 389; DB 4; Length 233;
 Best Local Similarity 72.5%; Pred. No. 1.1e-23;
 Matches 79; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 147 SSYELMQLPSVSVSPQQTASITGSGDNLGDKYACMYOQKGRSPVLYIGDNKRPSG 206
 DB 19 ASVELTOPSPSVSVSPQQTARITCGDLPKRYAVMYOQKSGRTFVLYIDTFRPSG 78
 QY 207 RFGSSGNTATLTITSGTQAMDEADYCCOAMDIST--VFGTGTXTLTVL 253
 DB 79 RFGSSGNTATLTITSGADEVADYCCOAMDSSDHPVFGGTXTLTVL 127

RESULT 10

OS1082 PRELIMINARY; PRT; 107 AA.
 AC OS1082.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berny S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RT Clin. Immunol. Immunopathol. 87:184-192 (1998).
 RL EMBL; AF035032; AAD56268.1; --

DR HSSP; P01703; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11445 MW; 52FOCC1AB26821DC CRC64;

Query Match 28.3%; Score 382.5; DB 4; Length 107;
Best Local Similarity 72.0%; Pred. No. 1.4e-23;
Matches 77; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 148 SYELMQLPSVSVPGQTASTICSGDNLGDKYACQYQKRGSRPVLYIGDNKRPSGIPER 207
DB 1 SYELTPSSVSVPGQTARTICSGDLAKRYARFPQKPGQADILVIFKTERPSGIPER 60
QY 208 FSGNSGNTATLTISGTOAMDEADYYC-QAMDSTAFTGTGTLTVL 253
DB 61 FSGSSGTTVTLTISGAQVEDADYYCYASNDNGRVFGGTLTVL 107

RESULT 11
043234 PRELIMINARY; PRT; 97 AA.
AC 043234;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DS Rheumatoid factor RF-ET13 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Borretzen M., Natvig J.B., Thompson K.M.;
RT "Heterogenous RF structures between and within healthy individuals are
RT not related to HLA DRB1*0401.";
RL Mol. Immunol. 0:0-0(1997).
DR EMBL; AF035802; AAB88534.1; -.
DR HSSP; P01789; IMCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;

Query Match 27.8%; Score 376; DB 4; Length 97;
Best Local Similarity 76.0%; Pred. No. 4.3e-23;
Matches 73; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 3 TLKESGPTLVKPTQTLTTLTSGFISISGVGMIRPPGALMLASINNDKCYIS 62
DB 1 TLKESPPALVKPTETLTCTVSGFISINRMGVSMIRPPGALVEMLAHIFANDEKSYS 60
QY 63 PSLSKRLITTKDPRKQOVVLAMNMDPADATATSCA 98
DB 61 TSLKSLITLTKDTSKQOVVLAMNMDPADATATYCA 96

RESULT 12
Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypoetical protein (Fragment).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Lymphocytes;
RA Hermann A.;
RT "Autoimmunity.";
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; LA3092; AAA69746.2; -.
DR HSSP; P01709; 2MCG.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 27.7%; Score 374; DB 4; Length 107;
Best Local Similarity 70.8%; Pred. No. 7e-23;
Matches 75; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 150 ELMQLPSVSVPGQTASTICSGDNLGDKYACQYQKRGSRPVLYIGDNKRPSGIPERPS 209
DB 1 ELTQDPVSVVAGQYTRITCGQDSLSYASVYQKPGQAPVLYIGKNRPSGIPDRS 60
QY 210 GSNAGNTATLTISGTOAMDEADYYCOAMDTS--TAVFTGTGTLTVL 253
DB 61 GSSSGNTATLTISGAQVEDADYYCNSRDSGNHNVFGGTLTVL 106

RESULT 13
Q722U7 PRELIMINARY; PRT; 234 AA.
AC Q722U7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.T., Utsid T.B., Toshlyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalski U., Smailus D.E., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RP Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC054883; AAH54883.1; --
KM Hypothetical protein.
SQ SSEQUENCE 234 AA; 25015 MW; 9A5723ABC393A06F CRC64;
Query Match 27.3%; Score 368.5; DB 4; Length 234;
Best Local Similarity 65.5%; Pred. No. 5e-22;
Matches 72; Conservative 12; Mismatches 23; Indels 3; Gaps 1;
QY 147 SSYELMLPVSVPSPGQTASITCGDNLGDKYACWYQKRGSPVLVIYGDNRKPSGIPR 206
DB 19 ASYVLTPPSVSAVPAQTARITCGADNIGKASVHWYQKTDQAPVLVHDDNRPSPGIPR 78
QY 207 RFGSGNSGNTATLTISGTOAMDADYCCQAMDSTA--VFGTGTLTVL 253
DB 79 RFGSGNSGNTATLTISGTPDEADYFCQVWDSGGQJLWFGGTLTVL 128
RESULT 14
Q96169 PRELIMINARY; PRT; 233 AA.
AC Q96169;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RL Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007782; AAH07782.1; --
DR PIR; S12440; S12440.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004812; F:RNA ligase activity; IEA.
DR GO; GO:0006418; P:amino acid activation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR001412; CRNA-synt_1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SSEQUENCE 233 AA; 24802 MW; C694F8397827650B CRC64;
Query Match 26.1%; Score 353; DB 4; Length 233;
Best Local Similarity 60.7%; Pred. No. 8.9e-21;
Matches 68; Conservative 15; Mismatches 27; Indels 2; Gaps 1;
QY 144 GGGSSYELMLPVSVPSPGQTASITCGDNLGDKYACWYQKRGSPVLVIYGDNRKPSG 203
DB 16 GGGTSSYVLTPPSVSAVPAQTARITCGGNSLGSVHWYQKTDQAPVLVYENKERKPSG 75
QY 204 IPRFSGNSGNTATLTISGTOAMDADYCCQAMDSTA--VFGTGTLTVL 253
DB 76 IPRFSGNSGNTATLTISGTPDEADYFCQVWDTTSQOYVFGTGTQVTVL 127
RESULT 15
Q72374 PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN DKFZp686C02218.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Wewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; --
KM Hypothetical protein.
FT NON TER 1
SQ SSEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
Query Match 25.6%; Score 346; DB 4; Length 492;
Best Local Similarity 38.1%; Pred. No. 8.1e-20;
Matches 91; Conservative 26; Mismatches 84; Indels 38; Gaps 6;
QY 1 QYTLKESGTLVKEPTQTLTLTCTLSGFSISTGVSVMTRPPGKALEWIASINWDDKC 60
DB 32 QQLQDSGGLVKEPTSLTCTVSGSVSNENYMGWIRPPGKLEWISIVYENYTY 91
QY 61 YSPSLKSRLLTIKDPKQVVLAMGNMPPADATYSCALDMPHDSGQSPFASDVMGPG 120
DB 92 YSPSLKSRLLTIKDPKQVVLAMGNMPPADATYSCALDMPHDSGQSPFASDVMGPG 145
QY 121 TWYTVSSGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG 180
DB 146 TLVTVSSASP-----TSPYVFPJSLDSTPDGIVV---VAC 178
QY 181 WYQKRGSPVLVIY---GDNRKPSGIP--RFGSGNSGNTATLTISGTOAMDADYCC 234
DB 179 LVQGFPPQEPFLSVTSSGQNTATNPPSPQASGDLYTTSQTLTPATQCCKSVTC 237

Search completed: May 13, 2004, 15:06:55
Job time : 36.0199 secs

PT Vaccines against conformation-dependent or non-peptide antigens, based on
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
PT vaccines.

PS Disclosure; Page 13; 36pp; German.

CC This invention describes a novel vaccine (V1) against conformation-
CC dependent antigens (CDA) comprising DNA (1) and/or an antibody, or
CC peptide which immunologically imitates CDA, is new. (1) encodes a region
CC of an antidiotytic antibody (Ab2) or another peptide which: (a)
CC specifically binds to the binding site of an antibody (Ab1) or an antigen
CC binding molecule; and (b) immunologically mimics the initial antigen. The
CC epitope is partially or completely conformation-dependent, and has an
CC immunogenic structure defined by a specific spatial conformation of amino
CC acids. (1) is used in the form of linear or circular naked DNA and/or
CC with a viral vector and/or adjuvants. The products of the invention have
CC cytostatic, virucidal, antibacterial and antiparasitic. The invention
CC also describes (1) a corresponding vaccine (V2) against antigens which
CC are not proteins or peptides, as defined above but which have epitopes
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
CC human antidiotytic antibody fragments against the MUC1-conformation
CC epitope having one of 31 approximately 60 residue amino acids sequences,
CC all fully defined in the specification; (4) MUC1-conformation epitope
CC mimics having one of 16-9-17 residue amino acid sequences, all fully in
CC the specification; (5) antidiotytic antibody fragments against the TF
CC antigen having one of 24 approximately 200 residue amino acid sequences,
CC fully defined in the specification; (6) TF carbohydrate epitope mimics
CC having one of 25-7-13 residue amino acid sequences, all fully defined in
CC the specification; and (7) DNA sequences encoding the fragments and
CC derivatives defined in (3), 4, 5, or 6). (V1) and (V2) are used to treat
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
CC and parasites. The vaccines are effective in cases where vaccination has
CC previously not been possible

XX Sequence 240 AA;

Query Match 72.2%; Score 981.5; DB 4; Length 240;

Best Local Similarity 75.3%; Pred. No. 5.9e-52;

Matches 192; Conservative 15; Mismatches 27; Indels 21; Gaps 3;

QY 1 QVQLQESGGPVLPSEETLSITCTVSGSI-GHDYMSWIRPPGEGLEWIGFIFFDSTNY 59
DB 1 QVQLQESGGPVLPSEETLSITCTVSGSISSSNMWVWVPPKGLGEMIGEIHSGSTNY 60
QY 60 NPSLNGRVITSLDTSKQQLSLRTSYTADTAVYFCARLKGAWLSEPPYFSGDKDWG 119
DB 61 NPSLNGRVITSLDTSKQQLSLRTSYTADTAVYFCARLKGAWLSEPPYFSGDKDWG 105
QY 120 OGTTVVPSSGGSGSGSGSGSGSGSGSMFLTOPSASGTPGQSVISCSGSSSDIGS 179
DB 106 OGTLTVV-----SSGGSGSGSGSGSGSGSALQSVLTQPPSASGTPGQSVISCSGSSSDIGS 160
QY 180 NTVNMTQQLPGTAPKLLIYSNNRPPSGVDPDRFSGFSGTSSASIVISGLSEDEADYYCA 239
DB 161 NTVNMTQQLPGTAPKLLIYSNNRPPSGVDPDRFSGFSGTSSASIVISGLSEDEADYYCA 220
QY 240 WDESLNGVVFSGGPR 254
DB 221 WDSLRLVFGGGTK 235

RESULT 4

AAE36248 standard; protein; 244 AA.

XX AAE36248;

XX 26-JUN-2003 (first entry)

XX TRAIL receptor protein binding scfv protein, T1014A02.

DE TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;
XX hyperproliferative disorder; neurodegenerative disorder; immune disorder;
KM

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;
KW rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;
KW biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;
KW glomerulonephritis; immune deficiency syndrome; myasthenia gravis;
KW polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;
KW infectious disease; acquired immunodeficiency syndrome; viral infection;
KW AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;
KW ischaemic injury; myocardial infarction; reperfusion injury; cachexia;
KW anorexia; stroke; cardiovascular disorder; peripheral artery disease;
KW limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;
KW ocular disorder; wound healing; angiogenesis; transplantation.

XX Unidentified.

OS	Key	Location/Qualifiers
XX	Domain	1..118
XX	Region	/note="VH domain"
XX	Region	26..35
XX	Region	/note="VH domain complementarity determining region 1 (CDR1)"
XX	Region	50..65
XX	Region	/note="VH domain complementarity determining region 2 (CDR2)"
XX	Region	98..105
XX	Region	/note="VH domain complementarity determining region 3 (CDR3)"
XX	Domain	134..244
XX	Region	/note="VL domain"
XX	Region	156..168
XX	Region	/note="VL domain complementarity determining region 1 (CDR1)"
XX	Region	184..190
XX	Region	/note="VL domain complementarity determining region 2 (CDR2)"
XX	Region	223..233
XX	Region	/note="VL domain complementarity determining region 3 (CDR3)"
XX	WO200297033-A2.	
XX	05-DEC-2002.	
XX	07-MAY-2002; 2002WO-US014268.	
XX	25-MAY-2001; 2001US-0293473P.	
XX	04-JUN-2001; 2001US-0294981P.	
XX	02-AUG-2001; 2001US-0309176P.	
XX	21-SEP-2001; 2001US-0323807P.	
XX	09-OCT-2001; 2001US-0327364P.	
XX	07-NOV-2001; 2001US-0331044P.	
XX	14-NOV-2001; 2001US-0331310P.	
XX	20-DEC-2001; 2001US-0341237P.	
XX	05-APR-2002; 2002US-0369860P.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TV;	
XX	WPI; 2003-140454/13.	
XX	N-PSDB; AAD54849.	
XX	Novel antibody useful for treating cancers and other hyperproliferative	
XX	disorders, immunospecifically binds to TRAIL receptor and comprises	
XX	variable heavy or light chain complementarity determining regions.	
XX	Claim 1; Page 285-286; 301pp; English.	
XX	The present invention relates to novel antibodies that immunospecifically	
XX	bind to TRAIL receptor (TR4). Sequences of the invention are useful for	
XX	treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,	
XX	pancreatic, lung, gastrointestinal or central nervous system cancer e.g.	
XX	medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in	

RESULT 6
ABP45631
ID ABP45631 standard; protein; 255 AA.
XX AC ABP45631;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scfv SEQ ID 1642.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN MO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2362-2363; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 255 AA;
XX
Query Match 71.7%; Score 975; DB 5; Length 255;
Best Local Similarity 74.5%; Pred. No. 1.5e-51;
Matches 190; Conservative 23; Mismatches 36; Indels 6; Gaps 2;
XX
QY 1 QVQLQSSGGGLVPSSTLSITCVSGSGSIQGHYWMIRPPRGLEWIGFIFPDGSTNNY 60
DB 1 QVQLQDMGAGLKPSSTLSITCAVVGSGSYGYWMSIRPSGKLEWIEIHNGGSTNNY 60
QY 61 PSINGRVTISLPTSKNQLSLRLSVTAADTAAYVFCARLKGAW-ILSEPPYFSSDGDWVG 119

DB 61 PSILKSRVTISVDASKNQFSLKLSVTAADTAAYVCARERSYDILTGVPKRYGMDWVG 120
QY 120 QGTVTVVPSGGGGSGGGGGSGGGGSGNFMULTOPPSASGTPGQVVISCSGSSSDIGS 179
DB 121 RGTLLVTV-----SSGGGSGGGGGSGGGGSSQSVLTOPPSASGTPGQVTVISCSGSSSDIGS 175
QY 180 NTVMNMYQQLPGTAPKLLIYSNNQRPSPGVDPDRSPGSPKSGTSASLVISGLQSEADYYCA 239
DB 176 NTVMNMYQRLPGAAPOLLITNNDRPSGIRPDRSPGSGSGTSGLSVISGLQSEADYYCAS 235
QY 240 WDESLNGVVFGGGPR 254
DB 236 WDSLNGRVFGGGTK 250
XX
RESULT 7
AAB46060
ID AAB46060 standard; peptide; 244 AA.
XX
AC AAB46060;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human TF anti-Idiotypic antibody fragment ZA14.
XX
KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
KW antidiabetic antibody; cytostatic; virucidal; antibacterial; TF antigen;
KW antiparasitic; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200073430-A2.
XX
PD 07-DEC-2000.
XX
PF 29-MAY-2000; 2000WO-DE001809.
XX
PR 27-MAY-1999; 99DE-01024405.
PR 09-SEP-1999; 99DE-01043016.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Goletz S, Karsten U;
XX
XX WPI; 2001-049937/06.
XX
PT Vaccines against conformation-dependent or non-peptide antigens, based on
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
PT vaccines.
XX
PS Disclosure; Page 14; 36pp; German.
XX
CC This invention describes a novel vaccine (V1) against conformation-
CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or
CC peptide which immunologically imitates CDA, is new. (I) encodes a region
CC of an antidiabetic antibody (Ab2) or another peptide which: (a)
CC specifically binds to the binding site of an antibody (Ab1) or an antigen
CC binding molecule; and (b) immunologically mimics the initial antigen. The
CC epitope is partially or completely conformation-dependent, and has an
CC immunogenic structure defined by a specific spatial conformation of amino
CC acids. (I) is used in the form of linear or circular naked DNA and/or
CC with a viral vector and/or adjuvants. The products of the invention have
CC cytostatic, virucidal, antibacterial, and antiparasitic. The invention
CC also describes (1) a corresponding vaccine (V2) against antigens which
CC are not proteins or peptides, as defined above but which have epitopes
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
CC human antidiabetic antibody fragments against the MUC1-conformation
CC epitope having one of 31 approximately 60 residue amino acids sequences,
CC all fully defined in the specification; (4) MUC1-conformation epitope
CC mimics having one of 16 9-17 residue amino acid sequences, all fully in
CC the specification; (5) antidiabetic antibody fragments against the TF
CC antigen having one of 24 approximately 200 residue amino acid sequences,

CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25-7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3), (4), (5), or (6). (VI) and (VII) are used to treat
 CC cancer and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible

Sequence 244 AA:

Query Match 71.7%; Score 974.5; DB 4; Length 244;
 Best Local Similarity 74.9%; Pred. No. 1.6e-51;
 Matches 191; Conservative 17; Mismatches 30; Indels 17; Gaps 4;

QY 1 QVLOESGPGVLVPSSETLSLTCTVSGSGSI-GHDVMSWIRPPREGLEWIGFIFDGSITNN 59
 Db 1 QVLOESGPGVLVPSSETLSLTCTVSGSGSI-GHDVMSWIRPPREGLEWIGFIFDGSITNN 59
 QY 60 NSLNGRVITISLDTKNOULSLTSTVTAADTAAYVFCARLKGAWLSEPPYFSSDGMWVG 119
 Db 61 NSLNGRVITISLDTKNOULSLTSTVTAADTAAYVFCARLKGAWLSEPPYFSSDGMWVG 119
 QY 120 QCTTVTPPSGGSGSGSGSGSGSGSGSNFMLTOPPSASGTPGQVVISCSGSSSDIGS 179
 Db 110 QCTTVTPPSGGSGSGSGSGSGSGSGSNFMLTOPPSASGTPGQVVISCSGSSSDIGS 179
 QY 180 NTVMVYQQLPETAAPKLLIYSNNORPSGVDPDRFSGFSGTSASLVISGLQSEDEADYCA 239
 Db 165 NTVMVYQQLPETAAPKLLIYSNNORPSGVDPDRFSGFSGTSASLVISGLQSEDEADYCA 239
 QY 240 WDESLNGVPPGGGR 254
 Db 225 WDESLNGVPPGGGR 239

RESULT 8

AA21883
 ID AA21883 standard; protein; 244 AA.

AC AA21883;

DT 24-SEP-1999 (first entry)

DE Amino acid sequence of antibody BIOA8.

KM Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;
 KW diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy; BIOA8.

OS Homo sapiens.

Key Location/Qualifiers
 FT Misc-difference 201
 FT /label= unknown
 FT /note= "encoded by TST"

EP34953-A2.
 11-AUG-1999.

PD 01-DEC-1998; 98EP-00122546.

PR 03-DEC-1997; 97US-0067428P.

PA (BOE) BOEHRINGER MANNHEIM CORP.
 PI Winter GP, Mahoney W, Sawyer JR;
 XX WPI; 1999-432068/37.
 DR N-PSDB; AA86940.
 XX

PS New anti-complex antibody useful for diagnosing prostate cancer.
 Claim 28; Page 25-27; 42pp; English.

XX The invention relates to an antibody that binds a complex between
 CC prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an
 CC affinity for the complex which is at least 10 fold higher than the
 CC affinity for either PSA or ACT alone. The antibody is used in diagnostic
 CC assays to detect PSA-ACT in serum samples from patients. The levels of
 CC PSA-ACT complex increase in patients suffering from prostate cancer
 CC compared to the levels in patients with benign or no growth in the
 CC prostate. Therefore detection of PSA in complex with ACT is useful for
 CC the early detection of prostate tumours, by distinguishing between benign
 CC patients with prostate cancer, such as the disclosure of metastasis and
 CC the monitoring of the PSA levels after treatment. The antibodies may also
 CC be used in immunotherapy, affinity chromatography and isolation or
 CC purification of PSA-ACT, unlike prior art antibodies which bind to PSA-
 CC specific for PSA-ACT alone. Diagnostic assays using the antibody is
 CC more accurate in diagnosing prostate cancer as they only detect the
 CC intact complex of PSA-ACT. Sequences AA21880-884 represent specific
 CC examples of antibodies directed against PSA-ACT. The present sequence
 CC represents the amino acid sequence of antibody BIOA8

Sequence 244 AA:

Query Match 71.4%; Score 970.5; DB 2; Length 244;
 Best Local Similarity 74.8%; Pred. No. 2.0e-51;
 Matches 190; Conservative 14; Mismatches 33; Indels 17; Gaps 3;

QY 1 QVLOESGPGVLVPSSETLSLTCTVSGSGSI-GHDVMSWIRPPREGLEWIGFIFDGSITNN 60
 Db 3 QVLOESGPGVLVPSSETLSLTCTVSGSGSI-GHDVMSWIRPPREGLEWIGFIFDGSITNN 60
 QY 61 NSLNGRVITISLDTKNOULSLTSTVTAADTAAYVFCARLKGAWLSEPPYFSSDGMWVG 120
 Db 63 NSLNGRVITISLDTKNOULSLTSTVTAADTAAYVFCARLKGAWLSEPPYFSSDGMWVG 120
 QY 121 GTTYVTPPSGGSGSGSGSGSGSGSNFMLTOPPSASGTPGQVVISCSGSSSDIGS 180
 Db 111 GTTYVTPPSGGSGSGSGSGSGSGSNFMLTOPPSASGTPGQVVISCSGSSSDIGS 180
 QY 181 TVVMVYQQLPETAAPKLLIYSNNORPSGVDPDRFSGFSGTSASLVISGLQSEDEADYCA 240
 Db 166 TVVMVYQQLPETAAPKLLIYSNNORPSGVDPDRFSGFSGTSASLVISGLQSEDEADYCA 240
 QY 241 WDESLNGVPPGGGR 254
 Db 226 WDESLNGVPPGGGR 239

RESULT 9

ABP45983
 ID ABP45983 standard; protein; 252 AA.

AC ABP45983;

DT 19-AUG-2002 (first entry)

DE Human Bly6 binding scFv SEQ ID 1994.

KM Bly6; B lymphocyte stimulator; TNF superfamily; human; cytotoxic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

XX 10-JAN-2002.
 XX 15-JUN-2001; 2001WO-US019110.

DB 228 EADYCCASWDDSLNGRVFGGQTK 250

RESULT 12

ID ABP45499 standard; protein; 251 AA.

XX AC ABP45499;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1510.

XX KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumor necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2205-2206; 3148pp; English.

XX XX

CC This invention describes novel antibodies that immunospecifically bind to B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the tumor necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

XX SQ Sequence 251 AA;

XX

QY Query Match 70.6%; Score 959; DB 5; Length 251;

DB Best Local Similarity 74.6%; Pred. No. 1.4e-50;

Matches 101; Conservative 20; Mismatches 33; Indels 12; Gaps 4;

QY 1 QVQLQSGGPGGVVPSSETLSLTCTVSGSGSIGH--DYMSWIRQPPGSGLEWIGFIFFDGSIN 58

DB 1 QVQLQSGGPGGVVPSSETLSLTCTVSGSGFISRTSRYGMIRQPPGKLEWIGNIYYGKTY 60

QY 59 YNPSLNGRVTLISLDTSKNQLSLRTSVTAADTAVYFCARLKGAMLLSEPPYFSSDDMDVW 118

DB 61 YSPSLKSRVTIADTSKKNLSLSTSVTAADTAVYCAAGADLTGYFFYF-----DSW 115

QY 119 GGGTIVTVPSGGGSGGGSGGGGSGGGSNFMLTQPPASAGTQGVRSISGSGSSDID 178

DB 116 GRGTLVTVSSGGGSGGGSGGGGSGGGS----AQAVLTQPSASAGTQGVRSISGSGSSNIG 171

QY 179 SNTVAMVYQQLPQTAPKLLIYSNNQRPSPGVPPDRPSGKSTASALVTSGLQSEDEADYCA 238

DB 172 STTVAMVYQGVPPGTAPQLIYSNDRPSGVPPDRPSGKSTASALVTSGLQSEDEADYCA 231

QY 239 AWDESLNGVVPFGGPPR 254

DB 232 SWDDSPH-VVFGGQTK 246

RESULT 13

ID AAB46059

XX AAB46059 standard; peptide; 239 AA.

XX AC AAB46059;

XX DT 23-MAR-2001 (first entry)

XX DE Human TF anti-idiotypic antibody fragment ZA36.

XX KM MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antidiabetic antibody; cytostatic; virucidal; antibacterial; TF antigen; antiparasitic; infectious disease.

XX KM Homo sapiens.

XX OS Homo sapiens.

XX PN WO200073430-A2.

XX PD 07-DEC-2000.

XX PF 29-MAY-2000; 2000WO-DE001809.

XX PR 27-MAY-1999; 99DE-01024405.

XX PR 09-SEP-1999; 99DE-01043016.

XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX PI Goletz S, Karsten U;

XX DR WPI; 2001-049937/06.

XX PT Vaccines against conformation-dependent or non-peptide antigens, based on DNA encoding peptide which mimics the antigen, useful e.g. as antitumor vaccines.

XX PS Disclosure; Page 14; 36pp; German.

XX XX

CC This invention describes a novel vaccine (V1) against conformation-dependent antigens (CDA) comprising DNA (1) and/or an antibody, or peptide which immunologically imitates CDA, is new. (1) encodes a region of an antidiabetic antibody (Ab2) or another peptide which: (a) specifically binds to the binding site of an antibody (Ab1) or an antigen binding molecule; and (b) immunologically mimics the initial antigen. The epitope is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of amino acids. (1) is used in the form of linear or circular naked DNA and/or with a viral vector and/or adjuvants. The products of the invention have cytostatic, virucidal, antibacterial and antiparasitic. The invention also describes (1) a corresponding vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which show an immunogenic structure; (2) preparing (V1) and (V2); (3) human antidiabetic antibody fragments against the MUC1-conformation epitope having one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (4) MUC1-conformation epitope mimics having one of 16 9-17 residue amino acid sequences, all fully in

CC the specification; (5) antiidiotypic antibody fragments against the TF
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TF carbohydrate epitope mimics,
 CC having one of 25-73 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3), (4), (5), or (6). (VI) and (V2) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible
 XX
 SQ Sequence 239 AA;

Query Match 70.4%; Score 957; DB 4; Length 239;
 Best Local Similarity 73.3%; Pred. No. 1.8e-50;
 Matches 187; Conservative 17; Mismatches 29; Indels 22; Gaps 3;

QY 1 QVQLQESGGPGLVKRSSETLSLTCTVSGSI-GHYWYMTROPGEGLWGTFFPDGNTY 59
 DB 1 QVQLQESGGPGLVKRSSETLSLTCAVSGSISNNMWMVQPPGKGLWGTFFPDGNTY 60
 QY 60 NPSLNGRVTISLDTSKNQSLRLTSTVTAADTAVYFCARLKAWLSEPPYFSSDMDVWG 119
 DB 61 NPSLKSRTVTSADKSKNLSLSVTAADTAVYFCAR-----PSSIMG 104
 QY 120 QGTIVYVPSGGSGSGSGSGSGSGSNFMTLTPPSASGTPGQVRSISCGSSSDIGS 179
 DB 105 QGTIVY-----SSGGSGSGSGSGSGSALQSVLTQPPSASGTPGQVRSISCGSSSDIGS 159
 QY 180 NTWNWYQQLPGTAPKLLIYSNNORPBGVDPDRSGFSGTSASLVISGLQSEDEADYYCA 239
 DB 160 NYWYMQQLPGTAPKLLIYRNORPBGVDPDRSGFSGTSASLVISGLQSEDEADYYCA 219
 QY 240 WDSLSLNGVYVGGGPR 254
 DB 220 WDSLSLNGVYVGGGPR 234

RESULT 14

ABP45535
 ID ABP45535 standard; protein; 251 AA.

XX
 AC ABP45535;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1546.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytoactive;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; rheumatoid
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.

PN NO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001MO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 21-MAR-2001; 2001US-0276248P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMP-) CAMBRIDGE ANTI-BODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 PT
 XX
 XX
 PS Claim 1; Page 2247-2249; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytoactive, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineoplastic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantify the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC acquired immunodeficiency syndrome (AIDS). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 251 AA;

Query Match 70.0%; Score 951; DB 5; Length 251;
 Best Local Similarity 72.7%; Pred. No. 4.3e-50;
 Matches 189; Conservative 19; Mismatches 32; Indels 20; Gaps 5;

QY 1 QVQLQESGGPGLVKRSSETLSLTCTVSGSI-GHYWYMTROPGEGLWGTFFPDGNTY 59
 DB 1 QVQLQESGGPGLVKRSSETLSLTCAVSGDSIRGHNMMWVQPPGKGLWGTFFPDGNTS 60
 QY 60 NPSLNGRVTISLDTSKNQSLRLTSTVTAADTAVYFCAR-----LKGAWLSEPPYFSSDG 114
 DB 61 NPSLKSRTVTSADKSKNLSLSVTAADTAVYFCAR-----YLRK-- 110
 QY 115 MDVWGGQITVYVPSGGSGSGSGSGSGSNFMTLTPPSASGTPGQVRSISCGSS 174
 DB 111 LDYWGKGTIVYVPSGGSGSGSGSGSGS-----AQPVLQPPSASGTPGQVRSISCGSS 166
 QY 175 SDIGSNWYQQLPGTAPKLLIYSNNORPBGVDPDRSGFSGTSASLVISGLQSEDEAD 234
 DB 167 SNIGSKTVMYQQLPGTAPKLLIYSTNLRPBGVDPDRSGFSGTSASLVISGLQSEDEAD 226
 QY 235 YTCAMDSLNGVYVGGGPR 254
 DB 227 YTCAMDSLNGVYVGGGPR 246

RESULT 15

ABP45970
 ID ABP45970 standard; protein; 247 AA.

XX
 AC ABP45970;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1981.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytoactive;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; rheumatoid
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.

PN NO200202641-A1.

PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2764-2765; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 247 AA;
XX
Query Match 69.0%; Score 938; DB 5; Length 247;
Best Local Similarity 71.5%; Pred. No. 2.6e-49;
Matches 183; Conservative 22; Mismatches 35; Indels 16; Gaps 4;
QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIG--HDYWSWIRPPGEGLEWIGFIIPDGSTN 58
DB 1 QQLQESGPGIVVPLETTLSTCTVSGSGSVGRTHYWGWIIRLPKGMENIASISFDGTF 60
QY 59 YNPSLNGRYTISLDTSKNQLSLRLTSVTAADTAIVFCARLKGMWLSEPPYFSSDGMVW 118
DB 61 YNPSLKSRYSVSRLDTSKNQFSLKTSVTAADTAIVYCAR-----HDY--GDLFDYW 110
QY 119 GGGTTVTVSGGGSGGGSGGGSGGSGNFMLTQPPSASGTPGQRVASISGSSSDIG 178
DB 111 GGGTWTVTSSGGSGGGSGGGSGGSGS---AQSVLTQPPSASGTPGQRPVPSGSGSSNIG 166
QY 179 SNTVMNYQQLPGTAPKLLIYSNNQRPSPGVDPRSPGKSGTSASLVISGLQSEDEADYYCA 238
DB 167 SNSVSWYQVPGTAPKLLIYNNNRPSGVDPRSPGKSGTSASLVISGLQSEDEADYYCA 226
QY 239 ANDESLNGVVFPGGGPR 254
DB 227 SWDDSLTVPVFPGGTX 242

Search completed: May 13, 2004, 15:00:56
Job time : 53.2796 secs

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us-10-072-301-19.ra1

[illegible]

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RESULT 2
US-10-039-785-50
/ Sequence 50, Application US/10039785
/ Patent No. 6538938
GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: P5550
/ CURRENT APPLICATION NUMBER: US/10/039,785
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 60/369,860
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/331,310
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/331,044
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: 60/327,364
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/323,807
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/309,156
/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/294,981
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/293,473
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 250
/ TYPE: PRT
/ ORGANISM: Artificial sequence
FEATURE:
/ OTHER INFORMATION: T1015A02 scFv
/ NAME/KEY: SITE
/ LOCATION: (250)
/ OTHER INFORMATION: Xaa equals either Gly or Ser
US-10-039-785-50

```

QY	179	SNTVNNYQQLPGTAPKLLIYNNQPPSGVDRFSGFSKSGTASLVISGLQSEBDADYYCA	238
Db	170	GNIVNNYQQLPGTAPKLLIYNNQPPSGVDRFSGFSKSGTASLVISGLQSEBDADYYCA	
QY	239	AMDESILGVVFGG	252
Db	230	AMDDSLIGVFGTG	243

```

RESULT 3
US-08-918-148-79
/ Sequence 79 / Application US/06918148A
/ Patent No. 6342220
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camellia
/ APPLICANT: W.
/ APPLICANT: Carter, Paul J.
/ APPLICANT: Fendly, Brian M.
/ APPLICANT: Gurney, Austin L.
/ TITLE OF INVENTION: Agent Bodies
/ FILE REFERENCE: P0970
/ CURRENT APPLICATION NUMBER: US/08/918,148A
/ CURRENT FILING DATE: 1997-08-25
/ SEQ ID NO 79
/ LENGTH: 244
/ TYPE: RT
/ ORGANISM: artificial
US-08-918-148-79

```

Query Match	65.4%	Score 888.5	DB 4	Length 244
Best Local Similarity	67.5%	Pred. No. 1.5e-57		
Matches 172	Conservative 34	Mismatches 28	Indels 2	Gaps 5
QY				
	1	QVQLQSSGPGLVPSSETLSLTCTVSGSGSGTHDYMWIRPPRPGELRWIGFIFPDGSTNYN	60	
	3	QVQLQSSGPGLVPSSETLSLTCTVSGDSISSTYMWIRPPKGLGEMIGYIYSGSTNYN	60	
QY	61	PSLNGRVTISLPTSSKKQSLRLTSTAADTANYFCARLKGMULSEPPYFSSDGMDDVWQ	62	
Db	63	PSLKSRLTISVDTISKQPSLKLSISVTAAADTANYVCAR-----YF-----DVMGR	120	
QY	121	GTTTNYVPSGGGGSGGGGSGGGGSGGGSNFMILTPPSASGTPGQARVSLSGSGSSDITGS-	108	
Db	109	GTMATV-----SSGGGSGGGGSGGGGSGGGGSYLTLPSPISGSPGGSITISCTGTSIDVG	179	
QY	180	NFTNNVYQQLPGTAPELTLTYSNNOBPSGVPRPFSQFSGKGTASLIVISGLQSEDEADYYCA	163	
Db	164	NVYSVYQGHPPGKAPRLMTIYESGSKRPSGVSNRFSGSKSGNTASLTISGLQSEDEADYYCS	239	
QY	240	WDESLNGVPRGGGR	254	
Db	224	Y-TTRSTVRFGGGTK	237	

	Query Match	70.7%	Score 960.5	DB 4	Length 250
	Best Local Similarity	74.0%	Pred. No. 8.7e-63		
	Matches 189	Conservative 22	Mismatches 31	Indels 13	Gaps 5
QY	1	QVQLDSEGPGLVKPSETLSLTCTVSGSGIGHD--YMSNINQPPGEGLENIIGTFIDGSTN	58		
Db	1	QVQLDSESGPGLVKPSQTLSTLKNVSGSGISGIGDPTMSMINKPPGKLEMIIGIHSGSGLTY	60		
QY	59	YNPSLNGRVTISLPTSRKNQSLRLTSTADTVAVFCARLKGAMLLSEPPYSQMDVW	118		
Db	61	YKPSLRSLRTVSMQTSNRQPSLKLTSVTADTALTYCVR---EM--ANGDHMSA--PDLW	113		
QY	119	GQGTVTVYPPSGGGSGSGGGSGGGSGGGSGNFMLLTPPASGTPGQARYSISCGSSSDIG	178		
Db	114	GQGLTVTVSSGGGSGSGGGSGGGSGGGSG---AQAIVLNPSSASGTPQQRVTLIPCSGSSSNIG	169		

```

RESULT 4
US-09-260-527-3
: Sequence 3, Application US/09260527A
: Patent No. 622859
: GENERAL INFORMATION:
: APPLICANT: Knox, J.P.
: APPLICANT: Miklesen, J.D.
: APPLICANT: Willats, W. G.
: TITLE OF INVENTION: ANTIBODY
: CURRENT APPLICATION NUMBER: 1999-0014AS
: CURRENT FILING DATE: 1999-02-26
: NUMBER OF SEQ. ID NOS: 7
: SOFTWARE: PatsSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 278
: TYPE: PRT
: ORGANISM: UNKNOWN

```



```

; FEATURE: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

```

Query Match	57.9%;	Score 787;	DB 3;	Length 278;
Best [Local] Similarity	62.0%;	Pred No 4	2a-50;	

QY 1 QVQLQSSGGSLVPESETLTCTVSGGS-I-GHDVSMIRQPGSGLEWIGIFPDGSTNY 59
 QY 23 QVQLQSSGGSLVPESETLTCTVSGGS-I-GHDVSMIRQPGSGLEWIGIFPDGSTNY 82
 QY 60 NPSLNGRVITSLDTSKNQLSLRLTSTYTAADTAIVYCAALKKAMLLSEPPYFSSGMDVWG 119
 Db 83 NPSLKSRLVMSVDTSKNQPSLKLSTVATDIAVYCAFP-----HPRVYD-----WG 129
 QY 120 QGTVTVVPSGGGGSGGGSGGGSGGGGSGNFLLTPGASGPGQGRVVISGCSGSSSDIGS 179
 Db 130 QGTLIVTVSSKGGGSGGGSGGGGSG-----ELTPDPAVVALQGVYARITQGIS--LRS 181
 QY 180 NTVMVTQQLPGTAPKLLIYSNNQRPBGVDPRFSGFKSGTSLVSIQSLQSEDEADYCAA 239
 Db 182 YVASMTQQRPGQAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQADEADYCNSS 241
 QY 240 WDSLNGVYVFGGSPR 254
 Db 242 RDSGNNHVVFGGQTK 256

```

RESULT 5
US-09-079-029-11
: Sequence 11, Application US/09079029
: Patent No. 6342369
: GENERAL INFORMATION:
: APPLICANT: Adams, Camilla W.
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Chuntharapaj, Anan
: APPLICANT: Kim, Kyung J.
: TITLE OF INVENTION: Apo-2 Receptor
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/079.029
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Marchang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1101R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 310 amino acids
: TYPE: Amino acid
: TOPOLOGY: Linear
: US-09-079-029-11

```

Query Match	57.2%	Score 778;	DB 4;	Length 310;
Best Local Similarity	60.2%;	Pred. No. 2.1e-49;		
Matches 154;	Conservative 32;	Mismatches 52;	Indels 18;	Gaps 4;

```

OY 1 QVQLQSGGGLVYPKPSSTLTCTVSGGSIIGHDYMSWIRQPPGELEWIGFTFPDGSTN-Y 59
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 40 QVQLVSGGGGVYPGSRILRSCASGPIFSSYGMHWYQAQKGLEWVAGIFYDGKHY 99

OY 60 NBSLNARVITSLDTSNQSLRLTSTVTAADTVAFCARLKAMTLSEPPFPSSGMDVWG 119
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 100 ADSVKRFITSDNSNNTLYIQMNSLRADPAVYYCAADRGYY-----MDVWG 148

OY 120 QGTTVYPSGGGSGGGGSGGGSAGGASNFMLTQPPSASGTPQQRVVISCSGSSPDIGS 179
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 149 KGTIVY-----SSGGGSGGGGSGGGSGGSQSVLTQPPVSGAPQQRVITISCTGRSSNIGA 203

OY 180 -NTVNNYQQLPGTAPKLLIYSNNQPPGVPDRPFGSGFSGTSSASLVISGLOSEADYYCA 228
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 204 GHVHWYQQLPGTAPKLLIYDPSNRPSPGVDRPFGSGRGTSSASLAIIGLQAEDADYYCQ 263

OY 239 AMDESLNGVYFGGGR 254
Db 264 SYDSILRGSVFGGGR 279

```

```

: RESULT 6
: US-08-665-202-5
: Sequence 5, Application US/08665202
: Patent No. 5977322
: GENERAL INFORMATION:
: APPLICANT: Marks, James D.
: APPLICANT: Schier, Robert
: TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
: TITLE OF INVENTION: Tumor Antigens
: NUMBER OF SEQUENCES: 141
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,202
: FILING DATE: 13-JUN-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,238
: FILING DATE: 14-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,250
: FILING DATE: 15-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hunter, Tom
: REGISTRATION NUMBER: 38,498
: REFERENCE/DOCKET NUMBER: 02307E-061410
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0300
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 258 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-665-202-5

```

Best Local Similarity 60.2%; Pred. No. 4e-49;
Matches 157; Conservative 32; Mismatches 54; Indels 18; Gaps 6;

```

Qy 1 QVQLQESGGPGLVPSRFTLSLTCTVSGSGSIQHDYWM-SMIRPPGDELWIGTIF-FDGSTN 58
Db 1 QVQLQESGALKKPKGSLIKSCGSGYSF-TSYWIAWYKQMGKLEWGLIYFGSDTK 59
Qy 59 YNPSLNGRVITISLDTSKNQLSLRLTSVTAADTAIVYFCARLKGAWLLSE-----PPYSSD 113
Db 60 YSPSPGQGVITISVDKSVSTAYLQWMSLKPDSAVYFCARHDVGYCSSNCAKMPDYFOH- 118
Qy 114 GMDWVGQGVITTVPSGGGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 173
Db 119 ---WGQGLTVTV-----SSGGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 169
Qy 174 SSDIGSNTVNMVYQQLPGTAPKLLIYSNNQPSGVDPDFSGFKSGTSAIVISGLQSEDEA 233
Db 170 SSNIGNNVYVMYQQLPGTAPKLLIYGHTRPAGVDPDFSGSKGTSASIALISGFRSEDA 229
Qy 234 DYCAAMDSESLNGVVFGGGPR 254
Db 230 DYCAAMDSESLNGVVFGGGPR 250

```

RESULT 7

US-09-315-574-5
Sequence 5, Application US/09315574
Patent No. 6512097

GENERAL INFORMATION:

APPLICANT: Matke, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-4106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER:

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411

TELEPHONE:

TELEPHONE: (415) 576-0200

TELEFAX:

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-315-574-5

Query Match
Best Local Similarity 56.9%; Score 773; DB 4; Length 258;
Matches 157; Conservative 32; Mismatches 54; Indels 18; Gaps 6;

```

Qy 1 QVQLQESGGPGLVPSRFTLSLTCTVSGSGSIQHDYWM-SMIRPPGDELWIGTIF-FDGSTN 58
Db 1 QVQLQESGALKKPKGSLIKSCGSGYSF-TSYWIAWYKQMGKLEWGLIYFGSDTK 59
Qy 59 YNPSLNGRVITISLDTSKNQLSLRLTSVTAADTAIVYFCARLKGAWLLSE-----PPYSSD 113
Db 60 YSPSPGQGVITISVDKSVSTAYLQWMSLKPDSAVYFCARHDVGYCSSNCAKMPDYFOH- 118
Qy 114 GMDWVGQGVITTVPSGGGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 173
Db 119 ---WGQGLTVTV-----SSGGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 169
Qy 174 SSDIGSNTVNMVYQQLPGTAPKLLIYSNNQPSGVDPDFSGFKSGTSAIVISGLQSEDEA 233
Db 170 SSNIGNNVYVMYQQLPGTAPKLLIYGHTRPAGVDPDFSGSKGTSASIALISGFRSEDA 229
Qy 234 DYCAAMDSESLNGVVFGGGPR 254
Db 230 DYCAAMDSESLNGVVFGGGPR 250

```

RESULT 8

US-09-646-028-53
Sequence 53, Application US/09646028
Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014,0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FaetsEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 334
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of artificial sequence: /note=synthetic construct

Query Match
Best Local Similarity 51.5%; Score 700; DB 4; Length 334;
Matches 146; Conservative 30; Mismatches 62; Indels 22; Gaps 6;

```

Qy 1 QVQLQESGGPGLVPSRFTLSLTCTVSGSGSIQHDYWMIRPPGDELWIGTIFPDGSTN-Y 59
Db 80 EVQLLESGGGLVGGSGSLRLSCVAGSLTFSASITWRAQPAKGLAWSGISFSDITTY 139
Qy 60 NPSLNGRVITISLDTSKNQLSLRLTSVTAADTAIVYFCARLKGAWLLSEPPYSSDQ---MD 116
Db 140 ADSYKGRFASASRDSKNTVYLLQNNLRPNDDTAIVFCAN-----NQGNFELD 186
Qy 117 VMGGQGVITTVPS-GGGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 175
Db 187 NMGGGTLVTVSSRGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSG 243
Qy 176 DIGSN-TVMWYQQLPGTAPKLLIYSNNQPSGVDPDFSGFKSGTSAIVISGLQSEDEAD 234
Db 244 NIGAGYDVWYQKFPETAPKLLIYSNNRPFSGVDPDFSGSKGTSASIALISGFRSEDA 229
Qy 235 YCAAMDSESLNGVVFGGGPR 254
Db 304 YTCQCNDSLSGLMFLFGGQTK 323

```


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```

Qy 181 TVNMYQQLPCTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYCAAM 240
Db 181 TVNMYQQLPCTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYCAAM 240
Qy 241 DESLNGVVFQGGPR 254
Db 241 DESLNGVVFQGGPR 254

```

RESULT 2

```

US-10-071-866-19
/ Sequence 19, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 19
/ LENGTH: 254
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.11
US-10-071-866-19

```

Query Match

```

Best Local Similarity 100.0%; Score 1359; DB 14; Length 254;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 QVOLOESGPGLVKPESETLSLCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFFDGSNTYN 60
Db 1 QVOLOESGPGLVKPESETLSLCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFFDGSNTYN 60
Qy 61 PSLNGRVITSLDTSKNQSLRLTSVTADTAFFCARLKGAMLLSEPPYSSDGMVWQ 120
Db 61 PSLNGRVITSLDTSKNQSLRLTSVTADTAFFCARLKGAMLLSEPPYSSDGMVWQ 120
Qy 121 GTTVVPSGGGGSGGGSGGGSGGSGSNFMTLTPPSASGTPQORVSISSGSSSDIGSN 180
Db 121 GTTVVPSGGGGSGGGSGGGSGGSGSNFMTLTPPSASGTPQORVSISSGSSSDIGSN 180
Qy 181 TVNMYQQLPCTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYCAAM 240
Db 181 TVNMYQQLPCTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYCAAM 240
Qy 241 DESLNGVVFQGGPR 254
Db 241 DESLNGVVFQGGPR 254

```

RESULT 3

```

US-10-360-828-19
/ Sequence 19, Application US/10360828
/ Publication No. US20030206909A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-727
/ CURRENT APPLICATION NUMBER: US/10/360,828
/ PRIOR FILING DATE: 2003-02-07
/ PRIOR APPLICATION NUMBER: US 10/071,866
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: US 10/072,301

```

```

/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: US 10/133,978
/ PRIOR FILING DATE: 2002-04-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 19
/ LENGTH: 254
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.11
US-10-360-828-19

```

Query Match

```

Best Local Similarity 100.0%; Score 1359; DB 15; Length 254;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 QVOLOESGPGLVKPESETLSLCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFFDGSNTYN 60
Db 1 QVOLOESGPGLVKPESETLSLCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFFDGSNTYN 60
Qy 61 PSLNGRVITSLDTSKNQSLRLTSVTADTAFFCARLKGAMLLSEPPYSSDGMVWQ 120
Db 61 PSLNGRVITSLDTSKNQSLRLTSVTADTAFFCARLKGAMLLSEPPYSSDGMVWQ 120
Qy 121 GTTVVPSGGGGSGGGSGGGSGGSGSNFMTLTPPSASGTPQORVSISSGSSSDIGSN 180
Db 121 GTTVVPSGGGGSGGGSGGGSGGSGSNFMTLTPPSASGTPQORVSISSGSSSDIGSN 180
Qy 181 TVNMYQQLPCTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYCAAM 240
Db 181 TVNMYQQLPCTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYCAAM 240
Qy 241 DESLNGVVFQGGPR 254
Db 241 DESLNGVVFQGGPR 254

```

RESULT 4

```

US-10-072-301-27
/ Sequence 27, Application US/10072301
/ Publication No. US20030152913A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
/ FILE REFERENCE: 25636-718
/ CURRENT APPLICATION NUMBER: US/10/072,301
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 27
/ LENGTH: 258
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.11
US-10-072-301-27

```

Query Match

```

Best Local Similarity 98.6%; Score 1340; DB 14; Length 258;
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 QVOLOESGPGLVKPESETLSLCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFFDGSNTYN 60
Db 1 QVOLOESGPGLVKPESETLSLCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFFDGSNTYN 60
Qy 61 PSLNGRVITSLDTSKNQSLRLTSVTADTAFFCARLKGAMLLSEPPYSSDGMVWQ 120
Db 61 PSLNGRVITSLDTSKNQSLRLTSVTADTAFFCARLKGAMLLSEPPYSSDGMVWQ 120

```


Oy	12	GTTVTPSGGGGSGGGGSGGGGSFMTLTOPPSASGPGRVSTSCGSSSDJGNS	180
	121	GTTVTYSSGGGSGGGGSGGGGSFMTLTOPPSASGPGRVSTSCGSSSDJGNS	180
Db	181	TVMNVOQLPCTAPKLLIYSNNORPSCGVPDRFGSPGSASIVTSGLOSEDEADYYCAAW	240
Oy	181	TVMNVOQLPCTAPKLLIYSNNORPSCGVPDRFGSPGSASIVTSGLOSEDEADYYCAAW	240
Db	241	DESINGVFEGGPR 254	
Oy	241	DESINGVFEGGPR 254	
Db	241	DESLNGVIFGGGTK 254	

```

RESULT 5
US-10-071-866-27
; Sequence 27, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071, 866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.11
US-10-071-866-27

```

```

Query Match 59.6%; Score 1340; DB 14; Length 258;
Best Local Similarity 98.8%; Pred. No. 4e-85;
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKSESETSLTCTVSGSGIGHDYSWIRQPGEGLEWIGTIFPDSTNYN 60
Db      1 QVQLQESGPGLVKSESETSLTCTVSGSGIGHDYSWIRQPGEGLEWIGTIFPDSTNYN 60

QY      61 PSILNGRVTISLDTSKNQSLRLTSVTAADTAIVYFCARLKGAWLISEPPYFSSDGDWVGQ 120
Db      61 PSILNGRVTISLDTSKNQSLRLTSVTAADTAIVYFCARLKGAWLISEPPYFSSDGDWVGQ 120

QY      121 GTTATVPSGGGSGSGGGSGGGSGGSGSNFMLTPPPSASGTPGQRVSISSCGSSSDITSN 180
Db      121 GTTATVPSGGGSGSGGGSGGGSGGSGSNFMLTPPPSASGTPGQRVSISSCGSSSDITSN 180

QY      181 TVNNYQQLPGAPAKLLIYSNNORPSGVDPDRPSGFPSGSASLVISGLQSEBDADYYCAAW 240
Db      181 TVNNYQQLPGAPAKLLIYSNNORPSGVDPDRPSGFPSGSASLVISGLQSEBDADYYCAAW 240

QY      241 DESLNGVVFSGGSPR 254
Db      241 DESLNGVVFSGGSPR 254

RESULT 6
US-10-360-828-27
; Sequence 27, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT FILING DATE: US/10/360,828
; CURRENT FILING DATE: 2003-02-07

```

	Prior Application Number:	US 10/071,866
	Prior Filing Date:	2002-02-08
	Prior Application Number:	US 10/072,301
	Prior Filing Date:	2002-02-08
	Prior Application Number:	US 10/133,978
	Prior Filing Date:	2002-04-25
	Number of SEQ ID NOS:	64
	Software:	PatentIn version 3.1
	SEQ ID NO:	27
	Length:	258
	Type:	PRT
	Organism:	Artificial Sequence
	Feature:	
	Other Information:	Clone 15.150.11 Variant
	US-10-360-828-27	
Query Match	98.6%; Score 1340; DB 15; Length 258;	
Best Local Similarity	98.8%; Pred. No. 4e-85;	
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0		
Dy	1 QVQLOSSGGGLYKPSBETLSLTCTTVSGSIGHDWSMIRQPGBELMIGTIFPDGSTNN	60
	1 QVQLOSSGGGLYKPSBETLSLTCTTVSGSIGHDWSMIRQPGBELMIGTIFPDGSTNN	60
Dy	61 PSINGEVTISLDTSKNOQLSLRTSTYADTAIVYCARLKGMILSEPPYFSSDGDMDVWG	120
	61 PSINGEVTISLDTSKNOQLSLRTSTYADTAIVYCARLKGMILSEPPYFSSDGDMDVWG	120
Dy	121 GTTATVPSSGGGSGGGSGGGSGGGGSFMULTOPPSSASGTPEGRVSISCSGSSSDIGSN	180
	121 GTTATVPSSGGGSGGGSGGGSGGGGSFMULTOPPSSASGTPEGRVSISCSGSSSDIGSN	180
Dy	181 TTNWVYQQLPGTAPKLIIYSNORPBGVDPRSGFGKSASLVISGLQSEDEADYYCAAW	240
	181 TTNWVYQQLPGTAPKLIIYSNORPBGVDPRSGFGKSASLVISGLQSEDEADYYCAAW	240
Dy	241 DESLNAGVFEGGGR 254	
	241 DESLNAGVFEGGGR 254	
Dy	241 DESLNAGVFEGGGR 254	
	241 DESLNAGVFEGGGR 254	

```

RESULT 7
US-09-880-748-1223
; Sequence 1223, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyst
; FILE REFERENCE: p5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1223
; LENGTH: 252
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-880-748-1223

```

Query Match	73.6%;	Score 1000.5;	DB 10;	Length 252;
Best Local Similarity	76.6%;	Pred. No. 1.2e-61;		
Matches 196;	Conservative 16;	Mismatches 33;	Indels 11;	Gaps 3.


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Publication No. US20030190685A1
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 244
TYPE: PRT
ORGANISM: Artificial sequence
OTHER INFORMATION: T1014A02 scfv
US-10-139-785-44
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Query Match      71.8%; Score 975.5; DB 14; Length 244;
Best Local Similarity 74.0%; Pred. No. 66-60;
Matches 188; Conservative 18; Mismatches 33; Indels 15; Gaps 2;
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```
QY 1 QVQLQESGGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRPPGEGLEWIGFIPFDGSTNN 60
DB 1 QVQLQESGGPGLVKPSETLSLTCTVSGSGSIDYMSWIRPPGEGLEWIGFIPFDGSTNN 60
QY 61 PSINQGVTTSLDTSKNQSLRLTSVTAADTAVYFCARLKAGAMLLSEPPYFSSDGMVWG 120
DB 61 PSINQGVTTSLDTSKNQSLRLTSVTAADTAVYFCARLKAGAMLLSEPPYFSSDGMVWG 120
QY 61 PSINQGVTTSLDTSKNQSLRLTSVTAADTAVYFCARLKAGAMLLSEPPYFSSDGMVWG 108
DB 61 PSINQGVTTSLDTSKNQSLRLTSVTAADTAVYFCARLKAGAMLLSEPPYFSSDGMVWG 108
QY 121 GTTVTVPSGGGGSGGGSGGGSGGSGSNFMLTOPPSASGTPGQRFVSISCGSSSDIGS 180
DB 109 GTTVTVPSGGGGSGGGSGGGSGGSGSNFMLTOPPSASGTPGQRFVSISCGSSSDIGS 180
QY 181 TVNMYQQLPQTAPKLIYNNORPSGVPPRFSGFKSGTSASLVISGLQSEDEADYYCAAM 240
DB 166 TVNMYQQLPQTAPKLIYNNORPSGVPPRFSGFKSGTSASLVISGLQSEDEADYYCAAM 225
QY 241 DESLNGVVFGGGPR 254
DB 226 DSRGGMVFGGGTK 239
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RESULT 11

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US-09-880-748-1642
Sequence 1642, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
```

```
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1642
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1642
```

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Query Match      71.7%; Score 975; DB 10; Length 255;
Best Local Similarity 74.5%; Pred. No. 6,8e-60;
Matches 190; Conservative 23; Mismatches 36; Indels 6; Gaps 2;
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QY 1 QVQLQESGGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRPPGEGLEWIGFIPFDGSTNN 60
DB 1 QVQLQESGGPGLVKPSETLSLTCTVSGSGSIDYMSWIRPPGEGLEWIGFIPFDGSTNN 60
QY 61 PSINQGVTTSLDTSKNQSLRLTSVTAADTAVYFCARLKAGAMLLSEPPYFSSDGMVWG 119
DB 61 PSINQGVTTSLDTSKNQSLRLTSVTAADTAVYFCARLKAGAMLLSEPPYFSSDGMVWG 120
QY 120 GTTVTVPSGGGGSGGGSGGGSGGSGSNFMLTOPPSASGTPGQRFVSISCGSSSDIGS 179
DB 121 GTTVTVPSGGGGSGGGSGGGSGGSGSNFMLTOPPSASGTPGQRFVSISCGSSSDIGS 175
QY 180 NTVMYQQLPQTAPKLIYNNORPSGVPPRFSGFKSGTSASLVISGLQSEDEADYYCAAM 239
DB 176 NTVMYQQLPQTAPKLIYNNORPSGVPPRFSGFKSGTSASLVISGLQSEDEADYYCAAM 235
QY 240 WDSLNGVVFGGGPR 254
DB 236 WDSLNGVVFGGGTK 250
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RESULT 12

```
US-10-293-418-1642
Sequence 1642, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1642
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1642
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Query Match 71.7%; Score 975; DB 12; Length 252;
Best Local Similarity 74.5%; Pred. No. 6,8e-60;
Matches 190; Conservative 23; Mismatches 36; Indels 6; Gaps 2;

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Qy 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--GHDYMSWIRQPPGSGLEWIGIFFDGSTN 60
Db 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--GHDYMSWIRQPPGSGLEWIGIFFDGSTN 60
Qy 61 PSLSKRVITISYDAKNSFKLSSTVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 119
Db 61 PSLSKRVITISYDAKNSFKLSSTVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 119
Qy 120 QGTTVTVPSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRYVSI--SCGSSSDIGS 179
Db 120 QGTTVTVPSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRYVSI--SCGSSSDIGS 179
Qy 121 RGLIVY----SSGGGSGGGGSGGGGSGGSGVLTQPPSASGTPGQRYVSI--SCGSSSDIGS 175
Db 121 RGLIVY----SSGGGSGGGGSGGGGSGGSGVLTQPPSASGTPGQRYVSI--SCGSSSDIGS 175
Qy 180 NTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 239
Db 180 NTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 239
Qy 176 NTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 235
Db 176 NTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 235
Qy 240 MDESLNGVVFSGGPR 254
Db 240 MDESLNGVVFSGGPR 254
Qy 236 MDESLNGVVFSGGPR 250
Db 236 MDESLNGVVFSGGPR 250
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RESULT 13

```
US-09-880-748-1994
/ Sequence 1994, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PFS23
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 1994
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1994
```

Query Match 70.9%; Score 963.5; DB 10; Length 252;
Best Local Similarity 73.0%; Pred. No. 4.2e-59;
Matches 187; Conservative 22; Mismatches 36; Indels 11; Gaps 3;

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Qy 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--GHDYMSWIRQPPGSGLEWIGIFFDGSTN 58
Db 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--GHDYMSWIRQPPGSGLEWIGIFFDGSTN 58
Qy 59 YNPSLNGRVITISLDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 118
Db 59 YNPSLNGRVITISLDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 118
Qy 61 YNPSLKS RVMSVDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 114
Db 61 YNPSLKS RVMSVDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 114
Qy 119 QGTTVTVPSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRYVSI--SCGSSSDIG 178
Db 119 QGTTVTVPSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRYVSI--SCGSSSDIG 178
Qy 179 SNTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 238
Db 179 SNTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 238
Qy 172 SNTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 231
Db 172 SNTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 231
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Qy 239 ANDESINGVVFSGGPR 254
Db 239 ANDESINGVVFSGGPR 254
Qy 232 TWDDRLRGLVFGGPR 247
Db 232 TWDDRLRGLVFGGPR 247
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RESULT 14

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US-10-293-418-1994
/ Sequence 1994, Application US/10293418
/ Publication No. US2003023996A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PFS23P2
/ CURRENT APPLICATION NUMBER: US/10/293,418
/ PRIOR FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1994
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-1994
```

Query Match 70.9%; Score 963.5; DB 12; Length 252;
Best Local Similarity 73.0%; Pred. No. 4.2e-59;
Matches 187; Conservative 22; Mismatches 36; Indels 11; Gaps 3;

```
Qy 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--GHDYMSWIRQPPGSGLEWIGIFFDGSTN 58
Db 1 QVQLQESGGPGLVKPSETLSLTCTVSGGSI--GHDYMSWIRQPPGSGLEWIGIFFDGSTN 58
Qy 59 YNPSLNGRVITISLDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 118
Db 59 YNPSLNGRVITISLDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 118
Qy 61 YNPSLKS RVMSVDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 114
Db 61 YNPSLKS RVMSVDTSKNQLSLRTSVTAADTAAYVFCARLKGMWLSSEPPYFSSDGMVW 114
Qy 119 QGTTVTVPSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRYVSI--SCGSSSDIG 178
Db 119 QGTTVTVPSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRYVSI--SCGSSSDIG 178
Qy 179 SNTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 238
Db 179 SNTVMYVQQLPGLTAPKLLIYSNNORPSGVDPDRFSGKSGTSAVLVSI--GLQSEDEADYCA 238
Qy 239 ANDESINGVVFSGGPR 254
Db 239 ANDESINGVVFSGGPR 254
Qy 232 TWDDRLRGLVFGGPR 247
Db 232 TWDDRLRGLVFGGPR 247
```

RESULT 15

```
US-10-039-785-50
/ Sequence 50, Application US/10039785
/ Publication No. US20020067646A1
/ GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL
/ FILE REFERENCE: PFS50
```

```

; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1015A02 scFv
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (250)
; OTHER INFORMATION: Xaa equals either Gly or Ser
US-10-039-785-50

```

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Query Match          70.7%; Score 960.5; DB 13; Length 250;
Best Local Similarity 74.0%; Pred. No. 6,7e-59;
Matches 188; Conservative 22; Mismatches 31; Indels 13; Gaps 5;

QY 1 QVQLQESGGPGGVKPSSTLSITCTVSGSGTGHG--YMSWIRQPPGEGLEWIGFIFPDGSTN 58
DB 1 QVQLQESGGPGGVKPSSTLSITCTVSGSGTGHG--YMSWIRQPPGEGLEWIGFIFPDGSTN 60
QY 59 YNPSTLNGRVYISLDTSKNQLSLRTSVTAADTAVFYCARLKGAWLSEPPYFSSDGMQDW 118
DB 61 YNPSTLNGRVYISLDTSKNQLSLRTSVTAADTAVFYCARLKGAWLSEPPYFSSDGMQDW 113
QY 119 GGGTIVTPSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 178
DB 114 GGGTIVTPSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 169
QY 179 SNTVMNYQQLPGTAPFLILYNNQRPSPGVDPDRFSGKSGTSASLVISGLQSEDEADYCA 238
DB 170 GNTVMNYQQLPGTAPFLILYNNQRPSPGVDPDRFSGKSGTSASLVISGLQSEDEADYCA 229
QY 239 AMDESLNGVVFSGG 252
DB 230 AMDDSLIGVFGTG 243

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Search completed: May 13, 2004, 15:43:31
Job time : 38.6068 secs

THE PUBLIC HEALTH SERVICE
(1951)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.467 Seconds

(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-19

Perfect score: 1359
Sequence: 1 QVQLQESGGLVKKPSETLSL.....YYCAMDESLNGVFGGGR 254Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559.5	41.2	268	2 AS6446	Ig heavy chain V r
2	534	39.3	249	2 S41374	single chain Fv an
3	509	37.5	233	2 S25752	Ig lambda chain -
4	490	36.1	112	2 D44151	Ig lambda chain V
5	487.5	35.9	135	2 S78051	Ig heavy chain pre
6	486.5	35.8	155	2 S31511	Ig heavy chain - h
7	485.5	35.7	149	2 S23626	Ig lambda chain V
8	483.5	35.6	155	2 S31512	Ig heavy chain - h
9	481	35.5	117	2 S25757	Ig lambda chain -
10	481	35.4	117	2 S23627	Ig lambda chain pr
11	479	35.2	112	2 A44151	Ig lambda chain V
12	479	35.2	112	2 B44151	Ig lambda chain V
13	478.5	35.2	140	2 I37782	Ig variable region
14	478.5	35.2	233	2 JCS322	p53 specific singl
15	478	35.2	98	2 S36047	Ig lambda chain -
16	478	35.2	129	2 S78058	Ig lambda chain pr
17	476	35.0	137	2 S31676	Ig heavy chain V r
18	475	35.0	110	2 S57408	Ig lambda chain V-
19	475	35.0	112	2 C44151	Ig lambda chain V
20	475	35.0	216	2 A42193	Ig lambda chain (B
21	474.5	34.9	130	2 S31690	Ig heavy chain V r
22	474.5	34.9	146	2 S09711	Ig heavy chain V r
23	474	34.9	130	2 S78057	Ig lambda chain pr
24	472.5	34.8	235	2 S25754	Ig lambda chain -
25	471	34.7	233	2 S25744	Ig lambda chain -
26	467	34.4	130	2 S30534	Ig heavy chain V r
27	466	34.3	235	2 S25750	Ig lambda chain -
28	464	34.1	118	2 S20780	Ig heavy chain V r
29	460	33.8	139	2 S31586	Ig heavy chain V r

30	456	33.6	110	2 S57428	Ig light chain V-J
31	453.5	33.4	147	2 S13519	Ig heavy chain V r
32	449	33.0	98	2 S36048	Ig lambda chain -
33	447	32.9	146	1 G1HDH2	Ig heavy chain pre
34	446.5	32.9	109	1 D2H0WA	Ig heavy chain V-I
35	444.5	32.7	105	2 S44125	Ig lambda chain V
36	444.5	32.7	121	2 S44113	Ig heavy chain V r
37	444	32.7	220	2 A49444	Ig gamma-1 heavy c
38	444	32.7	231	2 B23746	Ig Fab region IV-J
39	443.5	32.6	143	2 B45028	Ig heavy chain V-I
40	443	32.6	97	2 S26906	Ig heavy chain V r
41	442.5	32.6	146	2 S09710	Ig heavy chain V r
42	442	32.5	116	2 B26340	Ig heavy chain pre
43	440	32.4	97	2 S12415	Ig heavy chain V r
44	440	32.4	145	2 S78055	Ig heavy chain pre
45	439	32.3	118	2 S24443	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scfv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #ext_change 16-Aug-1996

C/Accession: A56446
R/Tang, P.W.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity dioxin-binding protein displayed on M13 is functionally identical

A/Reference number: A56446, PMID:95229583, PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TRAN>

A/Cross-references: GB:U20617
C/Keywords: heterotetramer; immunoglobulin

Query Match 41.2%; Score 559.5; DB 2; Length 268;

Best Local Similarity 47.3%; Pred. No. 2.2e-29;
Matches 121; Conservative 35; Mismatches 77; Indels 23; Gaps 6;

QY	1	QVQLQESGGLVKKPSETLSLCTVSGSGIGHYWSWIRPPGGLGFWIF-FDGSITY 59
DB	3	QVQLQESGGLVKKPSETLSLCTVSGSGIGHYWSWIRPPGGLGFWIF-FDGSITY 59
QY	60	NPSLNGRVTLISDTSKNQLSRLTSTVTAADTAVFPCARLKGMWLSPPYFSGDGMVWG 119
DB	63	DPKFGKATITADTSNTAVYQLSLTSEDVAVYCA-----SYILTRYENYWG 111
QY	120	QGTIVTPSGGSGSGSGSGSGSGSGSNFMULTQPPS-ASGTPOQVSISSGSSSDIG 178
DB	112	QGTIVTV-----SSGGSGSGSGSGSGSGSGSDIRLTPALMSASLGEKVTMSGRASS--- 163
QY	179	SVTVVMYQQLPGTAPRLILYSNNQRPSPGDRFSGKSGTSLVSGHSEADYYCA 238
DB	164	VNFITVYQKSDASPFKLWYITSHLPDGPVPAFSGSGSGSNSTLTISSMEGDAITTCO 223
QY	239	AMDESLNGVFGGGR 254
DB	224	QFTSS--PPTFGSGTK 237

RESULT 2

S41374
single chain Fv antibody - mouseC/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 06-Jan-1995

C/Accession: S41374

R/Artezenko, O.; Weller, B.W.; Whentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994A/Description: Construction and functional characterization of a single chain Fv antibody
A/Reference number: S41374

R.Chactagnier, P.; Demaison, C.; These, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 74.2%; Score 486.5; DB 2; Length 155;
Matches 95; Conservative 11; Mismatches 17; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI GHDYMSWIRPPGEGLEWIGIFPFPGSTNNY 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI SYWMSWIRPPGEGLEWIGIYYTGSATYN 92
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAYYFCARLKGAMILSEPPYFSSDGMVWQ 120
DB 93 PPLKSRVTISVDTSKNQLSLRLTSVTAADTAYYCAR--GGGISWYDY--GMDVWQ 147

QY 121 GTTIVTIPS 128
DB 148 GTTIVTIPS 155

RESULT 7
S23626
Ig lambda chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 21-Jan-2000
C:Accession: S23626
R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deflos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

A:Cross-references: EMBL:X59706; NID:g34204; PIDN:CAA42227.1; PID:g34205
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 83.8%; Score 485.5; DB 2; Length 149;
Matches 93; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

QY 145 GGSNFMILTPPSASGTPGQRYVISCSSGSSDIGNVTVMYQOLPGTAPKRLIYSNNORP 204
DB 16 GSWAQSVALTPPSASGTPGQRYVISCSSGSSDIGNVTVMYQOLPGTAPKRLIYSNNORP 75

QY 205 SGVPRFSGFKSGTSASLVISGLQSEDEADYYCAAMDESINLVVFGGGR 254
DB 76 SGVPRFSGFKSGTSASLVISGLQSEDEADYYCAAMDESINLVVFGGGR 126

RESULT 8
S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 23-Jul-1999
C:Accession: S31512
R:Chactagnier, P.; Demaison, C.; These, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31512

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 73.4%; Score 483.5; DB 2; Length 155;
Matches 94; Conservative 12; Mismatches 17; Indels 5; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI GHDYMSWIRPPGEGLEWIGIFPFPGSTNNY 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI SYWMSWIRPPGEGLEWIGIYYTGSATYN 92
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAYYFCARLKGAMILSEPPYFSSDGMVWQ 120
DB 93 PPLKSRVTISVDTSKNQLSLRLTSVTAADTAYYCAR--GGGISWYDY--GMDVWQ 147

QY 121 GTTIVTIPS 128
DB 148 GTTIVTIPS 155

RESULT 9
S25757
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #ext_change 21-Jan-2000
C:Accession: S25757
R:Combrato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(Lambda) and J(Lambda)-C(Lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25757
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-234 <CMA>
A:Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:149-217/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 80.9%; Score 483; DB 2; Length 234;
Matches 89; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 145 GGSNFMILTPPSASGTPGQRYVISCSSGSSDIGNVTVMYQOLPGTAPKRLIYSNNORP 204
DB 15 GSWAQSVALTPPSASGTPGQRYVISCSSGSSDIGNVTVMYQOLPGTAPKRLIYSNNORP 74

QY 205 SGVPRFSGFKSGTSASLVISGLQSEDEADYYCAAMDESINLVVFGGGR 254
DB 75 SGVPRFSGFKSGTSASLVISGLQSEDEADYYCAAMDESINLVVFGGGR 124

RESULT 10
S23627
Ig lambda chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #ext_change 21-Jan-2000
C:Accession: S23627
R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deflos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23627
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59707; NID:g34426; PIDN:CAA42228.1; PID:g34427
C:Genetics:

A;Intons: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 35.2%; Score 481; DB 2; Length 117;
Matches 91; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 145 GGGSNFMULTOPPSAGTGGORVSTSCSSSSDISNTVMYQOLPGTAPKLLYSNNORP 204
DB 16 GSMASQVLTOPPSAGTGGORVSTSCSSSSDISNTVMYQOLPGTAPKLLYSNNORP 75
QY 205 SGVPRRSGFSGTSASLVISGLQSEDEADYCAAMDSEINGVFGGPR 246
DB 76 SGVPRRSGFSGTSASLVISGLQSEDEADYCAAMDSEINGVFGGPR 117

RESULT 11

A44151
Ig lambda chain V region (BO-08) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C;Accession: A44151
R;Zebddee, S.L.; Barbac II, C.F.; Hom, Y.L.; Caethoven, R.H.; Graff, R.; Degraw, J.; Pyg
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A;Reference number: A44151; MUID:92228746; PMID:1373487
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-112 <ZEB>
A;Note: nucleotide translation not given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;14-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 35.2%; Score 479; DB 2; Length 112;
Matches 89; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 152 LTOPPSAGTGGORVSTSCSSSSDISNTVMYQOLPGTAPKLLYSNNORP 211
DB 3 LTOPPSAGTGGORVSTSCSSSSDISNTVMYQOLPGTAPKLLYSNNORP 62
QY 212 SGFSKTSASLVISGLQSEDEADYCAAMDSEINGVFGGPR 254
DB 63 SGFSKTSASLVISGLQSEDEADYCAAMDSEINGVFGGPR 105

RESULT 12

B44151
Ig lambda chain V region (BO-09) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C;Accession: B44151
R;Zebddee, S.L.; Barbac II, C.F.; Hom, Y.L.; Caethoven, R.H.; Graff, R.; Degraw, J.; Pyg
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A;Reference number: A44151; MUID:92228746; PMID:1373487
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-112 <ZEB>
A;Cross-references: GB:M88310; NID:G183954; PIDN:AAA3568.1; PID:G183955
C;Keywords: heterotrimer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 35.2%; Score 479; DB 2; Length 112;
Matches 89; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 152 LTOPPSAGTGGORVSTSCSSSSDISNTVMYQOLPGTAPKLLYSNNORP 211
DB 3 LTOPPSAGTGGORVSTSCSSSSDISNTVMYQOLPGTAPKLLYSNNORP 62
QY 212 SGFSKTSASLVISGLQSEDEADYCAAMDSEINGVFGGPR 254
DB 63 SGFSKTSASLVISGLQSEDEADYCAAMDSEINGVFGGPR 105

RESULT 13

137782
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: 137782; S25476
R;Demaison, C.; Chastagner, P.; These, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by
A;Reference number: A36876; MUID:9411917; PMID:8290556
A;Accession: 137782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: EMBL:X67906; NID:G33582; PIDN:CAA6104.1; PID:G33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 35.2%; Score 478.5; DB 2; Length 140;
Matches 95; Conservative 9; Mismatches 16; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISGHDYMSWIRPPRGLEWIGFIFPDSTNYN 60
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGSISGHDYMSWIRPPRGLEWIGFIFPDSTNYN 79
QY 61 PSILNGRTISLDPSSKNQSLRLSTVAADTAVYFCAR-LKGAWLSEPPYFSSDGMVYG 119
DB 80 PSILKSRITISVDTSKNQFSLKLSVTAADTAVYFCARHNSSEWY---GRYF-----DYWG 131
QY 120 QGTVTVPS 128
DB 132 QGTVTVPS 140

RESULT 14

JCS322
p53 specific single-chain antibody pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JCS322
R;Janot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JCS322; MUID:97168950; PMID:9016757
A;Accession: JCS322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hybridoma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match

Best Local Similarity 35.2%; Score 478.5; DB 2; Length 233;
Matches 109; Conservative 32; Mismatches 71; Indels 25; Gaps 5;

QY 5 QESGPGLVKPSSETLSLTCTVSGSISGHDYMSWIRPPRGLEWIGFIFPDSTNYNPSL 63
DB 1 QESGABLVSGASVSKLSTTSGFNINDYMMHWKRPFGGLWIGRIDPENGDADMTSS 60
QY 64 NGRVITSLDPSKNQSLRLSTVAADTAVYFCARLKGAWLSEPPYFSSDGMVYGQGT 123
DB 61 GVAITMTATLSTSTAVYQLSLSTSDTAVYVC-----MGMDVYGQGT 104
QY 124 VTVPSGGGSGGGGGGGGGGSGGSGNFMULTO-PPASGTPGQRVSTSC--SGSSSDIGSN 180

```

Db      105 VTV-----SSGGGGSGGRASGGGSDIBLTQSPASLAVSLGQRATISCRASKSVSTSGYS 159
QY      181 TVNMWYQOLPGTAPKLLIYSNNORPSGVPRFSGFKSGTASALVYISGLQSEDEADYYC 237
Db      160 YHWMNQKRPQPPRLIYLVSNLESVPAFSGSGSGTPTLNHPVEEDATYYC 216

```

RESULT 15

```

S36047
I9: lambda chain - human (fragment)
C:/Species: Homo sapiens (man)
C:/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:/Accession: S36047
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:/Reference number: S36046
A:/Accession: S36047
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-98 <Wtl>
A:/Cross-references: EMBL:Z22188; NID:g312291; PID:CAA80198.1; PID:g312292
C:/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:/Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

```

```

Query Match      35.2%; Score 478; DB 2; Length 98;
Best Local Similarity 93.8%; Pred. No. 1.4e-24;
Matches 90; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      151 MLTQPPSASGTGPGQRYISCSGSSSDIGSNTVMWYQOLPGTAPKLLIYSNNORPSGVPR 210
Db      3 VLTQPPSASGTGPGQRYITISGSSSNIGSNTVMWYQOLPGTAPKLLIYSNNORPSGVPR 62
QY      211 FSGFKSGTASALVYISGLQSEDEADYYCAAWDESLNG 246
Db      63 FSGSKSGTASALVYISGLQSEDEADYYCAAWDSLNG 98

```

Search completed: May 13, 2004, 15:08:42
Job time : 13.467 secs

...S PAGE 04/11 (USFO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.15146 Seconds
(without alignments)
1849.388 Million cell updates/sec

Title: US-10-072-301-19

Perfect score: 1359

Sequence: 1 QVQLQESGPGGLVKKPSETLSL.....YYCAAMDSESLNGVFGGPR 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.7	32.9	146	1 HV21_HUMAN	P06331 homo sapien
2	44.6	32.9	129	1 HV2F_HUMAN	P01824 homo sapien
3	43.6	32.1	112	1 LV1F_HUMAN	P06887 homo sapien
4	43.5	32.0	111	1 LV1A_HUMAN	P01699 homo sapien
5	42.9	31.6	109	1 LV1F_HUMAN	P04208 homo sapien
6	41.8	30.8	130	1 LV1G_HUMAN	P06316 homo sapien
7	41.6	30.6	111	1 LV1D_HUMAN	P01702 homo sapien
8	41.3	30.4	112	1 LV1B_HUMAN	P01700 homo sapien
9	40.3	29.7	117	1 LV1C_HUMAN	P01825 homo sapien
10	40.0	29.4	111	1 LV1C_HUMAN	P01701 homo sapien
11	39.4	29.0	109	1 LV1I_HUMAN	P06888 homo sapien
12	36.5	26.9	137	1 HV46_MOUSE	P01822 mus musculu
13	36.2	26.7	113	1 HV47_MOUSE	P01823 mus musculu
14	35.9	26.4	111	1 LV2G_HUMAN	P01710 homo sapien
15	34.6	25.5	111	1 LV6D_HUMAN	P06318 homo sapien
16	34.6	25.5	111	1 LV2F_HUMAN	P01709 homo sapien
17	34.4	25.3	116	1 HV6D_MOUSE	P18531 mus musculu
18	34.1	25.1	112	1 LV2K_HUMAN	P04209 homo sapien
19	34.1	25.1	144	1 HV43_MOUSE	P01819 mus musculu
20	34.0	25.0	111	1 LV2B_HUMAN	P01705 homo sapien
21	33.7	24.8	103	1 LV1E_HUMAN	P01703 homo sapien
22	33.5	24.7	111	1 LV2D_HUMAN	P01707 homo sapien
23	33.3	24.5	111	1 LV2C_HUMAN	P01706 homo sapien
24	33.3	24.5	111	1 LV2H_HUMAN	P01711 homo sapien
25	32.9	24.2	116	1 HV6I_MOUSE	P18532 mus musculu
26	32.4	23.9	110	1 LV2J_HUMAN	P01813 homo sapien
27	32.4	23.9	131	1 LV6E_HUMAN	P06319 homo sapien
28	32.4	23.8	109	1 LV2E_HUMAN	P01708 homo sapien
29	32.4	23.8	111	1 LV2I_HUMAN	P01712 homo sapien
30	32.0	23.6	117	1 HV6J_MOUSE	P18533 mus musculu
31	31.9	23.5	111	1 LV3B_HUMAN	P07448 homo sapien
32	31.9	23.5	111	1 LV3B_HUMAN	P80748 homo sapien
33	31.9	23.5	135	1 HV02_XENLA	P20957 xenopus lae

34	31.8	23.4	106	1 LV4B_HUMAN	P01716 homo sapien
35	31.6	23.3	111	1 LV2A_HUMAN	P01704 homo sapien
36	31.3	23.0	106	1 LV4A_HUMAN	P01715 homo sapien
37	30.9	22.7	106	1 LV4E_HUMAN	P06889 homo sapien
38	30.5	22.4	108	1 LV5A_HUMAN	P01719 homo sapien
39	30.5	22.4	120	1 HV2B_HUMAN	P01815 homo sapien
40	30.2	22.3	125	1 HV2D_HUMAN	P01817 homo sapien
41	30.1	22.1	107	1 LV4C_HUMAN	P01717 homo sapien
42	30.1	22.1	111	1 LV6C_HUMAN	P06317 homo sapien
43	30.0	22.1	115	1 HV44_MOUSE	P01820 mus musculu
44	29.9	22.0	147	1 HV2H_HUMAN	P04438 homo sapien
45	29.2	21.5	119	1 HV2C_HUMAN	P01816 homo sapien

ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	146 AA.
AC	P06331			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V-II region ARH-77 precursor.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85205332; PubMed=3922855;			
RA	Kudo A., Ichihara T., Nishimura T., Watanabe T.;			
RT	"A cloned human immunoglobulin heavy chain gene with a novel direct-			
RL	repeat sequence in 5' flanking region."			
RL	Gene 33:181-189(1985).			
DR	PIR; A02101; GIHQH2.			
DR	HSSP; P01825; 7FAB.			
DR	GO; GO:0005576; Cxcracellular; NAS.			
DR	GO; GO:0005823; Fc antigen binding; NAS.			
DR	GO; GO:0006955; P immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_V.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE; PS00835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	19	
FT	DOMAIN	20	146	IG HEAVY CHAIN V-II REGION ARH-77.
FT	DOMAIN	118	117	V SEGMENT.
FT	DOMAIN	128	127	D SEGMENT.
FT	DISULFID	42	115	J SEGMENT.
FT	NON TER	146	146	BY SIMILARITY.
SO	SEQUENCE	146 AA;	16228 MW;	8D7FDS2B218171F CRC64;
Query Match		32.9%	Score 447;	DB 1; Length 146;
Best Local Similarity		70.8%	Pred. No. 8.8e-25;	
Matches	92;	Conservative	8;	Mismatches 24; Indels 6; Gaps 3;
QY	1 QVQLQESGPGGLVKKPSETLSLCTCTGSGSGTGHGYSWIRQPPGEGLEWIGFIFPDSTNNY 60			
DB	21 QVQLQESGPGGLVKKPSETLSLCTCAVFGSGFGYSWIRQPPGEGLEWIGFIFPDSTNNY 80			
QY	61 PSLNGRVTISLDTSKNQLSLRTSYTAADTAVYFCAR--LKGAWLSEBPYSSDGMQDW 118			
DB	81 TSLKSRVTISLDTSKNQLSLRTSYTAADTAVYFCARGLRGW--NDVDYY--GMDVW 136			
QY	119 GGGTIVTVPS 128			
DB	137 GGGTIVTVPS 146			

RESULT 2

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ID HVZF_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Ig heavy chain V-II region MAH.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=8222235; PubMed=6806818;
RT Takahashi N., Tetsart D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01825; 7FAB.
DR GLYCOSUB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 113 IG-LIKE.
FT NON_TER 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match
Best Local Similarity 32.9%; Score 446.5; DB 1; Length 129;
Matches 88; Conservative 15; Mismatches 19; Indels 13; Gaps 3;

QY 1 QVQLQESGPGLVKPESTLSLTCTVSGSIGHD--YMSWIRPQEGLEGVFFPDGSGTN 58
DB 1 RLQLQESGPGLVKPESTLSLTCTVSGGIRRTGYMGWIMQPGKLEWIGVYTGSLY 60
QY 59 YNPSLNGSVTSLTSTKXQSLRLTSTYADIAVFCARLKAMLSEPPYF-----SSD 113
DB 61 YNPSLRGVTSLVDTSRNPSLNRSVSADTAMTCAR-----GNPPYTDIGTGSDD 114
QY 114 GMDVWGQGTITVTPS 128
DB 115 GIDVWGQGTITVHVS 129

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RESULT 3

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ID LV1H_HUMAN STANDARD; PRT; 112 AA.
AC P06867;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Ig lambda chain V-I region MEM.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=8525762; PubMed=2410269;
RT Mihalaco B., Roy J.P., Congy N., Peran-Rivat L., Mihalaco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features."

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RL Bur. J. Blochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
CC WERE POSITIONED BY HOMOLOGY.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC MARKERS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A25479; L1HUM.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Monoclonal antibody;
FT DOMAIN 1 106 IG-LIKE.
FT MOD_RES 1 106 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 112
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFBE4 CRC64;

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Query Match
Best Local Similarity 32.1%; Score 436.5; DB 1; Length 112;
Matches 84; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

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QY 151 MLTOPPSASGTPGQRVISCSGSSSDIGSN-TVNMVQQLPGTAPKLLIYNNOGRSGVDP 209
DB 3 VLTOPPSASGTPGQRVISCSGSSSNVGSZPAYVYQQLPGTAPKLLIYNNOGRSGVDP 62
QY 210 RFSGPKSGTSASLVISGLQSEDEADYCAAMPESLNGVYFGGQPR 254
DB 63 RFSASRSGTSASLVISGLQSEDEADYCAAMPDSLDGYVFGTGT 107

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RESULT 4

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ID LV1A_HUMAN STANDARD; PRT; 111 AA.
AC P01699;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Ig lambda chain V-I region VOR.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=76023790; PubMed=809332;
RT Engelhard M., Hilschmann N.;
RT "Pattern of antibody structure. The amino acid sequence of a
RT monoclonal immunoglobulin L-chain of lambda-type, subgroup I
RT (Bence-Jones-protein Vor.). A contribution to the elucidation of the
RT origin of antibody specificity."
CC -1- MISCELLANEOUS: Chem. 356:1413-1444(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01962; L1HVO.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein;
KW Pyriolidone carboxylic acid.

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FT DOMAIN 1 105 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11514 MW; 219DF64250DFC8E0 CRC64;

Query Match
Best Local Similarity 77.9%; Pred. No. 4.5e-24;
Matches 81; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 151 MLTQPPASAGTPOGQVRSISCSGSSSDIGSNTVMYQOOLPGTAPKLLIYSNNQPSGVPR 210
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 VLTQPPASAGTPOGQVRSISCSGSSSDIGSNTVMYQOOLPGTAPKLLIYSNNQPSGVPR 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 211 FSGFKSGTSASLIVISGLQSEDEADYCAAMDESLINGVFGGGR 254
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 FSGFKSGTSASLIVISGLQSEDEADYCAAMDESLINGVFGGGR 106
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
LVIF HUMAN STANDARD; PRT; 109 AA.
ID LVIF_HUMAN
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region MAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=83221661; PubMed=6407018;
RT Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
RT the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; LIHUMA.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match
Best Local Similarity 82.4%; Pred. No. 1.1e-23;
Matches 84; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

QY 151 MLTQPPASAGTPOGQVRSISCSGSSSDIGSNTVMYQOOLPGTAPKLLIYSNNQPSGVPR 210
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 VLTQPPASAGTPOGQVRSISCSGSSSDIGSNTVMYQOOLPGTAPKLLIYSNNQPSGVPR 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 211 FSGFKSGTSASLIVISGLQSEDEADYCAAMDESLINGVFGGGR 252
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 FSGFKSGTSASLIVISGLQSEDEADYCAAMDESLINGVFGGGR 102
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
LVIG HUMAN STANDARD; PRT; 130 AA.
ID LVIG_HUMAN
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85062823; PubMed=6095199;
RT Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
RT sequence.";
RL Nucleic Acids Res. 12:8407-8414(1984).

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CC EMBL; X01147; CAA25598.1; -
CC PIR; A01966; LIHUBL.
CC HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR PIR; A01967; LIHUMA.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON TER 130 130
SQ SEQUENCE 130 AA; 13564 MW; FA44B17D3A55EBF CRC64;

Query Match
Best Local Similarity 69.1%; Pred. No. 8.1e-23;
Matches 76; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 145 GGSNFMLTQPPASAGTPOGQVRSISCSGSSSDIGSNTVMYQOOLPGTAPKLLIYSNNQPSGVPR 204
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 GSAQSVLTQPPASAGTPOGQVRSISCSGSSSDIGSNTVMYQOOLPGTAPKLLIYSNNQPSGVPR 75
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 205 SGVPRFSGFKSGTSASLIVISGLQSEDEADYCAAMDESLINGVFGGGR 254
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 SGVPRFSGFKSGTSASLIVISGLQSEDEADYCAAMDESLINGVFGGGR 125
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
LVIG HUMAN STANDARD; PRT; 111 AA.
ID LVIG_HUMAN
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=83186114; PubMed=6404900;
RT Kamezani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RT Shimizu A.;

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"Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subgroup.",
 J. Blochem. 93:421-429(1983).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSP; P01703; 7FAB.

DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 105
 FT MOD RES 1 105
 FT DISTLFD 22 89
 FT NON TER 111
 FT BY SIMILARITY.
 SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match Best Local Similarity 30.6%; Score 416; DB 1; Length 111;
 Matches 77; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 151 MLTPPSASGTPGQRYVISCSSGSSSDIGSNVTYVYQQLPGTAPKLLIYSNNQPSGVDP 210
 DB 3 VLTPPSVSAPQGEVTVISCGSSNGTNNVYVYQQLPGTAPKLLIYDRDKRPSGVDP 62
 QY 211 FSGFKSGTASLVISGLQSEDEADYCAAMDESLNGVFGGG 254
 DB 63 FSGSKSGTATLGTGTGTGDEADYCCGMDSLSVGMFGGGTR 106

RESULT 8

LV1B HUMAN STANDARD; PRT; 112 AA.
 AC P01703;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-I region HA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71103824; PubMed=5532227;
 RA Shinoda T., Titani K., Putnam F.W.,
 RT "Amino acid sequence of human lambda chains. II. Chymotryptic
 RT peptides and sequence of protein Ha."
 RL J. Biol. Chem. 245:4475-4487(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A01963; L1HUNA.
 DR HSP; P01703; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein;
 KW Pyrrolidone carboxylic acid.
 KM Pyrrolidone carboxylic acid.
 FT DOMAIN 1 106
 FT MOD RES 1 106
 FT DISTLFD 22 90
 FT NON TER 112
 FT BY SIMILARITY.
 SQ SEQUENCE 112 AA; 11996 MW; 8D73378F3F5CD039 CRC64;

Query Match Best Local Similarity 30.4%; Score 413.5; DB 1; Length 112;
 Matches 80; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 151 MLTPPSASGTPGQRYVISCSSGSSSDIGSNVTYVYQQLPGTAPKLLIYSNNQPSGVDP 209
 DB 3 VLTPPSVSAPQGEVTVISCGSSNGTNNVYVYQQLPGTAPKLLIYDRDKRPSGVDP 62
 QY 210 FSGFKSGTASLVISGLQSEDEADYCAAMDESLNGVFGGG 252
 DB 63 FSGSKSGTATLGTGTGTGDEADYCCGMDSLSVGMFGGGTR 105

RESULT 9

HV2G HUMAN STANDARD; PRT; 117 AA.
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region NEMW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242302; PubMed=407927;
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the VH region of a human myeloma
 RT immunoglobulin (IgG New)."
 RL Biochemistry 16:3412-3420(1977).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE=78066916; PubMed=618887;
 RA Saul F.A., Amzel L.M., Poljak R.J.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 RT from human immunoglobulin new at 2.0-A resolution."
 RL J. Biol. Chem. 253:585-597(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGCl MYELOMA
 CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90404; G1HUM.
 DR PDB; 7FAB; 31-JAN-94.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 111
 FT MOD RES 1 111
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59
 FT TURN 61 63
 FT STRAND 64 66
 FT TURN 67 72
 FT STRAND 73 76
 FT TURN 77 82
 FT STRAND 87 89
 FT HELIX 91 98
 FT STRAND 104 107

FT STRAND 111 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D37 CRC64;
Query Match 29.7%; Score 403.5; DB 1; Length 117;
Best Local Similarity 58.5%; Pred. No. 7.4e-22;
Matches 76; Conservative 22; Mismatches 17; Indels 15; Gaps 2;
QY 1 QVQLQESGGPVGVKPSQSLTCTVSGGSIIGHDWMSIRPPGKLEWIGFIPFGDSTNN 60
1 QVQLQESGGPVGVKPSQSLTCTVSGGSIIGHDWMSIRPPGKLEWIGFIPFGDSTNN 60
DB 1 QVQLQESGGPVGVKPSQSLTCTVSGGSIIGHDWMSIRPPGKLEWIGFIPFGDSTNN 60
QY 61 PSINGRVITSLDTSKQQLSLRLTVAAADTAAYFCAR--LKGAMLLSEPPYFSSDDMDYV 118
61 PSINGRVITSLDTSKQQLSLRLTVAAADTAAYFCAR--LKGAMLLSEPPYFSSDDMDYV 118
DB 61 TPLRSVITMLVDTSKQQLSLRLTVAAADTAAYFCAR--LKGAMLLSEPPYFSSDDMDYV 107
QY 119 GGGTIVTVPS 128
119 GGGTIVTVPS 128
DB 108 GGGTIVTVPS 117
RESULT 10
LVIC_HUMAN STANDARD; PRT; 111 AA.
AC P01701;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=69060892; PubMed=4177823;
RX Langer B., Steinmetz-Kayne M., Hillechmann N.;
RT "The complete amino acid sequence of Bence Jones protein New (lambda-
RT type). Subgroups in the variable part of immunoglobulin L-chains of
RT the lambda-type."
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyroglutamate carboxylic acid.
FT DOMAIN 1 105
FT MOD_RES 1 105 IG-LIKE.
FT DISULFID 22 89 PYROGLUTAMATE CARBOXYLIC ACID.
FT NON TER 111 111 BY SIMILARITY.
SQ SEQUENCE 111 AA; 11453 MW; AAEBCA3C49F2AD3 CRC64;
Query Match 29.4%; Score 400; DB 1; Length 111;
Best Local Similarity 69.2%; Pred. No. 1.2e-21;
Matches 72; Conservative 16; Mismatches 16; Indels 0; Gaps 0;
QY 151 MTPPPSAGTGPGRVVISCGSSSDIGSNTVWYQQLPGTAPKLLIYSNNORPSGVPR 210
151 MTPPPSAGTGPGRVVISCGSSSDIGSNTVWYQQLPGTAPKLLIYSNNORPSGVPR 210
DB 3 VLTQPPSVAAPGQKVTISCGSSGNTVGNVYVSMHGLHETAPKLLIYEDNKRPSGIPDR 62
3 VLTQPPSVAAPGQKVTISCGSSGNTVGNVYVSMHGLHETAPKLLIYEDNKRPSGIPDR 62
QY 211 FSGFKSGTSASLVISGLQSEDEADYVCAAMDLSLNGVFGGPR 254
211 FSGFKSGTSASLVISGLQSEDEADYVCAAMDLSLNGVFGGPR 254
DB 63 ISAKSGTSATLIGTGLRTGDEADYVCAATWSSSLNAVVFVGQTK 106
63 ISAKSGTSATLIGTGLRTGDEADYVCAATWSSSLNAVVFVGQTK 106

RESULT 11
LVII_HUMAN STANDARD; PRT; 109 AA.
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=86000126; PubMed=3929803;
RX Toft K.G., Sletten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
RT containing amyloid fibril protein EPS (immunoglobulin light chain,
RT type lambda)."
CC Biol. Chem. Hoppe-Sevler 366:617-625 (1985).
CC -1- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
CC PEPTIDES WERE POSITIONED BY HOMOLOGY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT DOMAIN 1 105
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .).
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;
Query Match 29.0%; Score 394; DB 1; Length 109;
Best Local Similarity 73.5%; Pred. No. 3.1e-21;
Matches 75; Conservative 11; Mismatches 14; Indels 2; Gaps 1;
QY 151 MTPPPSAGTGPGRVVISCGSSSDIGSNTVWYQQLPGTAPKLLIYSNNORPSGVPR 210
151 MTPPPSAGTGPGRVVISCGSSSDIGSNTVWYQQLPGTAPKLLIYSNNORPSGVPR 210
DB 3 VLTQPPSVAAPGQKVTISCGSSGNTVGNVYVSMHGLHETAPKLLIYEDNKRPSGIPDR 62
3 VLTQPPSVAAPGQKVTISCGSSGNTVGNVYVSMHGLHETAPKLLIYEDNKRPSGIPDR 62
QY 211 FSGFKSGTSASLVISGLQSEDEADYVCAAMDLSLNGVFGG 252
211 FSGFKSGTSASLVISGLQSEDEADYVCAAMDLSLNGVFGG 252
DB 63 FSGKSGTSATLIGTGLRTGDEADYVCAATWSSSLNAVVFVGQ 102
63 FSGKSGTSATLIGTGLRTGDEADYVCAATWSSSLNAVVFVGQ 102
RESULT 12
HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment."
MOL. Immunol. 26:431-434 (1989).

[2]
 RN SEQUENCE OF 1-31.
 RX MEDLINE=78094475; PubMed=414225;
 RA Jilka R.L., Peckha S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse
 RL immunoglobulin heavy chain";
 RN Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
 [3]
 RN SEQUENCE OF 1-21.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemel R., Birstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors";
 RN Fed. Proc. 38:1839-1845(1979).
 [4]
 RN SEQUENCE OF 19-136.
 RX MEDLINE=74170779; PubMed=4524622;
 RA Francis S.H., Leslie R.G.O., Hood L., Bisen H.N.;
 RT "Amino acid sequence of the variable region of the heavy (alpha)
 RL chain of a mouse myeloma protein with anti-hapten activity";
 RN Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 [5]
 RN REVISION TO 53.
 RX MEDLINE=7724979; PubMed=268248;
 RA Hood L., Margolies M.N., Givol D., Zakut R.;
 RL Unpublished results, cited by:
 RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 CC -----
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 CC -----
 DR EMBL; M27638; AA61337.1; -;
 DR EMBL; X07880; CAA30727.1; -;
 DR PIR; P10102; AVMS35.
 DR HSRP; P01825; 7FAB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL.
 FT CHAIN 1
 FT DOMAIN 19 137
 FT DOMAIN 19 48
 FT DOMAIN 49 54
 FT DOMAIN 55 68
 FT DOMAIN 69 84
 FT DOMAIN 85 116
 FT DOMAIN 117 126
 FT DOMAIN 127 137
 FT DISULFID 40 114
 FT CONFLICT 15 15
 FT CONFLICT 15 15
 FT CONFLICT 77 78
 FT CONFLICT 102 102
 FT CONFLICT 123 123
 FT NON TER 137
 SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 26.9%; Score 365.5; DB 1; Length 137;
 Best Local Similarity 58.6%; Pred. No. 5.9e-19;
 Matches 75; Conservative 16; Mismatches 26; Indels 11; Gaps 3;

QY 2 VOLQSSGGGLVKKPSETSLTCTVSGSGSIGHDY-MSWIRPQPGGLGEMIGIFPDGDTNN 60
 DB 20 VOLQSSGGGLVKKPSETSLTCTVSGSGSIGHDY-MSWIRPQPGGLGEMIGIFPDGDTNN 60

QY 61 PSINGRVTISDTSKNQLSLRTSVTAADAVVFCARLKGAWLSEPPFSDDGMDVMQ 120
 DB 80 PSINGRVTISDTSKNQLSLRTSVTAADAVVFCARLKGAWLSEPPFSDDGMDVMQ 120
 QY 121 GTTATVPS 128
 DB 130 GTTATVPS 137
 RESULT 13
 HV47_MOUSE
 ID HV47_MOUSE STANDARD; PRT; 113 AA.
 AC P01823;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IG heavy chain V region 36-60.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=8402451; PubMed=6414509;
 RA Ujczak E.C., Margolies M.N.;
 RT "Amino acid sequence of the heavy chain variable region from the A/J
 RT mouse anti-azobenzene monoclonal antibody 36-60 bearing a minor
 RL idio-type";
 RL Biochemistry 22:4291-4296(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTARSONATE
 CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
 CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTARSONATE RESPONSE OF
 CC STRAIN A/J MICE.
 DR PIR; A02098; G2MS60.
 DR PDB; 1J10; 18-FEB-03.
 DR PDB; 1J1P; 18-FEB-03.
 DR PDB; 1J1X; 18-FEB-03.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT NON TER 113
 SQ SEQUENCE 113 AA; 12734 MW; 38DC0B03F507587 CRC64;

Query Match 26.7%; Score 362.5; DB 1; Length 113;
 Best Local Similarity 56.3%; Pred. No. 5.1e-19;
 Matches 71; Conservative 17; Mismatches 23; Indels 15; Gaps 1;

QY 1 OVQLOSGGGLVKKPSETSLTCTVSGSGSIGHDYMSWIRPQPGGLGEMIGIFPDGDTNN 60
 DB 1 OVQLOSGGGLVKKPSETSLTCTVSGSGSIGHDYMSWIRPQPGGLGEMIGIFPDGDTNN 60
 QY 61 PSINGRVTISDTSKNQLSLRTSVTAADAVVFCARLKGAWLSEPPFSDDGMDVMQ 120
 DB 61 PSINGRVTISDTSKNQLSLRTSVTAADAVVFCARLKGAWLSEPPFSDDGMDVMQ 120
 QY 121 GTTATVPS 128
 DB 121 GTTATVPS 128
 QY 121 GTTATVPS 128
 DB 121 GTTATVPS 128

RESULT 14
 LV2G_HUMAN
 ID LV2G_HUMAN STANDARD; PRT; 111 AA.
 AC P01710;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IG lambda chain V-II region BO.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=71103825; PubMed=5532228;
RA Wikler M., Putnam F.W.;
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
RT chymotryptic peptides, and sequence of protein Bo.";
RL J. Biol. Chem. 245:4488-4507(1970).
CC -1- SIMILARITY: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01976; 12HUBO.
DR HSSP; P01976; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyrolydine carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD_RES 1 1 PYROLYDINE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 26.4%; Score 359; DB 1; Length 111;
Best Local Similarity 65.4%; Pred. No. 8.7e-19;

Matches 68; Conservative 19; Mismatches 15; Indels 2; Gaps 2;

QY 152 LTQPPSASGTPGQRYVISCSSSSSDIGSNT-VNMYQQLPGTAPKLLIYNNQRPSPGVPDR 210
DB 4 LTQPPSASGTPGQRYVISCSSSSSDIGSNT-VNMYQQLPGTAPKLLIYNNQRPSPGVPDR 63

QY 211 FSGFKSGTASLVISGLQSEDEADYCAAMDESINGVFGGPR 254
DB 64 FSGFKSGTASLVISGLQSEDEADYCAAMDESINGVFGGPR 106

RESULT 15

LV6D_HUMAN STANDARD; PRT; 111 AA.
AC P06318;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region WLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86122667; PubMed=4089539;
RA Dwyer F.E., Strako K., Benson M.D.;
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein
RT (WLT).";
RL Scand. J. Immunol. 22:653-660(1985).
DR PIR; A01989; L6HULT.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region.
FT DOMAIN 1 22 FRAMEWORK-1.
FT DOMAIN 23 35 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 36 50 FRAMEWORK-2.
FT DOMAIN 51 57 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 58 91 FRAMEWORK-3.
FT DOMAIN 92 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 22 91 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;

Query Match 25.5%; Score 346.5; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 6.5e-18;

Matches 70; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 149 NFMLTQPPSASGTPGQRYVISCSSSSSDIGSNT-VNMYQQLPGTAPKLLIYNNQRPSPGVP 208
DB 1 NFMLTQPPSASGTPGQRYVISCSSSSSDIGSNT-VNMYQQLPGTAPKLLIYNNQRPSPGVP 60

QY 209 DRFSGF--KSGTASLVISGLQSEDEADYCAAMDESINGVFGG 251
DB 61 DRFSGSIDSSNSASLITISGLTEDEADYCAAMDESINGVFGG 104

Search completed: May 13, 2004, 15:02:04
Job time : 8.15146 secs

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Db      40 QVQLQSGGGLVYPGGSLKSCAASGSPSRVMSWVQAPGKLEWIGELNPDSSITNY 99
Qy      60 NPSLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCARLKGMALLSEPPYFSSDGMVWG 119
Db      100 TSLKDKFTISRDNAKNTLYLQMSKYSRESDTALYYCARAS-----YGHSA--YWG 148
Qy      120 QGTTVTVPSGGGSGGGSGGGGSGGSGSNFMFLTPPSASGTGQGVSTISCGSSSDIG 178
Db      149 QGTTVTV-----SSGGGSGGGSGGGGSDIELTQSPASLSASVGEVITTCRASGNI-- 201
Qy      179 SNTVMVYQOLPGTAPKLLIYNNQRPSPGVDPDRFSGFGSGTASAVISGLQSEDEADYCA 238
Db      202 HNYLWYQOKQKSKPKQLLVYNKATLADGVPSRFSGSGSGTGYSLKINSIQPEDPGSTYCO 261
Qy      239 -AMDESINGVFGGQPR 254
Db      262 HFW---TTPYTFGGGQTK 275

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RESULT 2
Q7TOM2 PRELIMINARY; PRT; 243 AA.
ID Q7TOM2
AC Q7TOM2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE SAGV 6H8 protein (fragment).
GN SAGV 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxId=10090;
RP SEQUENCE FROM N.A.
RA Peter J.C., Eftekhari P., Billiaid P., Wallukat G.;
RT the beta-2 adrenergic receptor.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAB00495.1; -.
FT NON_TER 1
SQ SEQUENCE 243 AA; 25976 MW; BFF64D2DC4F76 CRC64;

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Query Match
Best Local Similarity 37.94; Score 515.5; DB 11; Length 243;
Matches 114; Conservative 39; Mismatches 77; Indels 27; Gaps 8;
Qy      1 QVQLQSGGGLVYPGGSLKSCAASGSPSRVMSWVQAPGKLEWIGELNPDSSITNY 99
Db      1 QVQLQSGGGLVYPGGSLKSCAASGSPSRVMSWVQAPGKLEWIGELNPDSSITNY 99
Qy      60 NPSLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCARLKGMALLSEPPYFSSDGMVWG 119
Db      61 DEKFKKAGILTVDTSSSTAYMHLISLASDSAYYCAR-----GGRSLDWG 107
Qy      120 QGTTVTVPSGGGSGGGSGGGGSGGSGSNFMFLTPPSA-SGTPQQRVSISSGSSSDIG 178
Db      108 AGTTLTV-----SSGGGSGGGSGGGGSDIOMTSSSFVSICDRYITICK-ASEDI- 160
Qy      179 SNTVMVYQOLPGTAPKLLIYNNQRPSPGVDPDRFSGFGSGTASAVISGLQSEDEADYCA 238
Db      161 YNRIANYQOKPQNAAPLLISGATSLFETGVPSRFSGSGSGKDYSLISLQTEADVATYCO 220
Qy      239 A-WDESINGVFGGQPR 254
Db      221 QYWSTR---TFGGGQTK 233

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RESULT 3
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      Anti-CEA 79 single chain Fv fragment (fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxId=10090;
RP      SEQUENCE FROM N.A.
RA      MEDLINE=98170165; PubMed=9509426;
RA      Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA      Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT      Cloning and characterization of cDNAs encoding VH and VL of a
RT      monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RL      M01. Cells 7:816-819(1997).
DR      EMBL; U88067; AAB48044.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      Pfam; PF00047; Ig_2.
DR      SMART; SM00406; Ig_2.
DR      PROSITE; PS50835; Ig_LIKE; 2.
FT      NON_TER 1
FT      NON_TER 241
SQ      SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

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Query Match
Best Local Similarity 36.44; Score 494.5; DB 11; Length 241;
Matches 117; Conservative 34; Mismatches 78; Indels 31; Gaps 11;
Qy      1 QVQLQSGGGLVYPGGSLKSCAASGSPSRVMSWVQAPGKLEWIGELNPDSSITNY 99
Db      1 QVQLQSGGGLVYPGGSLKSCAASGSPSRVMSWVQAPGKLEWIGELNPDSSITNY 99
Qy      60 NPSLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCARLKGMALLSEPPYFSSDGMVWG 119
Db      61 ADDEKGFAPASLSTASVTAYLQINLNKEDTATYFCARD--LIR-----DYWG 109
Qy      120 QGTTVTVPSGGGSGGGSGGGGSGGSGSNFMFLTPPSA-SGTPQQRVSISSGSSSDIG 178
Db      110 QGTTVTV-----SSGGGSGGGSGGGGSDIELTQSPASLSASVGEVITTCRASGNI-- 201
Qy      179 SNTVMVYQOLPGTAPKLLIYNNQRPSPGVDPDRFSGFGSGTASAVISGLQSEDEAD 234
Db      163 NXRIANYQKPKKGRPSAHTLHTYQ---PQISRFSGSGSGRDYFSFISNLEPEDIA 218
Qy      235 YTCANDESINGVFGGQPR 254
Db      219 YTCALHYD---NLATPGGQTK 235

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RESULT 4
Q96EYO PRELIMINARY; PRT; 613 AA.
ID Q96EYO
AC Q96EYO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxId=9606;
RP SEQUENCE FROM N.A.
RA Tissue-B-cell;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AA011857.1; -.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.

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DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 36.1%; Score 491; DB 4; Length 613;
Best Local Similarity 47.5%; Pred. No. 5.5e-11;
Matches 114; Conservative 20; Mismatches 62; Indels 44; Gaps 5;

QY 1 QVQLQSGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGSGLEWIGIFPFDSSTNN 60
DB 20 QVQLQSGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGSGLEWIGIFPFDSSTNN 79
QY 61 PSILNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKAWLSEPPYSSDGMVWQ 120
DB 80 PSILKSRVTISVDTSKNQLSLRTSVTAADTAAYVCA-----SQPWELPTVGLPYWQ 131
QY 121 GTTVTVPSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVSISSGSSSDIGSN 180
DB 132 GTTVTVSSG-----SASAPTLFPLVSCENSPDTSV 163
QY 181 TVNMWYQQ--LPGTAPKRLIYSNNQRPSS---GVDPREFSGFKSGTSASLVISG---LQSEDE 232
DB 164 AVGCIAQDFLPDSITFSWKYKNNSDISSTRGFPVSVRGKRYAATSGVLLPSKDVWQGTDE 223

RESULT 5

Q9UL73 PRELIMINARY; PRT; 119 AA.

ID Q9UL73
AC Q9UL73
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
RP MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.U., Kalis N.N., Berner S.M.,
RT Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

Query Match 35.4%; Score 480.5; DB 4; Length 119;
Best Local Similarity 74.2%; Pred. No. 5.3e-11;
Matches 95; Conservative 8; Mismatches 16; Indels 9; Gaps 3;
QY 1 QVQLQSGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGSGLEWIGIFPFDSSTNN 60
DB 1 QVQLQSGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGSGLEWIGIFPFDSSTNN 60
QY 61 PSILNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKAWLSEPPYSSDGMVWQ 120
DB 61 PSILKSRVTISVDTSKNQLSLRTSVTAADTAAYVCA-----GPYV---FDYWQ 111
QY 121 GTTVTVPS 128

DB 112 GTTVTVSS 119

RESULT 6

Q8WUX4 PRELIMINARY; PRT; 588 AA.

ID Q8WUX4
AC Q8WUX4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
RP Straussberg R.;
RT Tissue-Lymph;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39ED7 CRC64;

Query Match 34.5%; Score 469.5; DB 4; Length 588;
Best Local Similarity 46.7%; Pred. No. 2.7e-29;
Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQSGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGSGLEWIGIFPFDSSTNN 60
DB 20 QVQLQSGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGSGLEWIGIFPFDSSTNN 79
QY 61 PSILNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKAWLSEPPYSSDGMVWQ 120
DB 80 PSILKSRVTISVDTSKNQLSLRTSVTAADTAAYVCA---ITRASPTDGRYGMVWQ 136
QY 121 GTTVTVPSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVSISSGSSSDIGSN 180
DB 137 GTTVTVSSG-----SASAPTLFPLVSCENSPDTSV 168
QY 181 TVNMWYQQ--LPGTAPKRLIYSNNQRPSS---GVDPREFSGFKSGTSASLVISG---LQSEDE 232
DB 169 AVGCIAQDFLPDSITFSWKYKNNSDISSTRGFPVSVRGKRYAATSGVLLPSKDVWQGTDE 228

RESULT 7

Q9BU10 PRELIMINARY; PRT; 597 AA.

ID Q9BU10
AC Q9BU10
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
RP Tissue-Lymph;
RL Straussberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.

DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Ig_1.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; 3.
 DR Hypothetical protein.
 SO SEQUENCE 597 AA; 65274 MW; 2DAFAPB7E055851 CRC64;

Query Match 34.5%; Score 469.5; DB 4; Length 597;
 Best Local Similarity 46.7%; Pred. No. 2.8e-29;
 Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSETSLTCTVSGSGSIGHDYMSWIRPQEGLEWIGTFFDGSNTYN 60
 DB 20 QVQLQOMWAGLTKPSETSLTCTGVYGSFSGYMSWIRPQEGLEWIGTFFDGSNTYN 79
 QY 61 PSILNGRVTISLDTSSKQSLRLTSTYADTAIVYFCARLKGMWLSSEPFSSDGMVWQ 120
 DB 80 PSLSKRVTISVDTSSKQSLRLTSSVNAADTAIVYCARV---ITRASFGTDGRYGMVWQ 136
 QY 121 GTTAVTPSGGGSGGGSGGGSGGGSNFMLTQPSASGTQQRVSISSGSSSDIGSN 180
 DB 137 GTTAVTSSG-----SASAPTLPELVSCENSPSDTSSV 168
 QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP-----GVDPDFSGFSGTSAALVLSG---LQSEDE 232
 DB 169 AVGLADFLPDSTITFSWKYKNNSDISSTRGFPSVLRGKGYAATQVLLPSKDVWQGTDE 228

RESULT 8

ID Q96AA6 PRELIMINARY; PRT; 618 AA.
 AC Q96AA6;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 OS Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017356; AAH17356.1; -
 DR InterPro: IPR007110; Ig_LIKE.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Ig_1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 DR Hypothetical protein.
 SO SEQUENCE 618 AA; 67758 MW; 96DBD4C7C69650A6 CRC64;

Query Match 34.5%; Score 469.5; DB 4; Length 618;
 Best Local Similarity 46.7%; Pred. No. 2.9e-29;
 Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSETSLTCTVSGSGSIGHDYMSWIRPQEGLEWIGTFFDGSNTYN 60
 DB 20 QVQLQOMWAGLTKPSETSLTCTGVYGSFSGYMSWIRPQEGLEWIGTFFDGSNTYN 79
 QY 61 PSILNGRVTISLDTSSKQSLRLTSTYADTAIVYFCARLKGMWLSSEPFSSDGMVWQ 120
 DB 80 PSLSKRVTISVDTSSKQSLRLTSSVNAADTAIVYCARV---ITRASFGTDGRYGMVWQ 136
 QY 121 GTTAVTPSGGGSGGGSGGGSGGGSNFMLTQPSASGTQQRVSISSGSSSDIGSN 180

DB 137 GTTAVTSSG-----SASAPTLPELVSCENSPSDTSSV 168
 QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP-----GVDPDFSGFSGTSAALVLSG---LQSEDE 232
 DB 169 AVGLADFLPDSTITFSWKYKNNSDISSTRGFPSVLRGKGYAATQVLLPSKDVWQGTDE 228

RESULT 9

ID Q9BQB8 PRELIMINARY; PRT; 597 AA.
 AC Q9BQB8;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 OS Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle, and Lymph;
 RA Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AAH06180.1; -
 DR EMBL; BC001872; AAH01872.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro: IPR007110; Ig_LIKE.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Ig_1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 DR Hypothetical protein.
 SO SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 34.1%; Score 463.5; DB 4; Length 597;
 Best Local Similarity 46.2%; Pred. No. 8.4e-29;
 Matches 111; Conservative 19; Mismatches 71; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSETSLTCTVSGSGSIGHDYMSWIRPQEGLEWIGTFFDGSNTYN 60
 DB 20 QVQLQOMWAGLTKPSETSLTCTGVYGSFSGYMSWIRPQEGLEWIGTFFDGSNTYN 79
 QY 61 PSILNGRVTISLDTSSKQSLRLTSTYADTAIVYFCARLKGMWLSSEPFSSDGMVWQ 120
 DB 80 PSLSKRVTISVDTSSKQSLRLTSSVNAADTAIVYCARV---ITRASFGTDGRYGMVWQ 136
 QY 121 GTTAVTPSGGGSGGGSGGGSGGGSNFMLTQPSASGTQQRVSISSGSSSDIGSN 180
 DB 137 GTTAVTSSG-----SASAPTLPELVSCENSPSDTSSV 168
 QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP-----GVDPDFSGFSGTSAALVLSG---LQSEDE 232
 DB 169 AVGLADFLPDSTITFSWKYKNNSDISSTRGFPSVLRGKGYAATQVLLPSKDVWQGTDE 228

RESULT 10

ID Q925S1 PRELIMINARY; PRT; 218 AA.
 AC Q925S1;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;

DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AAB68783.1; -.
DR PDB; 1KU4; 29-MAY-02.
DR InterPro; IPR003596; IG_1like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 32.7%; Score 445; DB 4; Length 108;
Best Local Similarity 84.8%; Pred. No. 3.2e-28;
Matches 84; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 151 MLTPPSASGTGPGORVYISGSGSSSDIGSNTVMYQOLPGTAPKLLIYSNNRPSGVPR 210
DB 3 VLTQPSASGTGPGORVYISGSGSSSDIGSNTVMYQOLPGTAPKLLIYSNNRPSGVPR 62

QY 211 FSGFKGTSASLVISGLQSEADADYCAAMDESINGVVF 249
DB 63 FSGSKGTSASLVISGLQSEADADYCAAMDDLSCGMW 101

RESULT 14
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CSDDL004YMI9 of B cells (Ramos cell line)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Genoscope;
RL Submitted (PEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA "Full-length cDNA libraries and normalization."
RT Submitted (PEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX243300; CAD62627.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmaid.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1B2302410B4F8C CRC64;

Query Match 32.6%; Score 443; DB 4; Length 139;
Best Local Similarity 84.5%; Pred. No. 6.3e-28;
Matches 82; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISG--HDYMSWIRPPGEGLEWIGFIFPDGSTN 60
DB 33 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSYWMSWIRPPGEGLEWIGIYSGSTN 92

QY 61 PSLNGRVITSLTSTKQQLSLRTSTYADTAVYFCAR 97
DB 93 PSLKRVITSLTSTKQQLSLRTSTYADTAVYFCAR 129

RESULT 15
Q95973 PRELIMINARY; PRT; 150 AA.
AC Q95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
RT Rheumatoid arthritis patient with arthritis."
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR HSSP; P01825; 7FAB
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1
FT CHAIN 20
FT NON_TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 31.6%; Score 429; DB 4; Length 150;
Best Local Similarity 65.4%; Pred. No. 9.1e-27;
Matches 89; Conservative 10; Mismatches 21; Indels 16; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISG--HDYMSWIRPPGEGLEWIGFIFPDGSTN 58
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSTNYWGWIRPPGEGLEWISLNSGSDY 79

QY 59 YNPSLNGRVITSLTSTKQQLSLRTSTYADTAVYFCARL-KGAWLLSEPPYFSSDGMV 117
DB 80 YNPSLKRVITSLTSTKQQLSLRTSTYADTAVYFCARLKGAWLLSEPPYFSSDGMV 126

QY 118 WGGGTVTVPSGGGGS 133
DB 127 WGGGTVTVPSGGGGS 142

Search completed: May 13, 2004, 15:06:56
Job time : 35.1544 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 51.4563 Seconds

(without alignments)
1372.754 Million cell updates/sec

Title: US-10-072-301-21

Sequence: 1 QVQLQQWKGAGLTKMCTLSL.....CLQHDNFPITFGGKVEIK 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_292a04:*

1: geneseqp1980a:***
2: geneseqp1990a:***
3: geneseqp2000a:***
4: geneseqp2001a:***
5: geneseqp2002a:***
6: geneseqp2003a:***
7: geneseqp2003b:***
8: geneseqp2004a:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	835	62.5	249	5	ABP45310 Human Bly
2	816.5	57.7	249	5	AAU75150 Human Bly
3	771.5	57.7	256	3	AAV55072 Interleuk
4	771.5	57.7	260	3	AAV55075 Single ch
5	771.5	57.7	367	3	AAV55078 Single ch
6	771.5	57.7	381	3	AAV55079 Single ch
7	771.5	57.7	519	3	AAV55080 Single ch
8	771.5	57.7	546	3	AAV55074 Single ch
9	771.5	57.7	626	3	AAV55081 Single ch
10	771.5	57.7	640	3	AAV55082 Single ch
11	756	56.6	251	5	ABP45038 Human Bly
12	740.5	55.4	252	5	ABP45315 Human Bly
13	738.5	55.3	248	5	ABP45349 Human Bly
14	738.5	55.3	250	5	ABP45402 Human Bly
15	735	55.0	255	5	ABP45631 Human Bly
16	733.5	54.9	250	5	ABP45634 Human Bly
17	730.5	54.7	253	5	AAU72867 PS-9 sing
18	729.5	54.6	253	5	ABP45322 Human Bly
19	729.5	54.6	254	5	ABP45648 Human Bly
20	728.5	54.5	244	2	AAV21883 Amino aci
21	718	53.7	241	4	AAAB6061 Human TF
22	716	53.6	209	2	AAK50092 Humanised
23	715	53.5	253	5	ABP44943 Human Bly
24	714.5	53.5	240	4	AAAB6020 Human MUC
25	713	53.4	249	5	ABP44946 Human Bly

26	712.5	53.3	241	7	ADC64791	ADC64791 Hu-B-A5 c
27	711.5	53.3	241	7	ADC64785	ADC64785 Hu-B4-1 c
28	709	53.1	255	5	ABP45586	ABP45586 Human Bly
29	708.5	53.0	240	4	AAAB5992	AAAB5992 Human MUC
30	705.5	52.8	242	3	AAV58236	AAV58236 Interleuk
31	704	52.7	253	5	ABP45591	ABP45591 Human Bly
32	700.5	52.4	240	4	AAAB6039	AAAB6039 Human TF
33	699.5	52.4	240	4	AAAB6021	AAAB6021 Human MUC
34	699	52.3	239	5	ABP45328	ABP45328 Human Bly
35	699	52.3	245	2	AAU06714	AAU06714 Antibody
36	698	52.2	237	5	ABP45895	ABP45895 Human Bly
37	697	52.2	255	5	ABP45615	ABP45615 Human Bly
38	696.5	52.1	240	4	AAAB6018	AAAB6018 Human MUC
39	696	52.1	249	5	ABP45911	ABP45911 Human Bly
40	695.5	52.1	231	7	ADC64788	ADC64788 Hu-A-B5 c
41	695.5	52.1	251	5	AAU72868	AAU72868 PS-10 sin
42	694.5	52.0	240	4	AAAB5993	AAAB5993 Human MUC
43	694.5	52.0	240	4	AAAB5991	AAAB5991 Human MUC
44	694	51.9	253	5	ABP45328	ABP45328 Human Bly
45	693.5	51.9	241	7	ADC64787	ADC64787 Hu-A-D2 c

ALIGNMENTS

RESULT 1
ABP45310
ID ABP45310 standard; protein, 249 AA.
XX
AC ABP45310;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1321.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX Tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX anti-IL1DS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001MO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SW, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 1979-1980; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

XX Screening libraries of tester proteins against protein, peptide or
PT nucleic acid target(s) using a two-hybrid method in yeast, useful for
PT generating recombinant human antibodies and screening for their affinity
PT binding with target antigens.
XX
PS
XX Example 8; Fig 16; 251pp; English.
XX
CC The present invention relates to compositions and methods for high
CC throughput generation and screening of a human antibody or immunoglobulin
CC (Ig) library in yeast. The method comprises expressing a library of
CC tester fusion proteins in yeast cells, each tester fusion protein
CC comprising either an activation domain or a DNA binding domain of a
CC transcription activator and a tester protein having a large diversity
CC within the library. The tester protein comprises a first polypeptide
CC subunit (e.g. human variable heavy-chain, VH) whose sequence varies
CC within the library, a second polypeptide subunit (e.g. human variable
CC light-chain, VL) whose sequence varies within the library independently
CC of the first polypeptide, and a linker peptide which links the first and
CC second polypeptide subunits. The method is useful for generating
CC recombinant human antibodies and screening for their affinity binding
CC with target antigens. The present sequence represents the amino acid
CC sequence for an anti-IL6 scFv clone as described in the methods of the
XX present invention
XX
Sequence 249 AA;
SQ

[illegible]

RESULT 3	
AAV55072	
ID	AAV55072 standard; protein; 256 AA.
XX	
XX	
AC	AAV55072;
XX	
DT	
XX	25-FEB-2000 (first entry)
XX	
DE	
XX	Interleukin-6 specific ScFv protein sequence.
XX	
KW	Gene isolation; membrane-bound protein; fusion protein; drug production;
KW	antigen-binding cell; secretable functional protein; antigenic protein;
KW	protein isolation; diagnosis; interleukin-6; ScFv.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
XX	
PN	MO996013-A1.
XX	
PD	25-NOV-1999.
XX	
XX	

PF 30-APR-1999; 99WO-JP002341.
 XX
 XX 20-MAY-1998; 98JP-00138652.
 PR 01-OCT-1998; 98JP-00279876.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Tauchiya M, Saito M, Ohtomo T;
 XX WPI; 2000-039382/03.
 DR N-PSDB; AAZ40291.
 XX
 XX Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.
 XX
 XX Example 1; Page 54-56; 120pp; Japanese.
 XX
 CC This sequence represents a ScFv specific for human interleukin-6. The
 CC invention relates to a method for isolating a gene encoding a membrane-
 CC bound protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein

SO Sequence 256 AA;

Query Match 57.7%; Score 771.5; DB 3; Length 256;
 Best Local Similarity 59.7%; Pred. No. 1.1e-40;
 Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

QY 1 QVQLQWGMGGLKSKMTLSLTCAVSGASF-SGYVWSMIRPPKGLGEMTGEINHRSTTY 59
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 DB 1 QVQLQSGGPGVLPSSQTLSTCTVSGYSTSDHAWMWVRPPRGLEWIGYISYGITTY 60
 60 NPSLDRVTISLDTSTNOISLKLTSMTADTAAYVCARTVAGTS--DYWGQGLTVTVSSG 117
 DB 61 NPSLKRVTMLKRTSKQPSLRSLSTADTAAYVCARTVAGTS--DYWGQGLTVTVSSG 118
 118 SASAPYGGGSGGGSGGGSGGGSKTTLTOSPAFMSATPDGKVISCKASRDVDDVN 177
 DB 119 -----SGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASGDISSYLN 168
 178 WYQQRGEAFPIFIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYVYCLQHDNF 237
 DB 169 WYQQRGKAPKLLIYTSRLHSGVPSRFSGSGSDTFTTISLLOPEDIAIATYVYCOQGNTL 228
 238 PLTFGGGTVEIK 250
 QY 229 PTFGGGTVEIK 241
 DB

RESULT 4
 AAY55075

ID AAY55075 standard; protein; 260 AA.

AC AAY55075;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM(deltaE).

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.
 XX

OS Synthetic.

PN WO960113-A1.

XX 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Tauchiya M, Saito M, Ohtomo T;

XX WPI; 2000-039382/03.

DR N-PSDB; AAZ40305.

XX Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.
 XX

XX Example 7; Page 80-82; 120pp; Japanese.

CC This sequence represents a single chain Fv (ScFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein

SO Sequence 260 AA;

Query Match 57.7%; Score 771.5; DB 3; Length 260;
 Best Local Similarity 59.7%; Pred. No. 1.1e-40;
 Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

QY 1 QVQLQWGMGGLKSKMTLSLTCAVSGASF-SGYVWSMIRPPKGLGEMTGEINHRSTTY 59
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 DB 20 QVQLQSGGPGVLPSSQTLSTCTVSGYSTSDHAWMWVRPPRGLEWIGYISYGITTY 79
 60 NPSLDRVTISLDTSTNOISLKLTSMTADTAAYVCARTVAGTS--DYWGQGLTVTVSSG 117
 DB 80 NPSLKRVTMLKRTSKQPSLRSLSTADTAAYVCARTVAGTS--DYWGQGLTVTVSSG 137
 138 SASAPYGGGSGGGSGGGSGGGSKTTLTOSPAFMSATPDGKVISCKASRDVDDVN 177
 DB 139 -----SGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASGDISSYLN 187
 178 WYQQRGEAFPIFIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYVYCLQHDNF 237
 DB 188 WYQQRGKAPKLLIYTSRLHSGVPSRFSGSGSDTFTTISLLOPEDIAIATYVYCOQGNTL 247
 238 PLTFGGGTVEIK 250
 QY 248 PTFGGGTVEIK 260
 DB

RESULT 5
 AAY55078

ID AAY55078 standard; protein; 367 AA.

AC AAY55078;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1-Kappa.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secreted functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.

OS Synthetic.

PN WO960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-UP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-Psdb; AAZ40308.

PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 production of drugs treating abnormal functions of the protein.

Example 7; Page 86-89; 120pp; Japanese.

This sequence represents a single chain Fv (ScFv) sequence. The invention
 relates to a method for isolating a gene encoding a membrane-bound
 protein, comprising introducing a vector into a cell, contacting an
 antigen with the cell expressing the fused protein encoded by the vector
 on its surface to select an antigen-binding cell, and isolating the cDNA.
 The vector contains DNA encoding a secreted functional protein with
 antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 of the 3' end of the coding sequence. The method can be used to isolate a
 membrane-bound protein for diagnosis and study. It can also be used for
 producing drugs treating abnormal functions of the protein. Such a
 technique is efficient and selective, which is different from the prior-
 art transmembrane trap (TMT) method wherein an epitope recognised by an
 antibody is carried in a fused protein

Sequence 367 AA;

Query Match

Best Local Similarity 57.7%; Score 771.5; DB 3; Length 367;
 Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

```

QY 1 QVQLQWGAQLKSWGTLSTCAVSGASF-SGYVMSWIRPQKLEWIGINRGSTTY 59
DB 20 QVQLQESGPGIVRPSQTLSTCTVSGVSTSDHANSWVRPGRKLEWIGIYISGITY 79
QY 60 NPSLDGVTSLDTSNNOISLKLSTMTADTVAVVYCARVAGTS--DYWGQGTIVTVSSG 117
DB 80 NPSLKSRYVIMLRDTSNNOISLKLSTMTADTVAVVYCARVAGTS--DYWGQGTIVTVSSG 117
QY 118 SASAPITGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDGVISCSAASRDVDDVN 177
DB 138 -----SGGGSGGGSGGGSGGGSDIQMOSBSLSASVGDVITTCRAQSDISSYN 187
QY 178 WYQQRPGAPFIPIEDATTLVPGISPRSGSGYGTDFTLTINNIDSEDAAYVFCIQHNF 237
DB 188 WYQQRPGAPFKILLIYTSRLHSGVSPRSGSGSGTDFTLTISLQPEDIATYICQAGNTL 247
QY 238 PLTGGGKTVEIK 250
DB 248 PTFGGGKTVEIK 260

```

RESULT 6
 AAY55079

ID AAY55079 standard; protein; 381 AA.

AC AAY55079;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1-MCH4.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secreted functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.

OS Synthetic.

PN WO960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-UP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-Psdb; AAZ40309.

PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 production of drugs treating abnormal functions of the protein.

Example 7; Page 90-94; 120pp; Japanese.

This sequence represents a single chain Fv (ScFv) sequence. The invention
 relates to a method for isolating a gene encoding a membrane-bound
 protein, comprising introducing a vector into a cell, contacting an
 antigen with the cell expressing the fused protein encoded by the vector
 on its surface to select an antigen-binding cell, and isolating the cDNA.
 The vector contains DNA encoding a secreted functional protein with
 antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 of the 3' end of the coding sequence. The method can be used to isolate a
 membrane-bound protein for diagnosis and study. It can also be used for
 producing drugs treating abnormal functions of the protein. Such a
 technique is efficient and selective, which is different from the prior-
 art transmembrane trap (TMT) method wherein an epitope recognised by an
 antibody is carried in a fused protein

Sequence 381 AA;

Query Match

Best Local Similarity 57.7%; Score 771.5; DB 3; Length 381;
 Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

```

QY 1 QVQLQWGAQLKSWGTLSTCAVSGASF-SGYVMSWIRPQKLEWIGINRGSTTY 59
DB 20 QVQLQESGPGIVRPSQTLSTCTVSGVSTSDHANSWVRPGRKLEWIGIYISGITY 79
QY 60 NPSLDGVTSLDTSNNOISLKLSTMTADTVAVVYCARVAGTS--DYWGQGTIVTVSSG 117
DB 80 NPSLKSRYVIMLRDTSNNOISLKLSTMTADTVAVVYCARVAGTS--DYWGQGTIVTVSSG 117
QY 118 SASAPITGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDGVISCSAASRDVDDVN 177
DB 138 -----SGGGSGGGSGGGSGGGSDIQMOSBSLSASVGDVITTCRAQSDISSYN 187
QY 178 WYQQRPGAPFIPIEDATTLVPGISPRSGSGYGTDFTLTINNIDSEDAAYVFCIQHNF 237
DB 188 WYQQRPGAPFKILLIYTSRLHSGVSPRSGSGSGTDFTLTISLQPEDIATYICQAGNTL 247
QY 238 PLTGGGKTVEIK 250

```

Db 248 PYTFGGGTKEIK 260

RESULT 7

ID AAY55080 standard; protein; 519 AA.

AC AAY55080;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence hPM1(deltaE)-BVGS3.

KM Gene isolation; membrane-bound protein; fusion protein; drug production;
KM antigen-binding cell; secretable functional protein; antigenic protein;
KM protein isolation; diagnosis; ScFv.

OS Synthetic.

PN MO960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI, 2000-039382/03.

DR N-PSDB; AA240312.

PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.

XX Example 7; Page 95-100; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
XX relates to a method for isolating a gene encoding a membrane-bound
XX protein, comprising introducing a vector into a cell, contacting an
XX antigen with the cell expressing the fused protein encoded by the vector
XX on its surface to select an antigen-binding cell, and isolating the CDNA.
XX The vector contains DNA encoding a secretable functional protein with
XX antigenicity and binding affinity, and a CDNA ligated to DNA downstream
XX of the 3' end of the coding sequence. The method can be used to isolate a
XX membrane-bound protein for diagnosis and study. It can also be used for
XX producing drugs treating abnormal functions of the protein. Such a
XX technique is efficient and selective, which is different from the prior-
XX art transmembrane trap (TMT) method wherein an epitope recognised by an
XX antibody is carried in a fused protein

SQ Sequence 519 AA;

Query Match 57.7%; Score 771.5; DB 3; Length 519;

Best Local Similarity 59.7%; Pred. No. 2.1e-40;

Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

QY 1 QVQLQGMAGLKLKSGTSLTCAVSGASF-SGYYSMTIRPPGKLEWIGELINHRGTTY 59

DB 20 QVQLQSGSGPGLVPSQTLSTCTVSGYSITSDHAWMVRPPRGLEWIGYISGITY 79

QY 60 NPSLDGRVITSLDTSTNQSLKLTSMYADTAAYVCARTVAGNS--DYNGGGTLTVSSG 117

DB 80 NPSLKRVTYVLRITSKNQSLKLSVTYADTAAYVCARTVAGNS--DYNGGGTLTVSSG 137

QY 118 SASAPYGGGSGGGSGGGSGGGSKTTLTQSPAPWSATPGDKVSIKASRDVDDVA 177

DB 138 -----SGGGSGGGSGGGSGGGSDIQWTPSPSSISASVGRVITTCRAAGDISSYLN 187

QY 178 WYQQRPGAPFIPIEDATTLVPGISPRFSGSGYGTDTFTLLINNIDSEDAAYFCLQDNF 237

DB 188 WYQQRPGAPFKLLITYTSLRHSVPSRFSGSGSTDPFTTISLQEDATYTCQGGNTL 247

QY 238 PLTFGGGTKEIK 250

DB 248 PYTFGGGTKEIK 260

RESULT 8

ID AAY55074 standard; protein; 546 AA.

AC AAY55074;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence hPM1-BVGS3.

KM Gene isolation; membrane-bound protein; fusion protein; drug production;
KM antigen-binding cell; secretable functional protein; antigenic protein;
KM protein isolation; diagnosis; ScFv.

OS Synthetic.

PN MO960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI, 2000-039382/03.

DR N-PSDB; AA240303.

PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.

XX Example 5; Page 73-78; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
XX relates to a method for isolating a gene encoding a membrane-bound
XX protein, comprising introducing a vector into a cell, contacting an
XX antigen with the cell expressing the fused protein encoded by the vector
XX on its surface to select an antigen-binding cell, and isolating the CDNA.
XX The vector contains DNA encoding a secretable functional protein with
XX antigenicity and binding affinity, and a CDNA ligated to DNA downstream
XX of the 3' end of the coding sequence. The method can be used to isolate a
XX membrane-bound protein for diagnosis and study. It can also be used for
XX producing drugs treating abnormal functions of the protein. Such a
XX technique is efficient and selective, which is different from the prior-
XX art transmembrane trap (TMT) method wherein an epitope recognised by an
XX antibody is carried in a fused protein

SQ Sequence 546 AA;

Query Match 57.7%; Score 771.5; DB 3; Length 546;

Best Local Similarity 59.7%; Pred. No. 2.2e-40;

Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

QY 1 QVQLQGMAGLKLKSGTSLTCAVSGASF-SGYYSMTIRPPGKLEWIGELINHRGTTY 59

DB 20 QVQLQSGSGPGLVPSQTLSTCTVSGYSITSDHAWMVRPPRGLEWIGYISGITY 79

QY 60 NPSLDGRVITSLDTSTNQSLKLTSMYADTAAYVCARTVAGNS--DYNGGGTLTVSSG 117

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Db      80  NPSLRSKRVTLMTARTSNGPSLRISVTAADTVAVYCARSLARTTAMDYWGQSLVYS-- 137
Qy      118 SASAPFGGGSGGGSGGGSGGGSKTTLTOSPAFMSATPGDKVSIKCAKRPVDDVN 177
Db      138 -----SGGGSGGGSGGGSGGGSDIQMTSPSLSASVGDVITTCRASQDISSYLN 187
Qy      178 WYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFLTITNNIDSEDAAYFCLQDNF 237
Db      188 WYQORPGEAPKLLIYTSRLHSGVSPRSFGSGSDFTFTISSLQPEDIATYYCOQGNL 247
Qy      238 PLTFGGGTVEIK 250
Db      248 PTFGGGTVEIK 260

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RESULT 9
AAY55081
ID      AAY55081 standard; protein, 626 AA.
XX
AC      AAY55081;
XX
DT      25-FEB-2000 (first entry)
XX
DE      Single chain Fv protein sequence sHPM1-kappa-BVGS3.
XX
KW      Gene isolation; membrane-bound protein; fusion protein; drug production;
KM      antigen-binding cell; secretable functional protein; antigenic protein;
XX      protein isolation; diagnosis; ScFv.
OS      Synthetic.
XX
PN      WO960113-A1.
XX
PD      25-NOV-1999.
XX
PF      30-APR-1999; 99WO-UP002341.
XX
PR      20-MAY-1998; 98JP-00138652.
XX      01-OCT-1998; 98JP-00279876.
XX
PA      (CHUS) CHUGAI SEIYAKU KK.
XX
PI      Tsuchiya M, Salto M, Ohtomo T;
XX
DR      WPI; 2000-039382/03.
XX
N-PSDB; AAZ40316.
XX

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```

PT      Efficient and selective isolation of a gene encoding membrane protein
XX      with low or no antigenic binding activity, for diagnosis, study of, and
XX      production of drugs treating abnormal functions of the protein.
XX
PS      Example 7; Page 103-109; 120pp; Japanese.
XX
CC      This sequence represents a single chain Fv (ScFv) sequence. The invention
CC      relates to a method for isolating a gene encoding a membrane-bound
CC      protein, comprising introducing a vector into a cell, contacting an
CC      antigen with the cell expressing the fused protein encoded by the vector
CC      on its surface to select an antigen-binding cell, and isolating the cDNA.
CC      The vector contains DNA encoding a secretable functional protein with
CC      antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC      of the 3' end of the coding sequence. The method can be used to isolate a
CC      membrane-bound protein for diagnosis and study. It can also be used for
CC      producing drugs treating abnormal functions of the protein. Such a
CC      technique is efficient and selective, which is different from the prior-
CC      art transmembrane trap (TMT) method wherein an epitope recognised by an
CC      antibody is carried in a fused protein.
XX
SQ      Sequence 626 AA;

```

```

Query Match      57.7%; Score 771.5; DB 3; Length 626;
Best Local Similarity 59.7%; Pred. No. 2.5e-40;
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

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```

Qy      1  QVALQOMGAGLTKKMGTLSTCAVSGNSFSGYVMSWIRPPCKGLEWIGENHRGSTTY 59
Db      20  QVALQESGPGIVRSQTLSTLCTVSGSITSDHAWMVRQPPQRGLEWIGYISGITY 79
Qy      60  NPSLDSKRVTLSDPTSTNQSLKLTSMATAADTVAYYCARTVAGNS--DWGGOTLYTVSSG 117
Db      80  NPSLRSKRVTLMTARTSNGPSLRISVTAADTVAVYCARSLARTTAMDYWGQSLVYS-- 137
Qy      118 SASAPFGGGSGGGSGGGSGGGSKTTLTOSPAFMSATPGDKVSIKCAKRPVDDVN 177
Db      138 -----SGGGSGGGSGGGSGGGSDIQMTSPSLSASVGDVITTCRASQDISSYLN 187
Qy      178 WYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFLTITNNIDSEDAAYFCLQDNF 237
Db      188 WYQORPGEAPKLLIYTSRLHSGVSPRSFGSGSDFTFTISSLQPEDIATYYCOQGNL 247
Qy      238 PLTFGGGTVEIK 250
Db      248 PTFGGGTVEIK 260

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RESULT 10
AAY55082
ID      AAY55082 standard; protein, 640 AA.
XX
AC      AAY55082;
XX
DT      25-FEB-2000 (first entry)
XX
DE      Single chain Fv protein sequence sHPM1-MCH4-BVGS3.
XX
KW      Gene isolation; membrane-bound protein; fusion protein; drug production;
KM      antigen-binding cell; secretable functional protein; antigenic protein;
XX      protein isolation; diagnosis; ScFv.
OS      Synthetic.
XX
PN      WO960113-A1.
XX
PD      25-NOV-1999.
XX
PF      30-APR-1999; 99WO-UP002341.
XX
PR      20-MAY-1998; 98JP-00138652.
XX      01-OCT-1998; 98JP-00279876.
XX
PA      (CHUS) CHUGAI SEIYAKU KK.
XX
PI      Tsuchiya M, Salto M, Ohtomo T;
XX
DR      WPI; 2000-039382/03.
XX
N-PSDB; AAZ40321.
XX

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PT      Efficient and selective isolation of a gene encoding membrane protein
XX      with low or no antigenic binding activity, for diagnosis, study of, and
XX      production of drugs treating abnormal functions of the protein.
XX
PS      Example 7; Page 111-117; 120pp; Japanese.
XX
CC      This sequence represents a single chain Fv (ScFv) sequence. The invention
CC      relates to a method for isolating a gene encoding a membrane-bound
CC      protein, comprising introducing a vector into a cell, contacting an
CC      antigen with the cell expressing the fused protein encoded by the vector
CC      on its surface to select an antigen-binding cell, and isolating the cDNA.
CC      The vector contains DNA encoding a secretable functional protein with
CC      antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC      of the 3' end of the coding sequence. The method can be used to isolate a
CC      membrane-bound protein for diagnosis and study. It can also be used for
CC      producing drugs treating abnormal functions of the protein. Such a
CC      technique is efficient and selective, which is different from the prior-
CC      art transmembrane trap (TMT) method wherein an epitope recognised by an
CC      antibody is carried in a fused protein.
XX

```

```

Query Match      57.7%; Score 771.5; DB 3; Length 626;
Best Local Similarity 59.7%; Pred. No. 2.5e-40;
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

```


[illegible]

tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antineuritic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and actively such as cancer, immune, and autoimmune disorders and diseases, e.g., systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

Sequence 251 AA;

Query Match 56.6%; Score 756; DB 5; Length 251;
Best Local Similarity 59.5%; Pred. No.: 9.8e-40;
Matches 156; Conservative 29; Mismatches 53; Indels 24; Gaps 6

Dy
1 QVQLQDQGAGLLKMKWGLTLTCAVSGASFSG--YYMSWIROPCKGLEWIGINRHSSTT 58
1 QLGQDSGPGLVKRSSETLSLTCTYSGGISRTSWGMIRPPCKGPEMIGNIYTGMTY 60

Dd
59 YNPSLDGRVTISLDTNSTOISLKLTSMTADTVAYYCARTVAGTS-----DYWGCG 109
61 YSPSLKSRVTISVDTSKNQSLSKINSVTAAADTAAYVCAR--AGYDLTLGYPFYFDWSKG 118

Dy
110 TLVVYSSGSASAPFGGGSGGGSGGGSGGGSKITLTOSTPAPMSATRPDKNVISCKRAS 169
119 TLVTVSS-----GGGSGGGSGGGSGGG---ALEIVLTOSPATLSLPGERATLSCRAS 168

Dd
170 RDVDDDVVMYQORPGEARPIFIIEBATTLVPGISPRFSGSGYGTPETLTINNIDSEDAVY 229
169 QSVSSTLAAMYQKKQQAPRLILYHNSNRATGI PARFSGSGSGGTPTLTIISSLERPDVAVY 228

Dy
230 FCLQHDPNP-LTFGGGTRVEIK 250
229 YCGQRSNMPFLTFGGGTRVEIK 250

Db

RESULT 12
ABP45315
ID ABP45315 standard; protein; 252 AA.
XX .
AC . ABP45315;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv seq ID 1326.
XX
KW BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineuritic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293459P.

PT diagnosis and treatment of cancers and immune disorders.
XX

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention
CC cross-react with BLyS and TNF.

antibodies, immunosuppressive, immunostimulant, immunomodulatory, antineoplastic and anti-AIDS activity and can be used in vaccines to inhibit the expression and activity of Blyss. The antibodies bind to Blyss and so may be used to detect and quantitate the presence of Blyss in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blyss. They may also be administered to treat diseases associated with aberrant Blyss expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP3950-ABP4728 represent the antibodies and fragments of the antibodies described in the method of

Query Match	55.4%	Score 740.5;	DB 5;	Length 252;
Best Local Similarity	58.6%	Pred. No. 9.1e-39;		
Matches 154:	Conserved			

[illegible]

ABP45349 standard; protein, 248 AA.

19-AUG-2002 (first entry)

Human Blys binding BCFV SEQ ID 1360.

Blvs; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; arthrumatic; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

MOZ00202641-A1.

10-JAN-2002.

XX
PF
15-JUN-2001; 2001WO-115019110

16-JUN-2000: 2000HS-0212210D

PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0270016P.

PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0277379P.

2001; 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC.
 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY

Ruben SM, Barash SC, Choi GR, Vasek M

WPI: 2002-114799/15

XX	Antibodies against
PT	

diagnosis and treatment of cancers and immune disorders

Claim 1; Page 2025-2026; 3148bp; English

CCC This invention describes novel antibodies that

B Lymphocyte Stimulator (Blys) polypeptides that immunospecifically bind to tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have antitumoric and immunosuppressive, immunostimulant, immunomodulatory, inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABB43990-ABB47226 represent the invention and fragments of the antibodies described in the method of

Sequence 248 AA;

Query Match	55.3%	Score 738.5	DB 5	Length 248
Best Local Similarity	58.9%	Pred. No. 1.2e-38		
Matches 152	Conservative	30	Mismatch	

1	0V0LO0MGAG1LKSWCST	57;	Indels	19,	Gaps	5
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[illegible][illegible]

04 FOLDSKVIISLDISTINOJSLKTSMADTAVYCAR---TWAGT---SDYMGQTEV 112

61 PSLRSRATMSIDTSKNQFSLNITSVTAADTAVYCARDHYDVLTGSLYQAFDVMGQITLV 120

113 TVSSGSASAPITGGGSGGGSGGGSGGGSKTTLTOSPAFMSATPGDKVISICKASRDV 172

173 DDDVNWYQOPGEAPFIIFIEDATTLVPGISPRFSGSGYTDFTLTINNINSEDAVVECT 333

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      :||||| | ||||| : ||| : ||||| ||||| :||| :||| :|
    171 GRYLWYQOKPGRAPRLITVTSLSHDVPSPFSGSCTMTSTTSM CDHDTMUTSA 232
```

233 QHDFPPLTFGGGTKEIK 250
-----LVLISNDQFEDFAIYYCQ 230

231 QSYTD-TEGQTRLRK 247

```

RESULT 14
ABP45402
ID ABP45402 standard; protein, 250 AA.
XX AC
XX DT
XX DT
AC ABP45402;
DT 19-AUG-2002 (first entry)
XX DE
XX DE Human BlyS binding scFv SEQ ID 1413.
XX KW
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antithumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX PN
XX PN WO200202641-A1.
XX PD
XX PD 10-JAN-2002.
XX PF
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR
XX PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
XX DR
XX XX
PS Claim 1; Page 2088-2089; 3148bp; English.
XX CC
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and actively such as cancer, immune, and autoimmune disorders and
CC diseases, e.g., systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g., common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX SQ
XX Sequence 250 AA;
SQ
Query Match 55.3%; Score 738.5; DB 5; Length 250;
Best Local Similarity 59.0%; Pred. No. 1.2e-38;
Matches 154; Conservative 26; Mismatches 56; Indels 25; Gaps 7
QY 1 QVQLQQWAGLLKSGTSLTLCAVSGASFGSYGYSWIROPKGGLWEIGINRGSTYYN 60
DB 1 QAQLQQWAGLLKSPETLSLTCLAVDGGPSGYGYSWIRPPKGGLWEIGISNSTYYN 60
OY PSLDGRVITLSDTSTNOISLKTSMTAAATVAYYCAR-----TVAG-----TSDPWGGCTLY 112

```

Dd		61	PSLKSRTVTSVDTSKNGQFLKLSSTVADTVAVYCARBERILLGVILDGMDWGRGTMV	127
Oy		113	TWSSGSASAPTGCGSGGGSGGGSGGGSGKTTLTQS PAFMATSPTDQVISICK-ASRD	171
Dd		121	TWS-----SGGGSGGGSGGGSGSGLTPPP--VSAAPOKVITISCTGSSD	167
Oy		172	VD---DDVMVYQORPGAPFIETEDTLVPGISPFSGSGGTDFTLTIINISEDAAY	229
Dd		168	VGGXNVSYMYQQHPGAPPLMTIYESKRPSPGNRFSKSGNTASLTISQLQHDEADY	227
Oy		230	FCLQH-DNFPALTGGGTKVEI 249	
Dd		228	YCSSLTRSTRVFCCGCTKLTV 248	
RESULT 15				
ABP45631				
ID		ABP45631	standard; protein; 255 AA.	
XX				
AC		ABP45631;		
XX				
DT		19-AUG-2002	(first entry)	
XX				
DE			Human BlyS binding scFv SEQ ID 1642.	
XX				
KW		BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;		
KW		tumour necrosis factor; B cell proliferation; B cell differentiation;		
KW		immunopressessive; immunostimulant; immunomodulatory; antitneumatic;		
KW		antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;		
KW		systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;		
KM		common variable immunodeficiency; acquired immunodeficiency syndrome.		
XX				
OS		Homo sapiens.		
XX				
PN		WO200202641-A1.		
XX				
PD		10-JAN-2002.		
XX				
PE		15-JUN-2001; 2001WO-US019110.		
XX				
PR		16-JUN-2000; 2000US-021221OP.		
PR		17-OCT-2000; 2000US-0240816P.		
PR		16-MAR-2001; 2001US-0276248P.		
ER		21-MAR-2001; 2001US-0277379P.		
PR		25-MAY-2001; 2001US-0293499P.		
XX				
PA		(HUMA-) HUMAN GENOME SCI INC.		
PA		(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.		
XX				
Xx		Ruben SW, Barash SC, Choi GH, Vaughan T, Hilbert D;		
XX				
DR		WPI; 2002-114799/15.		
XX				
PT		Antibodies against B lymphocyte Stimulating polypeptides, useful for the		
FT		diagnosis and treatment of cancers and immune disorders.		
XX				
PS		Claim 1; Page 2362-2363; 3148pp; English.		
XX				
CC		This invention describes novel antibodies that immunospecifically bind to		
CC		B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the		
CC		tumour necrosis factor (TNF) super family and induces B cell		
CC		proliferation and differentiation. The antibodies of the invention have		
CC		cytotoxic, immunosuppressive, immunostimulant, immunomodulatory,		
CC		antitneumatic and antiAIDS activity and can be used in vaccines to		
CC		inhibit the expression and activity of BlyS. The antibodies bind to BlyS		
CC		and so may be used to detect and quantitate the presence of BlyS in		
CC		biological samples and may be used in this way to diagnose disease		
CC		associated with aberrant expression of BlyS. They may also be		
CC		administered to treat diseases associated with aberrant BlyS expression		
CC		and activity such as cancer, immune, and autoimmune disorders and		
CC		diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,		
CC		immunodeficiency (e.g. common variable immunodeficiency (CVID) and		
CC		acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent		

CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 255 AA;

Query Match 55.0%; Score 735; DB 5; Length 255;
 Best Local Similarity 58.6%; Pred. No. 2e-38;
 Matches 156; Conservative 21; Mismatches 59; Indels 30; Gaps 6;

```

QY 1 QVQLQOMGAGLLKSMGTSLTCAVSGASFGSYTWSMIRQPPKGLIEWIGIHRGSTTYN 60
DB 1 QVQLQOMGAGLLKSPETLSLTCAVYGSFSGYWSMIRQSPKGLIEWIGIHRGSTTYN 60
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAHYTCAR-----TVAGTS-----DYWG 107
DB 61 PSLKSRVTISVDASRQFSLKLSVTADTAHYTCARERTYDILTGYSFRSKYGMVWG 120
QY 108 QGTLVTSSGASAPITGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSIQCK 167
DB 121 RGLVTVS-----SGGGSGGGSGGGSGGGSGSVLTQPPS-ASGTPGQRTVTS 167
QY 168 ASRD--VDDVNTQQRGPAFPIEDATTLVPGISPRPSGSGVGTDFTLTINNIDSED 225
DB 168 GSSSNIGSNTVNTYQRLPGAAPQLLYNNDQRPISGIPDRFSQSKSGSLVIGLQSD 227
QY 226 AAYYFCLQHDNF--PLTFGGGTVEI 249
DB 228 EADYYCASWDDSLNGRVFGGGLTV 253
  
```

Search completed: May 13, 2004, 15:00:57
 Job time : 52.4563 secs


```

/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-1GE Antibodies and Method of
/ NUMBER OF INVENTION: Improving Polypeptides
/ CORRESPONDENCE ADDRESSES:
/ ADDRESS: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/887,352B
/ FILING DATE: 03-Jul-1997
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Svoboda, Craig G.
/ REGISTRATION NUMBER: 39,044
/ REFERENCE/DOCKET NUMBER: P1123
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/952-1489
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 248 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
/ US-08-887-352B-22

```

Query Match
Best Local Similarity 51.5%; Score 688.5; DB 2; Length 248;
Matches 143; Conservative 33; Mismatches 58; Indels 29; Gaps 5;

```

QY 1 QVQLQOMGAGLLKSGTSLTCAVSGASF-SGYVMSWIRQPGKGLIEWIGINRGSTTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSMMNIRQAPGKGLIEWASITYDGSITNY 60
QY 60 NPSLDGRVTISLDTSTNOISLKTSMTADTAAYVYCARVAGTSDY-----WGQGTLL 111
DB 61 NPSVKGRTITSRDSSKNTFYLLQNNSLRAEDTAAYVYCAR-----GSHFGHMFPAWVGQGTLL 116
QY 112 VTVSSGSASAPRTGGSGSGSGSGSGSGSKTTLTQSPAFMSATPGDYSISCKASRD 171
DB 117 VTVS-----SEGGSGSGSGSGSGSGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY 172 VDDD-----VMYQQRPEAPFIETDATTLPGISPRFSGSGYGTDFTLTINNIDSEDA 227
DB 165 VDGGSDSYLNMWYQKPGAPKPLIYAASYLESGVPSRFSGSGSDTFTLTISLQPEDFA 224
QY 228 YFFCLQHDNFPPLTFGGGTKEYIK 250
DB 225 TYCCQSHEDPYTFGGGTKEYIK 247

```

RESULT 3
US-09-109-207C-22
Sequence 22, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1GE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123K1
CURRENT APPLICATION NUMBER: US/09/109,207C
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
NUMBER OF SEQ ID NOS: 44

```

/ SEQ ID NO 22
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-248
/ OTHER INFORMATION: sfv sequence derived from MAE11
/
/ US-09-109-207C-22

```

Query Match
Best Local Similarity 51.5%; Score 688.5; DB 3; Length 248;
Matches 143; Conservative 33; Mismatches 58; Indels 29; Gaps 5;

```

QY 1 QVQLQOMGAGLLKSGTSLTCAVSGASF-SGYVMSWIRQPGKGLIEWIGINRGSTTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSMMNIRQAPGKGLIEWASITYDGSITNY 60
QY 60 NPSLDGRVTISLDTSTNOISLKTSMTADTAAYVYCARVAGTSDY-----WGQGTLL 111
DB 61 NPSVKGRTITSRDSSKNTFYLLQNNSLRAEDTAAYVYCAR-----GSHFGHMFPAWVGQGTLL 116
QY 112 VTVSSGSASAPRTGGSGSGSGSGSGSKTTLTQSPAFMSATPGDYSISCKASRD 171
DB 117 VTVS-----SEGGSGSGSGSGSGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY 172 VDDD-----VMYQQRPEAPFIETDATTLPGISPRFSGSGYGTDFTLTINNIDSEDA 227
DB 165 VDGGSDSYLNMWYQKPGAPKPLIYAASYLESGVPSRFSGSGSDTFTLTISLQPEDFA 224
QY 228 YFFCLQHDNFPPLTFGGGTKEYIK 250
DB 225 TYCCQSHEDPYTFGGGTKEYIK 247

```

RESULT 4
US-09-296-005-22
Sequence 22, Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1GE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1R
CURRENT APPLICATION NUMBER: US/09/296,005
PRIOR FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 22
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-248
OTHER INFORMATION: sfv sequence derived from MAE11
US-09-296-005-22

Query Match
Best Local Similarity 54.4%; Score 688.5; DB 3; Length 248;
Matches 143; Conservative 33; Mismatches 58; Indels 29; Gaps 5;

```

QY 1 QVQLQOMGAGLLKSGTSLTCAVSGASF-SGYVMSWIRQPGKGLIEWIGINRGSTTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSMMNIRQAPGKGLIEWASITYDGSITNY 60
QY 60 NPSLDGRVTISLDTSTNOISLKTSMTADTAAYVYCARVAGTSDY-----WGQGTLL 111
DB 61 NPSVKGRTITSRDSSKNTFYLLQNNSLRAEDTAAYVYCAR-----GSHFGHMFPAWVGQGTLL 116
QY 112 VTVSSGSASAPRTGGSGSGSGSGSGSKTTLTQSPAFMSATPGDYSISCKASRD 171
DB 117 VTVS-----SEGGSGSGSGSGSGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY 172 VDDD-----VMYQQRPEAPFIETDATTLPGISPRFSGSGYGTDFTLTINNIDSEDA 227
DB 165 VDGGSDSYLNMWYQKPGAPKPLIYAASYLESGVPSRFSGSGSDTFTLTISLQPEDFA 224
QY 228 YFFCLQHDNFPPLTFGGGTKEYIK 250
DB 225 TYCCQSHEDPYTFGGGTKEYIK 247

```


US-09-109-207C-23

Query Match 51.2%; Score 684.5; DB 3; Length 248;
Best Local Similarity 54.0%; Pred. No. 8.1e-46;
Matches 142; Conservative 33; Mismatches 59; Indels 29; Gaps 5;

```
QY 1 QVQLQOMGAGLLKSWGTLSTLTCVAVGASF-SGYVNWIRPPGKLEWIGELNHRGTTY 59
DB 1 EVQLVDSGGGLVOPGSLRLSCAVSGYITSGYSNMWIRQAQKLEWVASIKYSGETKY 60
QY 60 NPSLDGRVTISLDTSTNQSLKLTSMTADTVVYTCARTVAGTSDY-----WGQGTLL 111
DB 61 NPSVKGRIITISRDSDSKNTFYLQMNLSLRADTVVYCAR-----GSHYFGHMFAVWGQGTLL 116
QY 112 VTVSSGSASAPRTGGGSGGGSGGGSGGSKTTLTQSPAFMAGTPEGDKVSISSCKASRD 171
DB 117 VTVS-----SEGGSGSGGGSGGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY 172 VDDD-----VNMVQORPGAPFIITEDATTLVPGISPRFGSGGYGTDFTLTINNIDSDAA 227
DB 165 VDGGSDSYLNMVYQQRPGAPKLLIYAASYLESGVPSRFGSGSGGSDTDTLTISLQPEDFA 224
QY 228 YVFCLOHDFPLTFGGGTKEIK 250
DB 225 TYVCOQSHEDPYTFGGGTKEIK 247
```

RESULT 8
US-09-296-005-23
Sequence 23, Application US/09296005

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides
CURRENT APPLICATION NUMBER: US/09/296,005
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 23
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial
NAME/KEY: Artificial
LOCATION: 1-248
OTHER INFORMATION: sFv sequence derived from MAE11
US-09-296-005-23

Query Match 51.2%; Score 684.5; DB 3; Length 248;
Best Local Similarity 54.0%; Pred. No. 8.1e-46;
Matches 142; Conservative 33; Mismatches 59; Indels 29; Gaps 5;

```
QY 1 QVQLQOMGAGLLKSWGTLSTLTCVAVGASF-SGYVNWIRPPGKLEWIGELNHRGTTY 59
DB 1 EVQLVDSGGGLVOPGSLRLSCAVSGYITSGYSNMWIRQAQKLEWVASIKYSGETKY 60
QY 60 NPSLDGRVTISLDTSTNQSLKLTSMTADTVVYTCARTVAGTSDY-----WGQGTLL 111
DB 61 NPSVKGRIITISRDSDSKNTFYLQMNLSLRADTVVYCAR-----GSHYFGHMFAVWGQGTLL 116
QY 112 VTVSSGSASAPRTGGGSGGGSGGGSGGSKTTLTQSPAFMAGTPEGDKVSISSCKASRD 171
DB 117 VTVS-----SEGGSGSGGGSGGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY 172 VDDD-----VNMVQORPGAPFIITEDATTLVPGISPRFGSGGYGTDFTLTINNIDSDAA 227
DB 165 VDGGSDSYLNMVYQQRPGAPKLLIYAASYLESGVPSRFGSGSGGSDTDTLTISLQPEDFA 224
QY 228 YVFCLOHDFPLTFGGGTKEIK 250
DB 225 TYVCOQSHEDPYTFGGGTKEIK 247
```

RESULT 9
US-09-920-171-23
Sequence 23, Application US/09920171

GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-1gE Antibodies (as amended)
FILE REFERENCE: P123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 23
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: sFv sequence derived from MAE11
US-09-920-171-23

Query Match 51.2%; Score 684.5; DB 4; Length 248;
Best Local Similarity 54.0%; Pred. No. 8.1e-46;
Matches 142; Conservative 33; Mismatches 59; Indels 29; Gaps 5;

```
QY 1 QVQLQOMGAGLLKSWGTLSTLTCVAVGASF-SGYVNWIRPPGKLEWIGELNHRGTTY 59
DB 1 EVQLVDSGGGLVOPGSLRLSCAVSGYITSGYSNMWIRQAQKLEWVASIKYSGETKY 60
QY 60 NPSLDGRVTISLDTSTNQSLKLTSMTADTVVYTCARTVAGTSDY-----WGQGTLL 111
DB 61 NPSVKGRIITISRDSDSKNTFYLQMNLSLRADTVVYCAR-----GSHYFGHMFAVWGQGTLL 116
QY 112 VTVSSGSASAPRTGGGSGGGSGGGSGGSKTTLTQSPAFMAGTPEGDKVSISSCKASRD 171
DB 117 VTVS-----SEGGSGSGGGSGGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY 172 VDDD-----VNMVQORPGAPFIITEDATTLVPGISPRFGSGGYGTDFTLTINNIDSDAA 227
DB 165 VDGGSDSYLNMVYQQRPGAPKLLIYAASYLESGVPSRFGSGSGGSDTDTLTISLQPEDFA 224
QY 228 YVFCLOHDFPLTFGGGTKEIK 250
DB 225 TYVCOQSHEDPYTFGGGTKEIK 247
```

RESULT 10
US-08-918-148-79

Sequence 79, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adame, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fenley, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 79
LENGTH: 244
TYPE: PRT
ORGANISM: artificial
US-08-918-148-79

Query Match 50.5%; Score 675; DB 4; Length 482;
Best Local Similarity 49.2%; Pred. No. 9,4e-45;
Matches 129; Conservative 52; Mismatches 63; Indels 18; Gaps 4;

QY 1 QVQLQOMGAGLLKSWTSLTCAVSGASPSGYWMSIRPPKGLWIGELINHRG--ST 57
DB 31 EVLVESGGGLVLPQGSIRLSCATGFTFSDYEMWVQPKGLEIIMASRNKNTYT 90
QY 58 TNPISLDGRVTISLDTSTNQISLKLSTMTADTAIVYCARVAGTS--DYMOGTLVTV 114
DB 91 EYSAVYKGRFIVSRDTSQSIILQNALRAEDTAIVYCARVYGSITWCFDVMGAGTVTV 150
QY 115 SSGSASAPITGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSISSKASRDVVD 174
DB 151 SSG-----GGGGSGGGSGGGSGGGSDIVMTQSPSSLSVAGGRVMSCKSSQSLTN 204
QY 175 DVN-----WYQRPGEAPFIIEDATTLVPGISPRSGSGYGTDTTLTINNISEDAAY 228
DB 205 SQNQKNFLAWYQOKPQPKLLICGASTRESGVPRFTGSGGTDFTLTISVQADLAV 264
QY 229 YFCLOHNFPLTFGGGTKEIK 250
DB 265 YTCNDHSYPLTFGAGTKEIK 286

RESULT 14
US-10-092-246-36
Sequence 36, Application US/10092246
Patent No. 6501314
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
FILE REFERENCE: NEI-0007
CURRENT APPLICATION NUMBER: US/10/092,246
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patent version 3.1
SEQ ID NO 36
LENGTH: 240
TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-36

Query Match 50.5%; Score 674.5; DB 4; Length 240;
Best Local Similarity 51.6%; Pred. No. 4,7e-45;
Matches 130; Conservative 48; Mismatches 57; Indels 17; Gaps 4;
QY 1 QVQLQOMGAGLLKSWTSLTCAVSGASPSGYWMSIRPPKGLWIGELINHRG--STT 58
DB 3 QVQLQESGPRLVKGASVKISCKASGYTFDYHVMWKGKPGGLEWIG-MTYPGFDTN 61
QY 59 YNPISLDGRVTISLDTSTNQISLKLSTMTADTAIVYCARVAGTS--DYMOGTLVTVSSGS 118
DB 62 YSETFKGATLTVDTSNTVYMWQLSLTSEDTAVYFCAGVG--LDYMOGTLTVVS--- 116
QY 119 ASAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSISSKASRDVDDVNM 178
DB 117 -----SGGGSGGGSGGGSGGGSDIELTQSPNSLSTISGRIRITCKASQDVDTAVGM 167
QY 179 YQRPGEAPFIIEDATTLVPGISPRSGSGYGTDTTLTINNISEDAAYFCLQHDNFP 238
DB 168 YQRPQGSFKLLIFMSSTRHGTVPDRFTGSGGTDFTLTISVQSEDLADYFCHQYSYSP 227
QY 239 LTFGGGTKEIK 250
DB 228 FTFGSGTKEIK 239

RESULT 15

US-10-092-246-37
Sequence 37, Application US/10092246
Patent No. 6501314
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
FILE REFERENCE: NEI-0007
CURRENT APPLICATION NUMBER: US/10/092,246
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patent version 3.1
SEQ ID NO 37
LENGTH: 240
TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-37

Query Match 50.5%; Score 674.5; DB 4; Length 240;
Best Local Similarity 51.6%; Pred. No. 4,7e-45;
Matches 130; Conservative 48; Mismatches 57; Indels 17; Gaps 4;
QY 1 QVQLQOMGAGLLKSWTSLTCAVSGASPSGYWMSIRPPKGLWIGELINHRG--STT 58
DB 3 QVQLQESGPRLVKGASVKISCKASGYTFDYHVMWKGKPGGLEWIG-MTYPGFDTN 61
QY 59 YNPISLDGRVTISLDTSTNQISLKLSTMTADTAIVYCARVAGTS--DYMOGTLVTVSSGS 118
DB 62 YSETFKGATLTVDTSNTVYMWQLSLTSEDTAVYFCAGVG--LDYMOGTLTVVS--- 116
QY 119 ASAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSISSKASRDVDDVNM 178
DB 117 -----SGGGSGGGSGGGSGGGSDIELTQSPNSLSTISGRIRITCKASQDVDTAVGM 167
QY 179 YQRPGEAPFIIEDATTLVPGISPRSGSGYGTDTTLTINNISEDAAYFCLQHDNFP 238
DB 168 YQRPQGSFKLLIFMSSTRHGTVPDRFTGSGGTDFTLTISVQSEDLADYFCHQYSYSP 227
QY 239 LTFGGGTKEIK 250
DB 228 FTFGSGTKEIK 239

Search completed: May 13, 2004, 15:10:47
Job time: 14.7136 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.0146 Seconds
(without alignments)
1879.405 Million cell updates/sec

Title: US-10-072-301-21

Perfect score: 1336
Sequence: 1 QVQLQOMGAGLKSGTSLT.....CLQHDFPLTGGGTVEIK 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	100.0	250	14	US-10-072-301-21
2	1336	100.0	250	14	US-10-071-866-21
3	1336	100.0	250	15	US-10-360-828-21
4	1332	99.7	250	14	US-10-072-301-29
5	1332	99.7	250	14	US-10-071-866-29
6	1332	99.7	250	15	US-10-360-828-29
7	835	62.5	249	10	US-09-880-748-1321
8	835	62.5	249	12	US-10-293-418-1321
9	805	60.3	286	12	US-10-406-830-8
10	756	56.6	251	10	US-09-880-748-1049
11	756	56.6	251	12	US-10-293-418-1049
12	740.5	55.4	252	10	US-09-880-748-1326
13	740.5	55.4	252	12	US-10-293-418-1326
14	738.5	55.3	248	10	US-09-880-748-1360
15	738.5	55.3	248	12	US-10-293-418-1360

16	738.5	55.3	250	10	US-09-880-748-1413	Sequence 1413, Ap
17	738.5	55.3	250	12	US-10-293-418-1413	Sequence 1413, Ap
18	735	55.0	255	10	US-09-880-748-1642	Sequence 1642, Ap
19	735	55.0	255	12	US-10-293-418-1642	Sequence 1642, Ap
20	733.5	54.9	250	10	US-09-880-748-1645	Sequence 1645, Ap
21	733.5	54.9	250	12	US-10-293-418-1645	Sequence 1645, Ap
22	730.5	54.7	253	12	US-10-293-656-63	Sequence 63, Appl
23	730	54.6	253	10	US-09-880-748-1333	Sequence 1333, Ap
24	730	54.6	253	12	US-10-293-418-1333	Sequence 1333, Ap
25	729.5	54.6	254	10	US-09-880-748-1659	Sequence 1659, Ap
26	729.5	54.6	254	12	US-10-293-418-1659	Sequence 1659, Ap
27	715	53.5	253	10	US-09-880-748-954	Sequence 954, App
28	715	53.5	253	12	US-10-293-418-954	Sequence 954, App
29	713	53.4	249	10	US-09-880-748-957	Sequence 957, App
30	713	53.4	249	12	US-10-293-418-957	Sequence 957, App
31	709	53.1	255	10	US-09-880-748-1597	Sequence 1597, App
32	709	53.1	255	12	US-10-293-418-1597	Sequence 1597, App
33	706	52.8	258	14	US-10-072-301-27	Sequence 27, Appl
34	706	52.8	258	15	US-10-071-866-27	Sequence 27, Appl
35	706	52.8	258	15	US-10-360-828-27	Sequence 27, Appl
36	704	52.7	253	10	US-09-880-748-1602	Sequence 1602, Ap
37	704	52.7	253	12	US-10-293-418-1602	Sequence 1602, Ap
38	699	52.3	239	10	US-09-880-748-1882	Sequence 1882, Ap
39	699	52.3	239	12	US-10-293-418-1882	Sequence 1882, Ap
40	698	52.2	237	10	US-09-880-748-1906	Sequence 1906, Ap
41	698	52.2	237	12	US-10-293-418-1906	Sequence 1906, Ap
42	697	52.2	255	10	US-09-880-748-1626	Sequence 1626, Ap
43	697	52.2	255	12	US-10-293-418-1626	Sequence 1626, Ap
44	696	52.1	239	10	US-09-880-748-1922	Sequence 1922, Ap
45	696	52.1	239	12	US-10-293-418-1922	Sequence 1922, Ap

ALIGNMENTS

RESULT 1
US-10-072-301-21
; Sequence 21, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.12
US-10-072-301-21

Query Match	100.0%	Score 1336;	DB 14;	Length 250;
Best local similarity	100.0%	Pred. No. 8e-85;		
Matches	250;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
QY	1 QVQLQOMGAGLKSGTSLTCAVSGASFGSYWIRPPQKLEWIGEIFHRRGSTYTN 60			
DB	1 QVQLQOMGAGLKSGTSLTCAVSGASFGSYWIRPPQKLEWIGEIFHRRGSTYTN 60			
QY	61 PSIDGRVTSLSPTSTNQSLKLTSMTPAATAYYCARVTAAGTSIDYWGQSTLVTSSSGSAS 120			
DB	61 PSIDGRVTSLSPTSTNQSLKLTSMTPAATAYYCARVTAAGTSIDYWGQSTLVTSSSGSAS 120			
QY	121 APTGGGSGSGGSGGSGGSGGSKTTLTQSPAFAFMSATPGDKVYSISCKASRDVDDDDVNWYQ 180			
DB	121 APTGGGSGSGGSGGSGGSGGSKTTLTQSPAFAFMSATPGDKVYSISCKASRDVDDDDVNWYQ 180			

QY 181 ORPGEAPFIIEEDATTLVPGISPRFSGSGYGTDFLTITINNIDSEDAAYFFCLOHNDNPLT 240
 DB 181 ORPGEAPFIIEEDATTLVPGISPRFSGSGYGTDFLTITINNIDSEDAAYFFCLOHNDNPLT 240
 QY 241 FGGGTKEIK 250
 DB 241 FGGGTKEIK 250

RESULT 2

US-10-071-866-21
 ; Sequence 21, Application US/10071866
 ; Publication No. US20030165988A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hua, Shao-bing
 ; APPLICANT: Pauling, Michelle H.
 ; APPLICANT: Zhu, Li
 ; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
 ; FILE REFERENCE: 25636-717
 ; CURRENT APPLICATION NUMBER: US/10/071,866
 ; CURRENT FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 21
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Clone 15.150.12
 US-10-071-866-21

Query Match 100.0%; Score 1336; DB 14; Length 250;
 Best Local Similarity 100.0%; Pred. No. 8e-85;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQQMGAGLLKSGMTSLTCAVSGASFGSYWMTIRPPGKGLFWIGELINHRGSTTYN 60
 DB 1 QVQLQQMGAGLLKSGMTSLTCAVSGASFGSYWMTIRPPGKGLFWIGELINHRGSTTYN 60
 QY 61 PSIDGRVTISLDTSTNQISLKTSMTADTAAYVCARTVAGTSDYWGQGLTVVSSGSAS 120
 DB 61 PSIDGRVTISLDTSTNQISLKTSMTADTAAYVCARTVAGTSDYWGQGLTVVSSGSAS 120
 QY 121 APTGGGSGGGGSGGGGSGGSKTTLTQSPAFMSATPGDKVSIKSKASRDVDDVNWYQ 180
 DB 121 APTGGGSGGGGSGGGGSGGSKTTLTQSPAFMSATPGDKVSIKSKASRDVDDVNWYQ 180
 QY 181 ORPGEAPFIIEEDATTLVPGISPRFSGSGYGTDFLTITINNIDSEDAAYFFCLOHNDNPLT 240
 DB 181 ORPGEAPFIIEEDATTLVPGISPRFSGSGYGTDFLTITINNIDSEDAAYFFCLOHNDNPLT 240
 QY 241 FGGGTKEIK 250
 DB 241 FGGGTKEIK 250

RESULT 3

US-10-360-828-21
 ; Sequence 21, Application US/10360828
 ; Publication No. US20030206909A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hua, Shao-bing
 ; APPLICANT: Pauling, Michelle H.
 ; APPLICANT: Zhu, Li
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
 ; FILE REFERENCE: 25636-727
 ; CURRENT APPLICATION NUMBER: US/10/360,828
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: US 10/071,866
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 10/072,301

; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 10/133,978
 ; PRIOR FILING DATE: 2002-04-25
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 21
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Clone 15.150.12
 US-10-360-828-21

Query Match 100.0%; Score 1336; DB 15; Length 250;
 Best Local Similarity 100.0%; Pred. No. 8e-85;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 PSIDGRVTISLDTSTNQISLKTSMTADTAAYVCARTVAGTSDYWGQGLTVVSSGSAS 120
 DB 61 PSIDGRVTISLDTSTNQISLKTSMTADTAAYVCARTVAGTSDYWGQGLTVVSSGSAS 120
 QY 121 APTGGGSGGGGSGGGGSGGSKTTLTQSPAFMSATPGDKVSIKSKASRDVDDVNWYQ 180
 DB 121 APTGGGSGGGGSGGGGSGGSKTTLTQSPAFMSATPGDKVSIKSKASRDVDDVNWYQ 180
 QY 181 ORPGEAPFIIEEDATTLVPGISPRFSGSGYGTDFLTITINNIDSEDAAYFFCLOHNDNPLT 240
 DB 181 ORPGEAPFIIEEDATTLVPGISPRFSGSGYGTDFLTITINNIDSEDAAYFFCLOHNDNPLT 240
 QY 241 FGGGTKEIK 250
 DB 241 FGGGTKEIK 250

RESULT 4

US-10-072-301-29
 ; Sequence 29, Application US/10072301
 ; Publication No. US20030152913A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hua, Shao-bing
 ; APPLICANT: Pauling, Michelle H.
 ; APPLICANT: Zhu, Li
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
 ; FILE REFERENCE: 25636-718
 ; CURRENT APPLICATION NUMBER: US/10/072,301
 ; CURRENT FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Clone 15.150.12 Variant
 US-10-072-301-29

Query Match 99.7%; Score 1332; DB 14; Length 250;
 Best Local Similarity 99.6%; Pred. No. 1.5e-84;
 Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQQMGAGLLKSGMTSLTCAVSGASFGSYWMTIRPPGKGLFWIGELINHRGSTTYN 60
 DB 1 QVQLQQMGAGLLKSGMTSLTCAVSGASFGSYWMTIRPPGKGLFWIGELINHRGSTTYN 60
 QY 61 PSIDGRVTISLDTSTNQISLKTSMTADTAAYVCARTVAGTSDYWGQGLTVVSSGSAS 120
 DB 61 PSIDGRVTISLDTSTNQISLKTSMTADTAAYVCARTVAGTSDYWGQGLTVVSSGSAS 120

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Db	121	APTGGGSGGGGSGGGGSETTLTOSPARMSATPGDKXISCKASADVDDVNNWQ	180
0y	181	ORPGAPFIIEDATTLVPGISPRFSGSGYDFTLTINNIDSEDAAYYFCLOHNPPLT	240
Db	181	ORGPAPFIIEDATTLVPGISPRFSGSGYDFTLTINNIDSEDAAYYFCLOHNPPLT	240
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Db	241	FGGGTKVEIK 250	

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1      RESULT 5
2      US-10-071-866-29
3      ; Sequence 29, Application US/10071866
4      ; Publication No. US20030165988A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Hua, Shao-bing
7      ; APPLICANT: Pauling, Michelle H.
8      ; APPLICANT: Zhu, Li
9      ; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST
10     ; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
11     ; FILE REFERENCE: 25636-717
12     ; CURRENT APPLICATION NUMBER: US/10/071,866
13     ; CURRENT FILING DATE: 2002-02-08
14     ; NUMBER OF SEQ ID NOS: 54
15     ; SOFTWARE: PatentIn version 3.1
16     ; SEQ ID NO 29
17     ; LENGTH: 250
18     ; TYPE: PRT
19     ; ORGANISM: Artificial Sequence
20     ; FEATURE:
21     ; OTHER INFORMATION: Clone 15.150.12 Variant
22     ; US-10-071-866-29

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Query Match 1332; Score 1332; DB 14; Length 250;
Best Local Similarity 99.6%; Pred. No. 1.5e-84;
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      1 QVQLQDQMGAGLLKSGWGLTSLTCAVSGASFSGYVSMWIRPGPKGLEWIGEINHRGSTTYPN 60

QY      61 PSLDGRVITISLDTSTNQISLKLTSMTADIAVYVCARTVAGTSDYWGQGLTVYSSGSAS 120
Db      61 PSLDGRVITISLDTSTNQISLKLTSMTADIAVYVCARTVAGTSDYWGQGLTVYSSGSAS 120

QY      121 APTGGGSGSGGSGSGGSGGSGKTTLTQSPAPFMSATPDGKVISICKASRDVDDVVMYQ 180
Db      121 APTGGGSGSGGSGSGGSGGSGSETTLTQSPAPFMSATPDGKVISICKASRDVDDVVMYQ 180

QY      181 QRPEAPFIEIEDATTVLPGISPRPSGSGCYTDPLTNNIDSDAAVYFCLQHDNPFLT 240
Db      181 QRPEAPFIEIEDATTVLPGISPRPSGSGCYTDPLTNNIDSDAAVYFCLQHDNPFLT 240

QY      241 FGGGTKEIK 250
Db      241 FGGGTKEIK 250

RESULT 6
US-10-360-828-29
: Sequence 29, Application US/10360828
: Publication No. US20030206909A1
: GENERAL INFORMATION:
: APPLICANT: Hua, Shaobing
: APPLICANT: Pauling, Michelle H.
: APPLICANT: Zhu, Li
: TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
: FILE REFERENCE: 25836-727
: CURRENT APPLICATION NUMBER: US/10/360, 828
: CURRENT FILING DATE: 2003-02-07

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; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: clone 15.150.12 Variant
US-10-360-828-29

Query Match          99.7%;   Score 1332;   DB 15;   Length 250;
Best Local Similarity 99.6%;   Pred. No. 1.5e-84;
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0

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	OTHER INFORMATION: Clone 15.150.12 Variant US-10-360-828-29	
Query Match	99.7%;	Score 1332; DB 15; Length 250;
Best Local Similarity	99.6%;	Pred. No. 1.5e-84;
Matches 249; Conservative	1; Mismatches 0; Indels 0; Gaps 0	
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DB	1 QVQLQQMAGLLKSWGTLSTLCVAGSAGSFSGYGMWIRPPQKGLMEINHRGSTTN 60	
QY	61 PSLDGRVTISLDTSTNOISLKLTSMTADPAVAYVCARTVAGTSDYWGCGTLTVTSSGSAS 120	
DB	61 PSLDGRVTISLDTSTNOISLKLTSMTADPAVAYVCARTVAGTSDYWGCGTLTVTSSGSAS 120	
QY	121 APTGGGSGGGSGGGSGGGSGKTTLQSPAFMSATPGDKSISCKASRDVDDVNWQ 180	
DB	121 APTGGGSGGGSGGGSGGGSGSETTLQSPAFMSATPGDKSISCKASRDVDDVNWQ 180	
QY	181 QRPGRAPFIILEDATTLVPGISPRESGSGYGTDFTLTINNIDSEDAAYVFCLOHDFPLT 240	
DB	181 QRPGRAPFIILEDATTLVPGISPRESGSGYGTDFTLTINNIDSEDAAYVFCLOHDFPLT 240	
QY	241 FGGGTKEIK 250	
DB	241 FGGGTKEIK 250	

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RESULT 7
US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben et al.
;   TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
;   FILE REFERENCE: PFS23
;   CURRENT APPLICATION NUMBER: US/09/880,748
;   CURRENT FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/212,210
;   PRIOR FILING DATE: 2000-06-15
;   PRIOR APPLICATION NUMBER: 60/240,816
;   PRIOR FILING DATE: 2000-10-17
;   PRIOR APPLICATION NUMBER: 60/276,248
;   PRIOR FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/293,499
;   PRIOR FILING DATE: 2001-05-25
;   NUMBER OF SEQ ID NOS: 3239
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 1321
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1321

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Query Match	62.5%	Score	835	DB	10	Length	249
Best Local Similarity	63.8%	Pred. NC	3.3e-50				
Matches	166	Conservative	26	Mismatches	46	Indels	22
						Gaps	3

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.2864 Seconds

(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-21

Perfect score: 1336

Sequence: 1 QVQLQQMGAGLKSMTLSL.....CLQHNFPPLTFGGGTVEIK 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	45.7	249	S41374	single chain Fv an
2	601.5	45.0	268	A56446	Ig heavy chain V r
3	532	39.8	233	JC5322	p53 specific singl
4	506	37.9	231	B23746	Ig Fab region IV-J
5	502.5	37.6	140	A49045	Ig heavy chain V r
6	498.5	37.3	143	B49028	Ig heavy chain V-I
7	490	36.7	140	S78052	Ig heavy chain pre
8	478	35.8	126	S47010	Ig heavy chain V4.
9	468	35.0	115	K3H015	Ig heavy chain pre
10	452	33.8	146	G1H012	Ig kappa chain pre
11	442.5	33.1	122	JL0047	Ig heavy chain V r
12	439	32.9	97	S26898	Ig heavy chain V r
13	436.5	32.7	140	I37782	Ig variable region
14	431.5	32.3	130	S31690	Ig heavy chain V r
15	431	32.3	129	S44114	Ig heavy chain V r
16	430	32.2	97	S14474	Ig heavy chain V r
17	429	32.1	97	G34964	Ig heavy chain V-I
18	429	32.1	145	S78055	Ig heavy chain pre
19	425.5	31.8	114	I72667	cold agglutinin F8
20	420	31.4	118	S24443	Ig heavy chain V r
21	419.5	31.4	147	S13519	Ig heavy chain V r
22	418	31.3	139	S31586	Ig heavy chain V r
23	416	31.1	220	A49444	Ig gamma-1 heavy c
24	415.5	31.1	155	S31511	Ig heavy chain - h
25	414	31.0	97	S26805	Ig heavy chain V r
26	413.5	31.0	155	S31512	Ig heavy chain - h
27	411.5	30.8	123	S30530	Ig heavy chain V r
28	410	30.7	137	S31676	Ig heavy chain V r
29	409.5	30.7	134	S54906	Ig heavy chain V r

30	409	30.6	97	2	JH0428	Ig gamma chain V r
31	408	30.5	130	2	S30534	Ig heavy chain V r
32	406	30.4	118	2	S20780	Ig heavy chain V r
33	405.5	30.4	121	2	S44113	Ig heavy chain V r
34	404	30.2	97	2	S26806	Ig heavy chain V r
35	401.5	30.1	139	2	S31696	Ig heavy chain V r
36	400.5	30.0	127	2	S19668	Ig heavy chain pre
37	398.5	29.8	135	2	S78051	Ig heavy chain V r
38	396.5	29.7	146	2	S09711	Ig heavy chain V r
39	393	29.4	97	2	S26808	Ig heavy chain V r
40	391.5	29.3	123	2	S30529	Ig heavy chain V r
41	385.5	28.9	146	2	S09710	Ig heavy chain V r
42	385	28.8	106	2	S37454	Ig mu chain - huma
43	385	28.8	139	2	A41287	Ig heavy chain pre
44	384	28.7	97	2	S12416	Ig heavy chain V r
45	383.5	28.7	140	2	A24770	hypothetical hybr

ALIGNMENTS

```
RESULT 1
S41374
single chain Fv antibody - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 06-Jan-1995
C/Accession: S41374
R:Artaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A/Description: Construction and functional characterization of a single chain Fv antibod
A/Reference number: S41374
A/Accession: S41374
A>Status: preliminary
A/Molecule type: DNA
A/Residue: 1-249 <ART>
A/Cross-references: EMBL:229480

Query Match
Best Local Similarity 48.1%; Score 611; DB 2; Length 249;
Matches 124; Conservative 39; Mismatches 75; Indels 20; Gaps 4;

QY 1 QVQLQQMGAGLKSMTLSLTCAVSGSPSYGYSWIRPPGKGLMEIGI-NHRGTTY 59
| | | | | : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 QVQLQSGSELRVPGASVSLCTASGPNKDYIHVVKRPEKGLMIRIAPASNVXY 60

QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADVAIVYCAR--TVAGTSIDYWGQGLTVTVSSG 117
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 VRFPODKATITADTSSNTAYLLSLTSSEDTAVYVCARDTLYTSIGYWGQGSTVTVS-- 118

QY 118 SASAPRTGGSGGSGGSGGSGGSGGSKTTLTQSPAFMSATPDQVSIICKAR-----DV 172
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 -----SRGGSGGGSGGSGGSGGSDIELTQSPPEVVIPEBSVSIICRSSISLLYSQ3 168

QY 173 DDVVMWYQORPEAPAFITEDATTVPGISPPFSGSGYGTDFTLTINIDSEDAAYVFC 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 DSYLWFLQRPQOSQLILYKMSNLASGVDPDFSGSGSTFTLRISRBAEDVGYCYCM 228

QY 233 QHNNPPLTFGGGTVEIK 250
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 229 QHREYPLTFGAGTKLEIK 246

RESULT 2
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C/Species: Mus musculus (house mouse)
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #ext_change 16-Aug-1996
C/Accession: A56446
R:Rang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident
A/Reference number: A56446; MUID:95229583; PMID:7713873
A/Accession: A56446
```

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <RNA>
A:Cross-references: GB:U20617
C:Keywords: heterotrimer; immunoglobulin

Query Match
Best Local Similarity 45.0%; Score 601.5; DB 2; Length 268;
Matches 123; Conservative 41; Mismatches 73; Indels 15; Gaps 4;

QY 1 QVQLQOMGAGLLKSMGTLSTLCAVSGASFGGYWSWIRPPGKLEWIGEI-NHRSSTY 59
DB 3 QVQLQOMGAGLLKSMGTLSTLCAVSGASFGGYWSWIRPPGKLEWIGEI-NHRSSTY 59
QY 60 NPSLDGRVTISLDTSTNOISLKTSMTPADTAAYVYCAR-TVAGTSYWGQGLTVVSSG 118
DB 63 DPKFGKATITADTSSMTAVLQSSLSLSTEDTAVYTCASYLTRYENYWGQGLTVVSSG 119
QY 119 ASAPTGG 178
DB 120 -----SGGG 178
QY 179 YQORPGEAPLFIIEDATTVPGISPRFGSGYGDPTLTINNIDEDAAVYFCLOHNDNP 238
DB 170 YQKSPASPKLWYVYSHLPQVPARFSSGSSGNSISLTSSMEGDEDAATYCCOFTSSP 229
QY 239 LTFGGGTXYEIK 250
DB 230 FTFGSGTKLEIK 241

RESULT 3

UC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: J05322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: J05322; MUID:97168950; PMID:9016757
A:Accession: J05322
A:Molecule type: mRNA
A:Residues: 1-233 <JUN>
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match
Best Local Similarity 39.8%; Score 532; DB 2; Length 233;
Matches 114; Conservative 40; Mismatches 74; Indels 22; Gaps 6;

QY 5 QOMGAGLLKSMGTLSTLCAVSGASFGGYWSWIRPPGKLEWIGEI-NHRSSTY 63
DB 1 QESGAEILVRSQASVKLSCTTSGFNINDYHMKRPEGLMIRIPENGDADMTKRS 60
QY 64 DGEVITISLDTSTNOISLKTSMTPADTAAYVYCARVAGTSYWGQGLTVVSSG 123
DB 61 GYATMTADTSSMTAVLQSSLSLSTEDTAVYTCN---AG-MDYWGQGLTVVSSG 108
QY 124 GGG 178
DB 109 -----SGGG 179
QY 180 QORPGEAPLFIIEDATTVPGISPRFGSGYGDPTLTINNIDEDAAVYFCLOHNDNP 239
DB 165 QOKPQPPRLILYVSNLESQVPAFSSGSGTPTLNIHVEBEDAATYCC-OHIRELT 223
QY 240 TFGGGTXYEIK 249
DB 224 RSEGGTKLEIK 233

RESULT 4

B23746
Ig Fab region IV-(H4)-C (Kau cold agglutinin) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: B23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein Kau, a monoclonal immuno-

A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: B23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-231 <LBO>
C:Superfamily: 1-231 <LBO>
F:140-209/Domain: immunoglobulin C region; immunoglobulin homology

Query Match
Best Local Similarity 37.9%; Score 506; DB 2; Length 231;
Matches 101; Conservative 4; Mismatches 17; Indels 4; Gaps 1;

QY 2 VQLQOMGAGLLKSMGTLSTLCAVSGASFGGYWSWIRPPGKLEWIGEI-NHRSSTY 61
DB 1 VQLQOMGAGLLKSMGTLSTLCAVSGASFGGYWSWIRPPGKLEWIGEI-NHRSSTY 60
QY 62 SLDSGRVTISLDTSTNOISLKTSMTPADTAAYVYCARVAGTS---DYWGQGLTVVSSG 117
DB 61 SLDSGRVTISLDTSTNOISLKTSMTPADTAAYVYCARVAGTS---DYWGQGLTVVSSG 120
QY 118 SASAPT 123
DB 121 SASAPT 126

RESULT 5

A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rasseant, L.Z.; Labaume, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autoantibody from a patient with Sjögren's syndrome which recognizes a b1
A:Reference number: A49045; MUID:92324290; PMID:1623923
A:Accession: A49045
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GRI>
A:Cross-references: GB:S39381; NID:9250899; PID:AA822441.1; PID:9250900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 37.6%; Score 502.5; DB 2; Length 140;
Matches 97; Conservative 5; Mismatches 14; Indels 5; Gaps 1;

QY 1 QVQLQOMGAGLLKSMGTLSTLCAVSGASFGGYWSWIRPPGKLEWIGEI-NHRSSTY 60
DB 20 QVQLQOMGAGLLKSMGTLSTLCAVSGASFGGYWSWIRPPGKLEWIGEI-NHRSSTY 79
QY 61 PSIDGRVTISLDTSTNOISLKTSMTPADTAAYVYCAR-TVAGTSYWGQGLTVVSSG 115
DB 80 PSIDGRVTISLDTSTNOISLKTSMTPADTAAYVYCAR-TVAGTSYWGQGLTVVSSG 139
QY 116 S 116
DB 140 S 140

RESULT 6

B49028
Ig heavy chain V-IV region - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
 C:Accession: B49028
 R:Timmer, E.; Kenter, M.; Thompson, A.; Kraakman, M.B.; Berman, J.E.; Alt, F.W.; Schuur
 Eur. J. Immunol. 21, 2355-2363, 1991
 A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
 A:Reference number: A49028; MUID:92008140; PMID:1915549
 A:Accession: B49028
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-143 <TIM>
 A:Cross-References: GB:S64473; NID:9236906; PIDN:AAB20012.1; PID:9236907
 A:Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
 A:Note: sequence extracted from NCBI backbone (NCBI:64473, NCBI:64472)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 37.3%; Score 498.5; DB 2; Length 143;
 Best Local Similarity 73.5%; Pred. No. 26-25;
 Matches 100; Conservative 4; Mismatches 19; Indels 13; Gaps 2;

QY 1 QVQLQOMGAGLLKSNWGLTSLTCAVSGASPSGYWMSIRPPKGLGWEIGINHRGTTYN 60
 1 QVQLQOMGAGLLKSPETSLTCAVVGSGPSGYWMSIRPPKGLGWEIGINHRGTTYN 60
 DB 1 QVQLQOMGAGLLKSPETSLTCAVVGSGPSGYWMSIRPPKGLGWEIGINHRGTTYN 60
 QY 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAVYYCAR-----TVAGTS-----DYWG 107
 61 PSLKSRVTISVDTSKNQFSLKLSVTADTAVYYCARGPVVVPAAMRGRGMDYGDVWG 120
 DB 61 PSLKSRVTISVDTSKNQFSLKLSVTADTAVYYCARGPVVVPAAMRGRGMDYGDVWG 120
 QY 108 QGTLVTSSSGSASAPT 123
 121 QGTLVTSSSGSASAPT 136
 DB 121 QGTLVTSSSGSASAPT 136

RESULT 7

S78052
 Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
 C:Accession: S78052; S23717
 R:Harindranath, N.
 submitted to the EMBL Data Library, August 1990
 A:Reference number: S78051
 A:Accession: S78052
 A:Molecule type: mRNA
 A:Residues: 1-140 <HAR>
 A:Cross-References: EMBL:X54441; NID:937815; PIDN:CA48308.1; PID:930118
 R:Harindranath, N.; Goldfarb, I.S.; Ikenatsu, H.; Burastero, S.E.; Wilder, R.L.; Nocklins
 Int. Immunol. 3, 865-875, 1991
 A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
 patient.
 A:Reference number: S23716; MUID:92031262; PMID:1718404
 A:Accession: S23717
 A:Molecule type: mRNA
 A:Residues: 15-111 <HAM>
 A:Cross-References: EMBL:X54441
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
 F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
 F:29-111/Domain: immunoglobulin homology <IMM>

Query Match 36.7%; Score 490; DB 2; Length 140;
 Best Local Similarity 76.0%; Pred. No. 6-8e-25;
 Matches 98; Conservative 3; Mismatches 12; Indels 16; Gaps 2;

QY 1 QVQLQOMGAGLLKSNWGLTSLTCAVSGASPSGYWMSIRPPKGLGWEIGINHRGTTYN 60
 15 QVQLQOMGAGLLKSPETSLTCAVVGSGPSGYWMSIRPPKGLGWEIGINHRGTTYN 74
 DB 15 QVQLQOMGAGLLKSPETSLTCAVVGSGPSGYWMSIRPPKGLGWEIGINHRGTTYN 74
 QY 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAVYYCARTVAGTS-----DYWG 107
 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAVYYCARTVAGTS-----DYWG 107

DB 75 PSLKSRVTISVDTSKNQFSLKLSVTADTAVYYCAR---GGSVIRFLEMLLYPAEDYWG 131
 QY 108 QGTLVTSS 116
 132 QGTLVTSS 140
 DB 132 QGTLVTSS 140

RESULT 8

S47010
 Ig heavy chain V4.21-UniqueD-J5 region - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S47010
 R:Mahoudi, M.; Gasyan, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
 submitted to the EMBL Data Library, July 1994
 A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bi
 A:Reference number: S47009
 A:Accession: S47010
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-126 <MAH>
 A:Cross-References: EMBL:Z35492; NID:9517254; PIDN:CA484625.1; PID:9517255
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 35.8%; Score 478; DB 2; Length 126;
 Best Local Similarity 75.4%; Pred. No. 3.6e-24;
 Matches 95; Conservative 3; Mismatches 18; Indels 10; Gaps 1;

QY 1 QVQLQOMGAGLLKSNWGLTSLTCAVSGASPSGYWMSIRPPKGLGWEIGINHRGTTYN 60
 1 QVQLQOMGAGLLKSPETSLTCAVVGSGPSGYWMSIRPPKGLGWEIGINHRGTTYN 60
 DB 1 QVQLQOMGAGLLKSPETSLTCAVVGSGPSGYWMSIRPPKGLGWEIGINHRGTTYN 60
 QY 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAVYYCAR-----TVAGTSDYWGQGT 110
 61 PSLKSRVTISVDTSKNQFSLKLSVTADTAVYYCARGGCCPKKASCYTKNMFDPWGQGT 120
 DB 61 PSLKSRVTISVDTSKNQFSLKLSVTADTAVYYCARGGCCPKKASCYTKNMFDPWGQGT 120
 QY 111 LVTSS 116
 121 LVTSS 126
 DB 121 LVTSS 126

RESULT 9

K3H015
 Ig kappa chain precursor V region (EV15) - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
 C:Accession: A01906
 R:Stavener, J.; Kekish, O.; Batter, D.; Grenier, J.; Balazs, I.; Henderson, E.; Zeger, S.
 Nucleic Acids Res. 13, 3495-3514, 1985
 A:Title: Aberrant recombination events in B cell lines derived from a kappa-deficient hu
 A:Reference number: A01906; MUID:85242052; PMID:3925437
 A:Accession: A01906
 A:Molecule type: DNA
 A:Residues: 1-115 <STA>
 A:Note: the sequence was determined from the germline gene
 C:Comment: This sequence does not belong to any of the previously described V-kappa sub
 its type.
 C:Comment: The gene was found to be aberrantly rearranged in an individual who does not
 A:Gene: GDB:IGKV
 A:Cross-References: GDB:119341; OMIM:146980
 A:Map position: 2p12-2p12
 A:Intons: 17/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k)
 b chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-115/Product: Ig kappa chain V region (EV15) #status predicted <MAT>
 F:21-43/Region: framework 1
 F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1
 F:55-69/Region: framework 2
 F:70-76/Region: complementarity-determining 2
 F:77-108/Region: framework 3
 F:109-115/Region: complementarity-determining 3
 F:43-108/Disulfide bonds: #status predicted

Query Match 35.0%; Score 468; DB 1; Length 115;
 Best Local Similarity 87.5%; Pred. No. 1,4e-23;
 Matches 84; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 143 SKTLTOSAPFMSATPPDKSISCKASRDVDDVNMVQSPGAPFIETDATTVPGIS 202
 DB 20 AETLTOSAPFMSATPPDKXNISCKASQDIDDMMVYQKPGRAAFIIQEATIVPGIP 79
 QY 203 PRFSGSGYGTDFLTITINNISEDAAYFCLOHNF 238
 DB 80 PRFSGSGYGTDFLTITINNISEDAAYFCLOHNF 115

RESULT 10

G1HHD2

IG heavy chain precursor V-II region (ARH-77) - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
 C:Accession: A02101

R:Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
 Gene 33, 181-189, 1985
 A>Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence
 A:Reference number: A02101; MUID:85205332; PMID:392855

A:Accession: A02101
 A:Molecule type: mRNA
 A:Residues: 1-146 <KUD>

A>Note: the sequence was determined from the differentiated gene
 A>Note: the authors translated the codon GGG for residue 17 as Arg

C:Genetics:

A:Gene: GDB:IGH@

A:Cross-references: GDB:128528; OMIM:147070
 A:Map position: 14q32.33-14q32.33

A:Intons: 16/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-146/Product: IG heavy chain V-II region (ARH-77) #status predicted <MAY>

F:20-117/Region: V segment

F:35-117/Domain: immunoglobulin homology <IMM>

F:118-127/Region: D segment

F:128-146/Region: J segment

F:42-115/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 33.8%; Score 452; DB 1; Length 146;
 Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;

QY 1 QVQLQOMGAGLISWGLSLTCAVSGASFGYVSWIRPPGKGLFWIGINHGSTTYN 60
 DB 21 QVQLQOMGAGLVPRSETSLTCAVFGSGYVSWIRPPGKGLFWIGINHGSGTNYK 80

QY 61 PSIDGRVTLISLDTSTNQISLKTSMPTADTAAYVYCARV--AGTS-----DYMGGQT 110
 DB 81 TSLKSRVTLISLDTSTNQISLKTSMPTADTAAYVYCARGLRGWMDVDYVYGMWVGQGT 140

QY 111 LVTVSS 116
 DB 141 TTVTSS 146

RESULT 11

JL0047

IG heavy chain V region precursor (clone CR18) - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
 C:Accession: JL0047

R:Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
 U. Exp. Med. 167, 2011-2016, 1988

A>Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new
 A:Reference number: JL0047; MUID:88258392; PMID:3133445

A:Accession: JL0047

A:Molecule type: mRNA

A:Residues: 1-122 <BAE>

A:Experimental source: T-cell line RPMI 8402

A>Note: the authors translated the reading frame which extends to the stop codon; the s
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin
 F:23-105/Domain: immunoglobulin homology <IMM>

Query Match 33.1%; Score 442.5; DB 2; Length 122;
 Best Local Similarity 84.3%; Pred. No. 6,4e-22;
 Matches 86; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLQOMGAGLISWGLSLTCAVSGASFGYVSWIRPPGKGLFWIGINHGSTTYN 60
 DB 9 QVQLQOMGAGLISWGLSLTCAVSGASFGYVSWIRPPGKGLFWIGINHGSGTNYN 68
 QY 61 PSIDGRVTLISLDTSTNQISLKTSMPTADTAAYVYCAR--TVAG 101
 DB 69 TSLKSRVTLISLDTSTNQISLKTSMPTADTAAYVYCARGTARG 110

RESULT 12

S26898

IG heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26898; S12420

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992

A>Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26898

A:Molecule type: DNA

A:Residues: 1-97 <TOM>

A:Cross-references: EMBL:Z12363; NID:G32944; PIDN:CAA78233.1; PID:G32945
 A:Experimental source: clone DP-63

R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
 EMBO J. 8, 3741-3748, 1989

A>Title: The smaller human V(H) gene families display remarkably little polymorphism.
 A:Reference number: S09421; MUID:90059975; PMID:2511001

A:Accession: S12420

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-97 <SAN>

A:Cross-references: EMBL:X56364

A:Experimental source: V(H)4.2

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 439; DB 2; Length 97;
 Best Local Similarity 85.6%; Pred. No. 8,5e-22;
 Matches 83; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLQOMGAGLISWGLSLTCAVSGASFGYVSWIRPPGKGLFWIGINHGSTTYN 60
 DB 1 QVQLQOMGAGLISWGLSLTCAVSGASFGYVSWIRPPGKGLFWIGINHGSGTNYN 60
 QY 61 PSIDGRVTLISLDTSTNQISLKTSMPTADTAAYVYCAR 97
 DB 61 TSLKSRVTLISLDTSTNQISLKTSMPTADTAAYVYCAR 97

RESULT 13

I37782

IG variable region (VDJ) (clone T23-9) - human (fragment)
 C:Species: Homo sapiens (man)

C>Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
 C/Accession: I37782; S25476
 R/Demaison, C.; Chastagner, P.; These, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
 A/Title: Somatic diversification in the heavy chain variable region genes expressed by h
 A/Reference number: A36876; MUID:94119917; PMID:8290556
 A/Accession: I37782
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-140 <RES>
 A/Cross-references: EMBL:X67906; NID:g33582; PID:CAA48104.1; PID:g33583
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 32.7%; Score 436.5; DB 2; Length 140;
 Best Local Similarity 71.9%; Pred. No. 1.8e-21;
 Matches 87; Conservative 8; Mismatches 21; Indels 5; Gaps 1;

QY 1 QVQLQDQWAGLLKSGTSLTCAVSGASPSGYWMSWIRPPGKGLWIGIINHRGSTTYN 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 20 QVQLDSESGPLVKEPSETISLTCTVSGGSISYWSWIRPPGKGLWIGIITYSGSTNN 79
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 PSIDGRVTISLDSTNQISLKLTSMTADTAAYVYCARVAGT-----SDYWGQGLTVYS 115
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 80 PSLSKRVITISVDTSKQPSLKLSTVTAADTAAYVYCARHNSSWYGRYFDYWGQGLTVYS 139
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 116 S 116
 DB 140 S 140

RESULT 14

S31690
 Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31690
 R/Cuisinier, A.M.; Gauchier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31690
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-130 <CU>
 A/Cross-references: EMBL:Z14199; NID:g30984; PID:CAA78568.1; PID:g30985
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:20-102/Domain: immunoglobulin homology <IMM>

Query Match 32.3%; Score 431.5; DB 2; Length 130;
 Best Local Similarity 68.8%; Pred. No. 3.5e-21;
 Matches 88; Conservative 7; Mismatches 18; Indels 15; Gaps 2;

QY 1 QVQLQDQWAGLLKSGTSLTCAVSGASPSGYWMSWIRPPGKGLWIGIINHRGSTTYN 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 6 QVQLDSESGPLVKEPSETISLTCTVSGGSISYWSWIRPPGKGLWIGIITYSGSTNN 65
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 PSIDGRVTISLDSTNQISLKLTSMTADTAAYVYCARVAGT-----DYWGQ 108
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 66 PSLSKRVITISVDTSKQPSLKLSTVTAADTAAYVYCAR-----GSSVLMFGEELLYFDYWGQ 122
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 109 GTLVTVSS 116
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 123 GTLVTVSS 130

RESULT 15

S44114
 Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
 C/Accession: S44114

R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
 submitted to the EMBL Data Library, March 1994
 A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
 A/Reference number: S44105
 A/Accession: S44114
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-129 <HAM>
 A/Cross-references: EMBL:Z31579; NID:g472968; PID:CAA83451.1; PID:g940525
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 32.3%; Score 431; DB 2; Length 129;
 Best Local Similarity 69.8%; Pred. No. 3.7e-21;
 Matches 88; Conservative 6; Mismatches 24; Indels 8; Gaps 2;

QY 1 QVQLQDQWAGLLKSGTSLTCAVSGASPSGYWMSWIRPPGKGLWIGIINHRGSTTY 59
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 1 QVQLDSESGPLVKEPSETISLTCTVSGGSISYWSWIRPPGKGLWIGIITYSGSTNY 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 60 NSLDGRVTISLDSTNQISLKLTSMTADTAAYVYCARVAGT-----VAGTSDYWGQGLTV 112
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 61 NSFSKRVITISADTSKQPSLKLSTVTAADTAAYVYCARHNDYFDYWGQGLTV 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 113 TVSSGS 118
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 121 TVSSAS 126

Search completed: May 13, 2004, 15:08:42
 Job time : 11.2864 secs

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Db 20 AETLTGSPAFMSATPEDKVNISCKASQDIDDMWYQOKPGEAIFLIQEAITLVPCIP 79
 QY 203 PRSSGGYGTDFLTITNNINISSEDAAYFCLQHDNFP 238
 Db 80 PRSSGGYGTDFLTITNNINISSEDAAYFCLQHDNFP 115

RESULT 2
 ID HV21_HUMAN STANDARD; PRT; 146 AA.
 AC P0631;
 DT 01-JUN-1988 (Rel. 06, Created)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region ARH-77 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85203332; PubMed=3922855;
 RA Kudo A., Ishihara T., Nishimura Y., Maranabe T.;
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
 RL repeat sequence in 5' flanking region.";
 Gene 33:181-189 (1985).
 DR PIR; A02101; GHHD2.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1 19
 FT DOMAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
 FT DOMAIN 118 127 D SEGMENT.
 FT DOMAIN 128 146 J SEGMENT.
 FT DISULFID 42 115 BY SIMILARITY.
 FT NON TER 146 146
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;
 Query Match
 Best Local Similarity 33.8%; Score 452; DB 1; Length 146;
 Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;
 QY 1 QVQLQDQAGLILKSGWGLSTLTCAVSGASPSFGYWMWIRPPGKGLIEWIGINRGSTTN 60
 Db 21 QVQLQDQAGLIVPSETLSLTCAVFGSGFGYWMWIRPPGKGLIEWIGINRGSTTNK 80
 QY 61 PSDLGRVTISLDTSTNQISLKTSMTAADTAAYVCARV-----DYWGQT 110
 Db 81 TSKSRVTISLDTSTNQISLKTSMTAADTAAYVCARV-----DYWGQT 110
 QY 111 LVTYSS 116
 Db 141 TVTVSS 146
 RESULT 3
 ID HV2F_HUMAN STANDARD; PRT; 129 AA.
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region WAW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=8222235; PubMed=6806818;
 RA Takehashi N., Tetsert D., Debure B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 RT immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 CC PROTEIN
 CC PIR; A02099; D2HWA.
 DR HSSP; P01825; 7FAB.
 DR GlycoSiteDB; P01824; -.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 113
 FT NON TER 129 129 IG-LIKE.
 SQ SEQUENCE 129 AA; 14117 MW; D5D53D47AB51319 CRC64;
 Query Match
 Best Local Similarity 28.0%; Score 374.5; DB 1; Length 129;
 Matches 79; Conservative 10; Mismatches 27; Indels 13; Gaps 3;
 QY 1 QVQLQDQAGLILKSGWGLSTLTCAVSGASR--SGYWMWIRPPGKGLIEWIGINRGSTT 58
 Db 1 RLQDSEGPGLVLPSETLSLTCAVSGGPIRRGYGMWIRPPGKGLIEWIGVYTSIX 60
 QY 59 YNPSLDGRVTISLDTSTNQISLKTSMTAADTAAYVCAR-----TVAGTS-----DYWG 107
 Db 61 YNPSLRGRVTISLDTSTNQISLKTSMTAADTAAYVCARPPYYDYGTSDDGIDWVG 120
 QY 108 QGTLVTYSS 116
 Db 121 QGTVTVSS 129
 RESULT 4
 ID HV2G_HUMAN STANDARD; PRT; 117 AA.
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region NEMW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=77242302; PubMed=407927;
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the VH region of a human myeloma
 RT immunoglobulin (IgG New)."
 RL Biochemistry 16:3412-3420 (1977).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE=78066916; PubMed=618887;
 RA Saul F.A., Amzel L.M., Poljak R.J.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 RT from human immunoglobulin new at 2.0-A resolution.";
 J. Biol. Chem. 253:585-597 (1978).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90404; GIHUM.
 DR PDB; 7FAB; 31-JAN-94.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 KW DOMAIN 1 111 IG-LIKE.
 FT MOD RES 1 7 PYRROLIDONE CARBOXYLIC ACID.
 FT STRAND 1 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59
 FT HELIX 61 63
 FT TURN 64 66
 FT TURN 72 76
 FT STRAND 73 76
 FT STRAND 82 87
 FT HELIX 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
 Query Match 27.4%; Score 365.5; DB 1; Length 117;
 Best Local Similarity 60.7%; Pred. No. 2, 1e-20;
 Matches 71; Conservative 20; Mismatches 25; Indels 1; Gaps 1;
 QY 1 QVLOQMGAGLKGWGLSLTCAVSGASFGYWSMIRPPGKGLWGEINHRGSTTYN 60
 DB 1 QVLOESGPGVLPSPQTLSTCTVSGSTFSNDYTWVRQPGRGLEWIGVYFVHGTSDDT 60
 QY 61 PSLDGRVITSLDTSTNQLSKLTSMTAATVATYTCART-VAGTSDYWGQGLTVTVSS 116
 DB 61 TPLRSRVTMLVDTSNKQFSLRLSSVTAAADTAVYVCARNLIAGCIDVWGQGLTVTVSS 117
 RESULT 5
 HY46_MOUSE STANDARD; PRT; 137 AA.
 ID HV46_MOUSE
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DS Ig heavy chain V region MOPC 315 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89238351; PubMed=2497341;
 RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 RT gene segment";
 RL Mol. Immunol. 26:431-434(1989).
 RN [2]
 RP SEQUENCE OF 1-31.
 RX MEDLINE=78094475; PubMed=414225;
 RA Jilka R.L., Peacock S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse

RT immunoglobulin heavy chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemel R., Buretein Y.;
 RT "Structure and function of immunoglobulin genes and precursors";
 RL Fed. Proc. 38:1839-1845(1979).
 RN [4]
 RP SEQUENCE OF 19-136.
 RX MEDLINE=74170779; PubMed=4524622;
 RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
 RT "Amino-acid sequence of the variable region of the heavy (alpha)
 RT chain of a mouse myeloma protein with anti-hapten activity";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP REVISION TO 53.
 RX MEDLINE=77244979; PubMed=268248;
 RA Hood L., Margolies M.N., Glyvol D., Zakut R.;
 RL Unpublished results, cited by:
 RL Padlan E.A., Davies D.R., Peck I., Glyvol D., Wright C.;
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; M27638; AAA61337.1; -
 CC EMBL; X07880; CAA30727.1; -
 CC DR PIR; P01012; AVMS35.
 CC DR HSSP; P01825; 7FAB.
 CC DR InterPro; IPR007110; IG-like.
 CC DR InterPro; IPR003596; IG_v.
 CC Pfam; PF00047; IG_v.
 CC DR SMART; SM00406; IGV; 1.
 CC DR PROSITE; PS50835; IG_LIKE; 1.
 CC Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
 FT DOMAIN 19 48 FRAMEWORK-1.
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 127 137 FRAMEWORK-4.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).
 FT CONFLICT 15 15 G -> H (IN REF. 2).
 FT CONFLICT 77 78 GY -> YG (IN REF. 4).
 FT CONFLICT 102 102 N -> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON_TER 137
 SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
 Query Match 25.0%; Score 334.5; DB 1; Length 137;
 Best Local Similarity 57.4%; Pred. No. 4, 7e-18;
 Matches 70; Conservative 14; Mismatches 27; Indels 11; Gaps 3;
 QY 2 VLOQMGAGLKGWGLSLTCAVSGASFGYWSMIRPPGKGLWGEINHRGSTTYN 60
 DB 20 VLOESGPGVLPSPQTLSTCTVSGSTFSNDYTWVRQPGRGLEWIGVYFVHGTSDDT 60
 QY 61 PSLDGRVITSLDTSTNQLSKLTSMTAATVATYTCART-VAGTSDYWGQGLTVTVSS 114
 DB 80 PSLKRSRVTMLVDTSNKQFSLRLSSVTAAADTAVYVCARNLIAGCIDVWGQGLTVTVSS 135

STRAND	70	75
HELIX	80	82
STRAND	84	90
STRAND	98	98
STRAND	102	106

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Query Match      24.7%; Score 330; DB 1; Length 108;
Best Local Similarity 56.7%; Pred. No. 7.7e-18;
Matches 59; Conservative 22; Mismatches 23; Indels 0; Gaps 0
147 LTPSPAFMSATPGDKVSTSCSKASRVDDVNMYYQORPGEAFLFIETDATTLVGDISPRFS 206
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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Db 4 MTQSPSSLSASVGDRTVITTCQASQDISIFLNTYQQRKAPKLLIYDASKLEAGVSPRS 63
 QY 207 GSGYGTDFLTITNNIDSEDAAYFCLQHNFPPLTFGGGTVKVEIK 250
 DB 64 GSGSGTDFLTITNLSLOPEDFATYTCQCFDMLPLTFGGGTVKVEIK 107

RESULT 8

KVIR HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxId=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal Igm
 (protein WEA) with antibody activity against 3,4-pyruvylated
 galactose in Klebsiella polysaccharides K30 and K33."
 RT Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 RL -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WADENSTROM'S MACROGLOBULINEMIA.
 CC PIR; A01876; KIHUWE.
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Monoclonal antibody.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 98 107 FRAMEWORK-4.
 FT NON TER 23 88 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 24.4%; Score 326; DB 1; Length 108;
 Best Local Similarity 56.7%; Pred. No. 1.5e-17;
 Matches 59; Conservative 23; Mismatches 22; Indels 0; Gaps 0;
 QY 147 LTQSPAFMSATPBDKVISISCKASRDVDDVNTYQQRPGAPFIITEDATLVPGISPRS 206
 DB 4 MTQSPSSLSASVGDRTVITTCQASQDISIFLNTYQQRKAPKLLIYDASKLEAGVSPRS 63
 QY 207 GSGYGTDFLTITNNIDSEDAAYFCLQHNFPPLTFGGGTVKVEIK 250
 DB 64 GSGSGTDFLTITNLSLOPEDFATYTCQCFDMLPLTFGGGTVKVEIK 107

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxId=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=75059271; PubMed=4435756;
 RA Eulitz M., Hilschmann N.;
 RT "The primary structure of a human immunoglobulin L-chain of
 kappa-type (Bence-Jones protein Scw.). II: The chymotryptic peptides
 and the complete amino acid sequence."
 RT Hoppe-Seiyler's Z. Physiol. Chem. 355:842-866(1974).
 RL -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01875; KIHUSW.
 DR HSSP; P01607; IRET.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 98 107 FRAMEWORK-4.
 FT NON TER 23 88 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11764 MW; 32CECDDF9644414 CRC64;
 Query Match 23.7%; Score 317; DB 1; Length 108;
 Best Local Similarity 54.8%; Pred. No. 6.9e-17;
 Matches 57; Conservative 22; Mismatches 25; Indels 0; Gaps 0;
 QY 147 LTQSPAFMSATPBDKVISISCKASRDVDDVNTYQQRPGAPFIITEDATLVPGISPRS 206
 DB 4 MTQSPSSLSASVGDRTVITTCQASQDISIFLNTYQQRKAPKLLIYDASKLEAGVSPRS 63
 QY 207 GSGYGTDFLTITNNIDSEDAAYFCLQHNFPPLTFGGGTVKVEIK 250
 DB 64 GSGSGTDFLTITNLSLOPEDFATYTCQCFDMLPLTFGGGTVKVEIK 107

RESULT 10

HV43 MOUSE STANDARD; PRT; 144 AA.
 AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 141 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Makl R., Kurosawa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes."
 RL Nature 286:676-683(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
 DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC or send an email to license@isb-sib.ch).

DR BMB; V00768; CAA24149.1; -
DR PIR; A02094; G2M614.
DR HSP; P01825; 7FAB.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; Ig, 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144
FT DOMAIN 20 130
FT NON TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 23.7%; Score 316.5; DB 1; Length 144;
Best Local Similarity 52.0%; Pred. No. 1e-16; Mismatches 35; Indels 9; Gaps 1;
Matches 65; Conservative 16; Mismatches 35; Indels 9; Gaps 1;

QY 1 QVQLQWGAIGLKSMTSLTCAVSGAFSGYWMIRPGKLEWIGINHGSTTN 60
DB 20 QVQLKSGPGLVAPSGSLITCVSGFSLTGVMVWNPQPKLEWIGINHGSTTN 79
QY 61 PSIDGKVTISLDTSTQISLKLSTMTADTAVYCARVA-----GTSIDYGGTLL 111
DB 80 STLKSLRTITKNSQVFLKNSLQTDINRYCAVSIIYGRSDKYFTLDYWGQTS 139
QY 112 VTVSS 116
DB 140 VTVSS 144

RESULT 11

KVLA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Tiltan K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence and the location of the disulfide bridges.";
RT J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR HSP; A01861; KIHUAG.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; Ig, 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FRAMEWORK-1.

FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DISULFD 98 107
FT NON TER 23 88
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 23.7%; Score 316; DB 1; Length 108;
Best Local Similarity 54.8%; Pred. No. 8.1e-17;
Matches 57; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

QY 147 LTQSPAFNSATPGDKVISISCKASRDVDDVMYQORPGKAFIFIEDATTLVPGISPRFS 206
DB 4 MTQSPASLSASVDGVITTCASQDINHYLWYQGGPKKPKILYDASNLGVSRFS 63
QY 207 GSGYGDTFTLTINNIDSDAAYFCLQHDNPLTFPGGTQYETK 250
DB 64 GSGGDTFTLTISGLQPEDATYTCQYDTLPTFGGTLEIK 107

RESULT 12

KVLA_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91653; KIHUAV.
DR PDB; 1UV5; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; Ig, 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.


```
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RL 5'-terminal regions of immunoglobulin variable-region genes.";
RN Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Mathysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RL genes.";
RN Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RL myeloma MPC 11.";
RN Biochem. J. 171:337-347(1978).
CC -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
CC -----
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CC -----
DR EMBL; J00561; AAA38776.1; -.
DR PIR; A90823; KYMS11.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 129 FRAMEWORK-3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 FRAMEWORK-4.
FT REPEAT 26 35
FT REPEAT 36 47
FT REPEAT 48 49
FT NON_TER 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3B CRC64;
Query Match 23.4%; Score 313; DB 1; Length 149;
Best Local Similarity 55.8%; Pred. No. 1.9e-16;
Matches 58; Conservative 19; Mismatches 27; Indels 0; Gaps 0;
QY 147 LTQSPAFMSATPDKYSISCKASRDVDDVMYQQRPGEAFFIREDATTLVGIISPPS 206
DB 45 MTQSHKFMNSTSVDRSITCKASQDVSTVAMVQQRKFGSPKLLIYSASRYRTGVDPRT 104
QY 207 GSGYGTDFLTINNIDSEDAAYFCLQHDNFPILTFGGGTRVEIK 250
DB 105 GSGSGTDFLTFTISSVQAEIDLAVYYCOQHYSTPPTFGGTRLEIK 148
```

Search completed: May 13, 2004, 15:02:04
Job time : 7.03884 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 33.6165 Seconds
(without alignments)
2346.453 Million cell updates/sec

Title: US-10-072-301-21

Perfect score: 1336
Sequence: 1 OVLOQWAGLTKSGTSLTCAVSGASFGYSWIRPPCKGLTWIGTINHRGST-TV 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.25:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	667	49.9	298	11	Q9GYFO mus musculu
2	603.5	45.2	241	11	Q921A6 mus musculu
3	585.5	43.8	243	11	Q7CWM2 mus musculu
4	509	38.1	588	4	Q8WUX4 homo sapien
5	509	38.1	597	4	Q9BU10 homo sapien
6	509	38.1	618	4	Q96A6 homo sapien
7	503	37.6	597	4	Q9BQ88 homo sapien
8	453	33.9	218	11	Q925S1 mus musculu
9	443.5	33.2	613	4	Q96EY0 homo sapien
10	437.5	32.7	116	4	Q7Z3Y6 homo sapien
11	437	32.7	150	4	Q9S973 homo sapien
12	416.5	31.2	119	4	Q9U173 homo sapien
13	415.5	31.1	496	4	Q96KX8 homo sapien
14	403.5	30.2	478	4	Q7Z379 homo sapien
15	398	29.8	492	4	Q7Z374 homo sapien
16	386.5	28.9	139	4	Q86SX2 homo sapien

17	378.5	28.3	479	11	Q99M22 mus musculu
18	369	27.6	473	4	Q8TC63 homo sapien
19	362	27.1	130	4	Q81ZD7 homo sapien
20	361	27.0	234	11	Q8R028 mus musculu
21	352	26.3	597	4	Q96BB9 homo sapien
22	339	25.4	482	11	Q91X92 mus musculu
23	334	25.0	487	11	Q99KA4 mus musculu
24	332	24.9	122	4	Q9UL75 homo sapien
25	327.5	24.5	613	4	Q8WUK1 homo sapien
26	325	24.3	108	11	Q8V100 mus musculu
27	323	24.2	143	11	Q824P9 mus musculu
28	319.5	23.9	142	11	Q924Q2 mus musculu
29	314	23.5	488	11	Q91WR1 mus musculu
30	313.5	23.5	140	11	Q924R2 mus musculu
31	312	23.4	108	4	Q9UL79 homo sapien
32	312	23.4	236	11	Q7TS98 mus musculu
33	312	23.4	482	11	Q8K172 mus musculu
34	312	23.4	484	11	Q8VEA0 mus musculu
35	311.5	23.3	109	4	Q9UL85 mus musculu
36	311.5	23.3	142	11	Q924O1 mus musculu
37	311.5	23.3	146	11	Q924R8 mus musculu
38	311.5	23.3	170	11	Q925S2 mus musculu
39	310.5	23.2	109	4	Q9UL78 homo sapien
40	310.5	23.2	480	11	Q91XE1 mus musculu
41	310	23.2	214	11	Q9RIA5 mus musculu
42	309.5	23.2	479	11	Q91WP5 mus musculu
43	309.5	23.2	480	11	Q8K0Z4 mus musculu
44	309	23.1	108	4	Q9UL83 mus musculu
45	309	23.1	469	11	Q8R3V9 mus musculu

ALIGNMENTS

RESULT 1	Q9GYFO	PRELIMINARY;	PRT;	298 AA.
AC	Q9GYFO;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	CN 8 scfv.			
GN	CN 8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	Taxid=10090;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RX	STRAIN-Balb/c; TISSUE=SpLeen;			
RX	MEDLINE=20183911; PubMed=10706631;			
RA	Shinohara N., Demura T., Fukuda H.;			
RT	"Isolation of a vascular cell wall-specific monoclonal antibody			
RT	recognizing a cell polarity by using a phase display subtraction			
RT	method."			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).			
DR	EMBL; AB036341; BAA86633.1; --			
DR	PIR; A33933; A33933.			
DR	PIR; S19112; S19112.			
DR	HSSP; P01607; IRET.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	PFAM; PF00047; Ig_2.			
DR	SMART; SM00406; IGV; 2.			
DR	PROSITE; P550835; IG_LIKE; 2.			
SQ	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;			
Query Match	49.9%;	Score 667;	DB 11;	Length 298;
Best Local Similarity	52.4%;	Pred. No. 2,2e-44;		
Matches 132;	Conservative 40;	Mismatches 66;	Indels 14;	Gaps 3;
1 OVLOQWAGLTKSGTSLTCAVSGASFGYSWIRPPCKGLTWIGTINHRGST-TV 59				

```

Db 40 QVQLQSGGGLVPCGSLKLSGASGDFSRVMSWROAPGKLEWIGINDSSTINY 99
QY 60 NPSLDGRVTISLDSTNQISLKLSTMTADTAAYVYCAR-TVAQSDYWGQGLVTVSSGS 118
Db 100 TPLSKDKFTISRDAKNTLYLQMSKRVSEDTALYYCARASYGHSAVWGQGLTVTVS--- 156
QY 119 ASAPTGGGGGGGGGGGGGGGGGGKTTLTQSPAFMSTAGDGVYISLCAKSRVDVDDVNW 178
Db 157 -----SGGGGGGGGGGGGGGGGGDIETQSPASLASVGETVTVTCASGGINHYLAW 207
QY 179 YQQRPGAPFIETIDATTLVPGISPRFSGGYGTDTFTLTNNIDSEDAAYFCLQHDNFP 238
Db 208 YQKQKGSFQULVYNATTLADGVPSRPSGSGGTQYSLKINSIQPEDFSGYCGHPMTTP 267
QY 239 LTFGGGTKEIK 250
Db 268 YTFGGGTKEIK 279

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RESULT 2

```

ID 0921A6 PRELIMINARY; PRT; 241 AA.
AC 0921A6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DB Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.T., Kim H.U., Kim I.J., Choi I.H., Lee S.D.,
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RL generation of a single-chain Fv molecule (scfv).";
DR EMBL; U88067; AAB48044.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IgV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

```

Query Match 45.2%; Score 603.5; DB 11; Length 241;
 Best Local Similarity 48.4%; Pred. No. 1.6e-39;
 Matches 124; Conservative 41; Mismatches 68; Indels 23; Gaps 6;

```

QY 1 QVQLQSGGGLVPCGSLKLSGASGDFSRVMSWROAPGKLEWIGINDSSTINY 59
Db 1 QVQLQSGGGLVPCGSLKLSGASGDFSRVMSWROAPGKLEWIGINDSSTINY 59
QY 60 NPSLDGRVTISLDSTNQISLKLSTMTADTAAYVYCAR-TVAQSDYWGQGLVTVSSGS 118
Db 61 ADDPKRFAFSLETSTASTAYLQINLNKNEDTATYCARLDLRYDYGQGLTVTVS--- 117
QY 119 ASAPTGGGGGGGGGGGGGGGGGGKTTLTQSPAFMSTAGDGVYISLCAKSRVDVDDVNW 178
Db 118 -----SGGGGGGGGGGGGGGGGGDIETQSPASLASVGETVTVTCASGGINHYLAW 207
QY 179 YQQRPGAPFIETIDATTLVPGISPRFSGGYGTDTFTLTNNIDSEDAAYFCLQHDNFP 238
Db 169 YQKQKGSFQULVYNATTLADGVPSRPSGSGGTQYSLKINSIQPEDFSGYCGHPMTTP 267
QY 239 LTFGGGTKEIK 250
Db 225 DNLH-TFGGGLTLEIK 239

```

RESULT 3

```

ID 070M2 PRELIMINARY; PRT; 243 AA.
AC 070M2;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DB scfv 6H8 protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Balb/C;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G.;
RT "scfv single chain antibody variable fragment as inverse agonist for
the beta-2 adrenergic receptor.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAFE0495.1; -
FT NON TER 1
FT NON TER 243
SQ SEQUENCE 243 AA; 25976 MW; B8FF64D2DCE4F76 CRC64;

```

Query Match 43.8%; Score 585.5; DB 11; Length 243;
 Best Local Similarity 47.0%; Pred. No. 4.2e-38;
 Matches 118; Conservative 47; Mismatches 71; Indels 15; Gaps 4;

```

QY 1 QVQLQSGGGLVPCGSLKLSGASGDFSRVMSWROAPGKLEWIGINDSSTINY 59
Db 1 QVQLQSGGGLVPCGSLKLSGASGDFSRVMSWROAPGKLEWIGINDSSTINY 59
QY 60 NPSLDGRVTISLDSTNQISLKLSTMTADTAAYVYCAR-TVAQSDYWGQGLVTVSSGS 119
Db 61 DEKFNKILTVDTSSSTAYVHSLASLSASDAAYTCARQGRG-DWVGAGTTLTVS---- 115
QY 120 SAPTGGGGGGGGGGGGGGGGGGKTTLTQSPAFMSTAGDGVYISLCAKSRVDVDDVNW 179
Db 116 -----SGGGGGGGGGGGGGGGGGDIETQSPASLASVGETVTVTCASGGINHYLAW 207
QY 180 YQQRPGAPFIETIDATTLVPGISPRFSGGYGTDTFTLTNNIDSEDAAYFCLQHDNFP 239
Db 168 YQKQKGSFQULVYNATTLADGVPSRPSGSGGTQYSLKINSIQPEDFSGYCGHPMTTP 267
QY 240 TFGGGLTLEIK 250
Db 227 TFGGGLTLEIK 237

```

RESULT 4

```

ID 08WUX4 PRELIMINARY; PRT; 588 AA.
AC 08WUX4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DB Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 5.

```

DR SMART, SM00406; IGV, 1.
DR PROSITE; PS50835; IG LIKE, 5.
DR PROSITE; PS00290; IG_MHC, 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 588;
Best Local Similarity 41.0%; Pred. No. 1.2e-31;
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQWAGLGLKSKWTSLITCAVSGASPSGYYMSWIRPPGKGLMEIGINRSGSTTN 60
DB QVQLQWAGLGLKPSSETLSITCGVYGSFSGYYMSWIRPPGKGLMEIGINSGSTNN 79
QY 61 PSIDGKVTISLDTSTNQISLKTSMRTADTAAYVCARTVAGTS-----DYMGGTL 111
DB 80 PSLKSRVTISVDTSKKQSLKLSVNAADTAAYVCARTVTRASPGRGKGMVWGQGT 139
QY 112 VYVSSGSGASAPL-----GGGSGGGSGGSGG-----GSGGSGSKTTLTQSPA 152
DB 140 VYVSSGSGASAPLFLPVSCGNSPDTSSVAVGLADFLPDSITFSWKYKNNSDISSTG 199
QY 153 FMSATPGDVSIISCKA---SRDY---DDVNMVYQORPG---EAPIFIED---ATT 196
DB 200 FSVLRGKGYAATSOVLPLSKDVMOGTDEHVCKQHFNKGNKKNVPLPVIAELPKVSV 259
QY 197 LVP-----GISPR-----FSGSGYGT-----213
DB 260 FVPRDGFPGNPRKSKLICQATGFSRQIQVSWLRGKQVGSVTTDVOAFAKESGPTT 319
QY 214 ----FTLTININIDSEDAAYFCLQHNPLTF 241
DB 320 YKVTSTLTIKESDMLSQSMFTC-RVDHRLTF 350

RESULT 5

Q9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=lymph;
RC Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AA002963.1; -
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG LIKE, 5.
DR PROSITE; PS00290; IG_MHC, 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E05851 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 597;
Best Local Similarity 41.0%; Pred. No. 1.2e-31;
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQWAGLGLKSKWTSLITCAVSGASPSGYYMSWIRPPGKGLMEIGINRSGSTTN 60
DB QVQLQWAGLGLKPSSETLSITCGVYGSFSGYYMSWIRPPGKGLMEIGINSGSTNN 79
QY 61 PSIDGKVTISLDTSTNQISLKTSMRTADTAAYVCARTVAGTS-----DYMGGTL 111

DB 80 PSLKSRVTISVDTSKKQSLKLSVNAADTAAYVCARTVTRASPGRGKGMVWGQGT 139
QY 112 VYVSSGSGASAPL-----GGGSGGGSGGSGG-----GSGGSGSKTTLTQSPA 152
DB 140 VYVSSGSGASAPLFLPVSCGNSPDTSSVAVGLADFLPDSITFSWKYKNNSDISSTG 199
QY 153 FMSATPGDVSIISCKA---SRDY---DDVNMVYQORPG---EAPIFIED---ATT 196
DB 200 FSVLRGKGYAATSOVLPLSKDVMOGTDEHVCKQHFNKGNKKNVPLPVIAELPKVSV 259
QY 197 LVP-----GISPR-----FSGSGYGT-----213
DB 260 FVPRDGFPGNPRKSKLICQATGFSRQIQVSWLRGKQVGSVTTDVOAFAKESGPTT 319
QY 214 ----FTLTININIDSEDAAYFCLQHNPLTF 241
DB 320 YKVTSTLTIKESDMLSQSMFTC-RVDHRLTF 350

RESULT 6

Q96AA6 PRELIMINARY; PRT; 618 AA.

AC Q96AA6; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=lymph;
RC Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AA017356.1; -
DR PIR; S15590; S15590.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG LIKE, 5.
DR PROSITE; PS00290; IG_MHC, 3.
KW Hypothetical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96BDA6C7C696E0A6 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 618;
Best Local Similarity 41.0%; Pred. No. 1.3e-31;
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQWAGLGLKSKWTSLITCAVSGASPSGYYMSWIRPPGKGLMEIGINRSGSTTN 60
DB QVQLQWAGLGLKPSSETLSITCGVYGSFSGYYMSWIRPPGKGLMEIGINSGSTNN 79
QY 61 PSIDGKVTISLDTSTNQISLKTSMRTADTAAYVCARTVAGTS-----DYMGGTL 111
DB 80 PSLKSRVTISVDTSKKQSLKLSVNAADTAAYVCARTVTRASPGRGKGMVWGQGT 139
QY 112 VYVSSGSGASAPL-----GGGSGGGSGGSGG-----GSGGSGSKTTLTQSPA 152
DB 140 VYVSSGSGASAPLFLPVSCGNSPDTSSVAVGLADFLPDSITFSWKYKNNSDISSTG 199
QY 153 FMSATPGDVSIISCKA---SRDY---DDVNMVYQORPG---EAPIFIED---ATT 196
DB 200 FSVLRGKGYAATSOVLPLSKDVMOGTDEHVCKQHFNKGNKKNVPLPVIAELPKVSV 259
QY 197 LVP-----GISPR-----FSGSGYGT-----213
DB 260 FVPRDGFPGNPRKSKLICQATGFSRQIQVSWLRGKQVGSVTTDVOAFAKESGPTT 319

Qy 214 ----FTLTNNIDSDAAYFCLQNDNPLTF 241
 Db 320 YKMTSTLTIKESDMLSGSMFTC-RVDHRLGTLF 350

RESULT 7

Q9B08 PRELIMINARY; PRT; 597 AA.
 AC Q9B08; 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle, and Lymph;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AA06180.1; -
 DR EMBL; BC001872; AA01872.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 37.6%; Score 503; DB 4; Length 597;
 Best Local Similarity 40.7%; Pred. No. 3.6e-31;
 Matches 135; Conservative 23; Mismatches 82; Indels 92; Gaps 11;

Qy 1 QVQLQOMAGLLKSGTSLTCAVSGASFGSYWMTROPFGKLEWIGINRGSTTVN 60
 Db 20 QVQLQOMAGLLKSGTSLTCAVSGASFGSYWMTROPFGKLEWIGINRGSTTVN 79
 Qy 61 PSLDGRVITSLDTSTNQISLKTMTADTAVYCAR--TVAGTSDYMGQGLTVTVS 118
 Db 80 PSLSRVITSLDTSTNQISLKTMTADTAVYCAR--TVAGTSDYMGQGLTVTVS 139
 Qy 112 VTVSSGSASAPT-----GGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 152
 Db 140 VTVSSGSASAPTLPPLVSCNSPSPDTSVAVGCLADPLPDSITFSMKYKKNSSDISSTRG 199
 Qy 153 FMSATPGDKVYSISCKA---SRDV---DDPVNMYOQPG---EAFIFIID---ATT 196
 Db 200 FPSVLRGKYAATSOVLPLPSKDVAGTDEHYVCKVHPGNKPKVPLVIAELPKVSV 259
 Qy 197 LVP-----GISPR-----FSGSGGYGTD----- 213
 Db 260 FVPRPGFGRNPKSKLICQATGFSRQIQVSMLEKRGKQVGGVTTDQVQAEAKESGPTT 319
 Qy 214 ----FTLTNNIDSDAAYFCLQNDNPLTF 241
 Db 320 YKMTSTLTIKESDMLSGSMFTC-RVDHRLGTLF 350

RESULT 8

Q92551 PRELIMINARY; PRT; 218 AA.
 AC Q92551; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE MRPs (Fragment).
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c;
 RX PubMed=11819679;
 RA Su C.;
 RA Su C.; Zeng G.; Yan X.; Wang F.; Tian F.; Ren D.; Zhao T.; Li X.;
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 RT the repair of intestinal epithelium after irradiation in mice."
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c;
 RA Su C.; Zeng G.; Yan X.; Li X.; Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain."
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240168; AA043733.1; -
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR NON TER 218
 FT SEQUENCE 218 AA; 23013 MW; 527E4F8F7962817 CRC64;

Query Match 33.9%; Score 453; DB 11; Length 218;
 Best Local Similarity 43.8%; Pred. No. 8.7e-28;
 Matches 98; Conservative 33; Mismatches 75; Indels 18; Gaps 4;

Qy 1 QVQLQOMAGLLKSGTSLTCAVSGASFGSYWMTROPFGKLEWIGINRGSTTVN 59
 Db 3 QVQLQOMAGLLKSGTSLTCAVSGASFGSYWMTROPFGKLEWIGINRGSTTVN 62
 Qy 60 NPSLDGRVITSLDTSTNQISLKTMTADTAVYCAR--TVAGTSDYMGQGLTVTVS 118
 Db 63 AEFKGRFARFLEISASTAVLQISNLKNEBDTATYFCRMWDYDGFYWGQGLTVTVS 119
 Qy 119 ASAPTGGSG 174
 Db 120 -----SGGGSG 174
 Qy 175 DVNMYOQPGKAPFIPIEDATTLVPGISPRFSGSGGYGTDFTLTI 218
 Db 171 FNMVFOQKPGQPKLITVAASKQSGVPAGLLASGSGTDFSLNTI 214

RESULT 9

Q96EYO PRELIMINARY; PRT; 613 AA.
 AC Q96EYO; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AA011857.1; -
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 5.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 5.
 DR PROSITE; PSS0290; IG_MHC; 3.
 KM Hypothetical protein.
 SO SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 33.2%; Score 443.5; DB 4; Length 613;
 Best Local Similarity 39.2%; Pred. No. 1,7e-26;
 Matches 129; Conservative 24; Mismatches 85; Indels 91; Gaps 12;

QY 1 QVQLQWAGLGLKSWGTLSTCAVSGASFGSYWMSIRPPGKGLWIGINHGSTTNN 60
 |||||
 DB 20 QVQLQSGPLVLPSETLSLTCTVSGGSSISYWSWIRPPAGKLEWIGIYSGSTNN 79
 |||||
 QY 61 PSLDGVTISLDTSTNOISLKLSTMTADPAVYVCAR-----TVAGTSYWGQGLTVY 114
 |||||
 DB 80 PSLKSRVYTSVDTSKQFSLKLSVTAADPAVYVCASQWELPTVG--LFTWQDGLTVY 137
 |||||
 QY 115 SSGSASAPL-----GGGSGGGSGSGG-----GGGSGGSKTTLTQSPAFMS 155
 |||||
 DB 138 SSGSASAPLFLPLVSCGNSPDSVAVGLADFLPDSITTFWKTKNNSDISTGFP 197
 |||||
 QY 156 APFGDVYSISCKA---SRDY---DDVWVYQORPG---EAPFLIED---ATLVP 199
 |||||
 DB 198 VLRGKYAATSYQLPLPSKDVWGCTDEHVCKVQHFNKNEKVPFLPVIALPKVSVFV 257
 |||||
 QY 200 -----GISPR-----FSGSGYGD----- 213
 |||||
 DB 258 PRDGFEGNPKRSKLIQATGFSPPQIQVSWLRGKGVSGSVTVDVQAEAKESGPTTYKV 317
 |||||
 QY 214 -FTLTINNIDSDAAYFCLQHDNPLTF 241
 |||||
 DB 318 TSTLTIKESDWLSQSMFTC-RVDHRLTF 345

RESULT 10

Q723Y6 PRELIMINARY; PRT; 116 AA.
 AC Q723Y6;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Rearranged VH4-34 V gene segment (Fragment).
 GN VH4-34.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hodgkin lymphoma;
 RA Tinsley M., Rosenquist R., Sundstroem C., Anini R.M., Kuppers R.,
 RA Hansmann M.L., Brauner A.;
 RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma
 RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
 RT cell precursor in a germinal center."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF564425; CAD92032.1; -
 FT NON TER 1
 FT NON TER 116
 SO SEQUENCE 116 AA; 12902 MW; CE3DBA846616C908 CRC64;

Query Match 32.7%; Score 437.5; DB 4; Length 116;
 Best Local Similarity 72.0%; Pred. No. 6.5e-27;
 Matches 85; Conservative 8; Mismatches 14; Indels 11; Gaps 1;

QY 1 QVQLQWAGLGLKSWGTLSTCAVSGASFGSYWMSIRPPGKGLWIGINHGSTTNN 60
 |||||
 DB 1 QVQLQWAGLGLKSWGTLSTCAVSGASFGSYWMSIRPPGKGLWIGINHGSTTNN 60
 |||||
 QY 61 PSLDGVTISLDTSTNOISLKLSTMTADPAVYVCARVAGTSDYWGQGLTVYSSGS 118
 |||||
 DB 61 PSLKSRVYTSVDTSKQFSLKLSVTAADPAVYVCAR-----GRTVVPAPAS 107

RESULT 11

Q95973 PRELIMINARY; PRT; 150 AA.
 AC Q95973;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE VH4 heavy chain variable region precursor (Fragment).
 GN IGM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
 RT "Clonal proliferation of IGM secreting B cell in the synovium of
 RT Behcet's patient with arthritis."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF103795; AAC79084.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 DR SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 >150
 FT NON TER 150
 SO SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 32.7%; Score 437; DB 4; Length 150;
 Best Local Similarity 68.0%; Pred. No. 9.8e-27;
 Matches 85; Conservative 13; Mismatches 25; Indels 2; Gaps 1;

QY 1 QVQLQWAGLGLKSWGTLSTCAVSGASFGSYWMSIRPPGKGLWIGINHGSTTNN 58
 |||||
 DB 20 QVQLQSGPLVLPSETLSLTCTVSGGSSISYWSWIRPPAGKLEWIGIYSGSTNN 79
 |||||
 QY 59 PSLDGVTISLDTSTNOISLKLSTMTADPAVYVCARVAGTSDYWGQGLTVYSSGS 118
 |||||
 DB 80 PSLKSRVYTSVDTSKQFSLKLSVTAADPAVYVCARVAGTSDYWGQGLTVYSSGS 139
 |||||
 QY 119 ASAPT 123
 |||||
 DB 140 ASAPT 144

RESULT 12

Q9UL73 PRELIMINARY; PRT; 119 AA.
 AC Q9UL73;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Xu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035041; AAD56277.1; -

DR HSP, P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420BA0BE CRC64;

Query Match 31.2%; Score 416.5; DB 4; Length 119;
Best Local Similarity 70.6%; Pred. No. 3e-25;
Matches 84; Conservative 6; Mismatches 26; Indels 3; Gaps 1;

QY 1 QVQLQWAGALLKSWGTLSTCAVSGASFGYQWMIKPPGKGLWIGINRGSTT 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGSISYTWMIKPPGKGLWIGIYSGSTYT 60
QY 61 PSIDGRVTISLDTSTNOISLKTSMTPADTAIVYCARVAQTS--DYWGQGLVTVSS 116
DB 61 PSLKSRVTISVDRSKNOFSLKTLTAADTAIVYCARLSNMGPYFDYWGQGLVTVSS 119

RESULT 13
Q96KX8

ID Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strubeberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 31.1%; Score 415.5; DB 4; Length 496;
Best Local Similarity 42.8%; Pred. No. 2.1e-24;
Matches 101; Conservative 20; Mismatches 54; Indels 61; Gaps 7;

QY 1 QVQLQWAGALLKSWGTLSTCAVSGASFGYQWMIKPPGKGLWIGINRGSTT 58
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGSISYTWMIKPPGKGLWIGIYSGSTYT 58
QY 59 YNPDLGRVTISLDTSTNOISLKTSMTPADTAIVYCAR-----TVAGTSDYWGQGLV 112
DB 80 YNPDLKRYTISVDRSKNOFSLKTLTAADTAIVYCARHGSISGSGALIDYWGQGLV 139
QY 113 TVSSGASAPVTGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 172
DB 140 TVSSASPTSPK-----VFLSLSTCTOPDGNVYIACLVG--- 172
QY 173 DDDVNMVQGRPGKAPFIIEADTTLVPGISPRFSGSGYGTDTLTINN--DSEDA 227
DB 173 ---GFFPQEP-----LSVTMSGSG---VTANRFPSPQDAS 203

RESULT 14

Q72379
ID Q72379 PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZP686K04218 (Fragment).
GN DKFZP686K04218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boeher M., Mewes H.W., Weil B., Amid C., Oeanger A.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1;
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 30.2%; Score 403.5; DB 4; Length 478;
Best Local Similarity 42.9%; Pred. No. 1.7e-23;
Matches 100; Conservative 28; Mismatches 46; Indels 59; Gaps 10;

QY 1 QVQLQWAGALLKSWGTLSTCAVSGASFGYQWMIKPPGKGLWIGINRGSTT 58
DB 19 QVQLQESGPGLVKPSQTLSTCTVSGSISYTWMIKPPGKGLWIGIYSGSTYT 78
QY 59 YNPDLGRVTISLDTSTNOISLKTSMTPADTAIVYCARVAQTS--DYWGQGLVTVSS 116
DB 79 YNPDLKRYTISVDRSKNOFSLKTLTAADTAIVYCARHGSISGSGALIDYWGQGLV 138
QY 117 GSAPPTGSGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 175
DB 139 ASPTSP-----KVPFLSLSTCTOPDGNVYVAVVAVVAVVAVVAVVAVVAVV 167
QY 176 VNMVQGRPGKAPFIIEADTTLVPGISPRFSGSGYGTDTLTINN--DSEDA 227
DB 168 ---GFFPQEP-----LSVTMSGSG---VTANRFPSPQDAS 198

RESULT 15
Q72374

ID Q72374 PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZP686C02218 (Fragment).
GN DKFZP686C02218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boeher M., Mewes H.W., Weil B., Amid C., Oeanger A.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1;
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A1576FOCA74B CRC64;

Query Match 29.8%; Score 398; DB 4; Length 492;
Best Local Similarity 41.9%; Pred. No. 4.8e-23;
Matches 98; Conservative 23; Mismatches 53; Indels 60; Gaps 8;

QY 1 QVQLQWAGALLKSWGTLSTCAVSGASFGYQWMIKPPGKGLWIGINRGSTT 58

```

Db      32  OLOQESGPGLVKPSFTLSLCTVSGSVNRRNYWGWIRPPGKLEWIGSIYNNETY 91
Qy      59  YNPSLDGRVTISLDSTNQISLKTSMFADPAVYVCARTVAGT---SDYWGQGLVTVS 115
Db      92  YSPSLKSRLLTFVDISKHPSLRLISVTAADIAVYCVRHVEGPGYGMFDPWGQGLVTVS 151
Qy     116  SCSASAPTEGSGSGSGSGSGSGSKTTLTQSPAFMSATPGD-KVISCKASRDVD 174
Db     152  SASPTSP-----KVFPISLSDSTPQDGNVYVACLVQ----- 181
Qy     175  DVNMVQQRPGEAPIFIEDATTLVPGISPRFSGSGYGTDFTLTINI-DSEDA 227
Db     182  --GFFPQBP-----LSVTWSESQO---NVTARNFPPSQDAS 212

```

Search completed: May 13, 2004, 15:06:57
 Job time : 34.6165 secs

THE PAPER HOUSE

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 13, 2004, 14:48:56 ; Search time 52.0738 Seconds
(without alignments)
1372.754 Million cell updates/sec

Title: US-10-072-301-23

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTTL.....CQGSQVLPVTFGGGTRVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq.294904:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84.4	62.6	256	3	AAVS5072 Interleuk
2	84.4	62.6	260	3	AAVS5075
3	84.4	62.6	367	3	AAVS5078
4	84.4	62.6	381	3	AAVS5079
5	84.4	62.6	519	3	AAVS5080
6	84.4	62.6	546	3	AAVS5074
7	84.4	62.6	626	3	AAVS5081
8	84.4	62.6	640	3	AAVS5082
9	822.5	61.0	259	3	AAVS5085
10	822.5	61.0	259	3	AAVS5085
11	811.5	60.2	251	5	ABP45038
12	811.5	60.2	251	5	ABP45038
13	803	59.6	248	5	ABP45039
14	801.5	59.5	255	5	ABP45039
15	800.5	59.4	249	5	ABP45039
16	789	58.5	248	5	ABP45039
17	787	58.4	240	4	ABP45039
18	787	58.4	240	4	ABP45039
19	786	58.3	248	5	ABP45039
20	786	58.3	240	4	ABP45039
21	781.5	58.0	243	5	ABP45039
22	781.5	58.0	249	5	ABP45039
23	779.5	57.8	272	2	AAAR21260
24	779.5	57.8	285	2	AAAR21260
25	779	57.8	240	4	AAAR21260

ALIGNMENTS

RESULT 1	AAVS5072	standard, protein, 256 AA.
XX	AAVS5072;	
AC	AAVS5072;	
XX	25-FEB-2000	(first entry)
DE	Interleukin-6 specific ScFv protein sequence.	
XX	Gene isolation; membrane-bound protein; fusion protein; drug production;	
KW	antigen-binding cell; secreted functional protein; antigenic protein;	
KM	protein isolation; diagnosis; interleukin-6; ScFv.	
XX	Synthetic.	
OS	Homo sapiens.	
XX	MO9960113-AL.	
PN	25-NOV-1999.	
XX	30-APR-1999;	99WO-JP002341.
PF	20-MAY-1998;	98JP-00138652.
PR	01-OCT-1998;	98JP-00279876.
XX	(CHUS) CHUGAI SEIYAKU KK.	
PI	Tsuchiya M, Saito M, Ohtomo T;	
XX	WPI, 2000-039382/03.	
DR	N-PSDB; AA240291.	
PT	Efficient and selective isolation of a gene encoding membrane protein	
PT	with low or no antigenic binding activity, for diagnosis, study of, and	
PT	production of drugs creating abnormal functions of the protein.	
XX	Example 1; Page 54-56; 120pp; Japanese.	
PS	This sequence represents a ScFv specific for human interleukin-6. The	
XX	invention relates to a method for isolating a gene encoding a membrane-	
CC	bound protein, comprising introducing a vector into a cell, contacting an	
CC	antigen with the cell expressing the fused protein encoded by the vector	
CC	on its surface to select an antigen-binding cell, and isolating the cDNA.	
CC	The vector contains DNA encoding a secreted functional protein with	
CC	antigenicity and binding affinity, and a cDNA ligated to DNA downstream	
CC	of the 3' end of the coding sequence. The method can be used to isolate a	
CC	membrane-bound protein for diagnosis and study. It can also be used for	

26	779	57.8	240	4	AAVS5072	Human MUC
27	777	57.6	249	5	AAVS5072	Human MUC
28	777	57.6	250	5	AAVS5072	Human MUC
29	775	57.5	240	4	AAVS5072	Human MUC
30	773	57.3	240	4	AAVS5072	Human MUC
31	772	57.3	240	4	AAVS5072	Human MUC
32	772	57.3	240	4	AAVS5072	Human MUC
33	771	57.0	240	4	AAVS5072	Human MUC
34	769	57.0	240	4	AAVS5072	Human MUC
35	769	57.0	240	4	AAVS5072	Human MUC
36	769	57.0	266	5	AAVS5072	Human MUC
37	769	57.0	266	5	AAVS5072	Human MUC
38	767	56.9	240	4	AAVS5072	Human MUC
39	767	56.9	240	4	AAVS5072	Human MUC
40	767	56.9	240	4	AAVS5072	Human MUC
41	767	56.9	240	4	AAVS5072	Human MUC
42	766	56.8	240	4	AAVS5072	Human MUC
43	766	56.8	667	6	AAVS5072	Human MUC
44	765	56.8	240	4	AAVS5072	Human MUC
45	765	56.8	240	4	AAVS5072	Human MUC

CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMR) method wherein an epitope recognized by an
 CC antibody is carried in a fused protein
 CC
 CC Sequence 256 AA;

Query Match 62.6%; Score 844; DB 3; Length 256;
 Best Local Similarity 65.6%; Pred. No. 3.1e-49;
 Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQLTLTCTPSGFSRLTSGVGVNRPQPKALSMALIIYMDDDR 60
 Db 1 QVQLQESGPGLVRSQTLSTCTVSGYSI-TSDHMSWVRQPPGRGLEWIGYISGITT 59
 QY 61 YSPSLKSRLLITTKDTSKKQVVLMTNVDPADTATYCTHEQYYDTSGCPYDFWGGQT 120
 Db 60 YNPSLKSRYVMTLRDTSKQPSLRISVTADTAVYCAR-----SLARTAMDYWGQS 113
 QY 121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASODIRKNTLN 180
 Db 114 LVTVS-----SGGGSGGGGSGGGGSGGSDIQWTPSSLSASVGDRTVITCRASQDISSYLN 168
 QY 181 WYQKPGKAPKRVLIYDASDLETGIPSRFSGSGGTDFTLTISLQPEDIATYYCCQSDYL 240
 Db 169 WYQKPGKAPKRLIYYTSRLHSGVPSRFSGSGGTDFFTLTISLQPEDIATYYCCQGNLT 228
 QY 241 PLTFGGGTAKVDIK 253
 Db 229 PYTFGGGTAKVEIK 241

RESULT 2
 AAY55075
 ID AAY55075 standard; protein; 260 AA.
 AC AAY55075;
 XX
 XX
 DT 25-FEB-2000 (first entry)
 XX
 XX
 DE Single chain Fv protein sequence shPM1(deltaEL).

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.
 XX
 OS Synthetic.
 XX
 PN WO9960113-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-JP002341.
 XX
 PR 20-MAY-1998; 98JP-00138652.
 PR 01-OCT-1998; 98JP-00279876.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Teuchiya M, Saito M, Ohtomo T;
 DR WPI; 2000-039382/03.
 DR N-PSDB; AA240305.
 XX
 XX
 PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 XX production of drugs treating abnormal functions of the protein.
 PS Example 7; Page 80-82; 120pp; Japanese.

CC This sequence represents a single chain Fv (ScFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an

CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMR) method wherein an epitope recognized by an
 CC antibody is carried in a fused protein
 CC
 CC Sequence 260 AA;

Query Match 62.6%; Score 844; DB 3; Length 260;
 Best Local Similarity 65.6%; Pred. No. 3.1e-49;
 Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQLTLTCTPSGFSRLTSGVGVNRPQPKALSMALIIYMDDDR 60
 Db 20 QVQLQESGPGLVRSQTLSTCTVSGYSI-TSDHMSWVRQPPGRGLEWIGYISGITT 78
 QY 61 YSPSLKSRLLITTKDTSKKQVVLMTNVDPADTATYCTHEQYYDTSGCPYDFWGGQT 120
 Db 79 YNPSLKSRYVMTLRDTSKQPSLRISVTADTAVYCAR-----SLARTAMDYWGQS 132
 QY 121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASODIRKNTLN 180
 Db 133 LVTVS-----SGGGSGGGGSGGGGSGGSDIQWTPSSLSASVGDRTVITCRASQDISSYLN 187
 QY 181 WYQKPGKAPKRVLIYDASDLETGIPSRFSGSGGTDFTLTISLQPEDIATYYCCQSDYL 240
 Db 188 WYQKPGKAPKRLIYYTSRLHSGVPSRFSGSGGTDFFTLTISLQPEDIATYYCCQGNLT 247
 QY 241 PLTFGGGTAKVDIK 253
 Db 248 PYTFGGGTAKVEIK 260

RESULT 3
 AAY55078
 ID AAY55078 standard; protein; 367 AA.
 AC AAY55078;
 XX
 XX
 DT 25-FEB-2000 (first entry)
 XX
 XX
 DE Single chain Fv protein sequence shPM1-Kappa.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.
 XX
 OS Synthetic.
 XX
 PN WO9960113-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-JP002341.
 XX
 PR 20-MAY-1998; 98JP-00138652.
 PR 01-OCT-1998; 98JP-00279876.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Teuchiya M, Saito M, Ohtomo T;
 DR WPI; 2000-039382/03.
 DR N-PSDB; AA240308.

CC Efficient and selective isolation of a gene encoding membrane protein
 CC with low or no antigenic binding activity, for diagnosis, study of, and
 CC production of drugs treating abnormal functions of the protein.

XX Example 7; Page 86-89; 120pp; Japanese.

CC This sequence represents a single chain Fv (scFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein

XX Sequence 367 AA;

Query Match 62.6%; Score 844; DB 3; Length 367;

Best Local Similarity 65.6%; Pred. No. 4.4e-49; Mismatches 46; Indels 12; Gaps 3;

Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKSGPTLVKPTQTLLTCTFGSGLRTTGEVGVWROPGKALEMLALYMDDDR 60
 DB 20 QVQLDSGSGVLRPSQTLLTCTVSGYSI-TSDHMSWVRQPRGLRWIGYISGITT 78
 QY 61 YPSLSKRLITTKDTSKQOVLTMTNVPADPATYCTHEQYVDTSGOPYDFDGGGT 120
 DB 79 YPSLSKRLITTKDTSKQOVLTMTNVPADPATYCTHEQYVDTSGOPYDFDGGGT 132
 QY 121 LVTVSSGGSG 180
 DB 133 LVTVSSGGSG 187
 QY 181 WTQOKRGKAPKVLIDASDLDTGIPSRFSGSGSGTDFITLISLQPEDIAATYCCQGS 240
 DB 188 WTQOKRGKAPKVLIDASDLDTGIPSRFSGSGSGTDFITLISLQPEDIAATYCCQGS 247
 QY 241 PLTFGGGTVDIK 253
 DB 248 PYTFGGGTVDIK 260

RESULT 4

AAVS5079 standard; protein; 381 AA.

XX AAVS5079;

XX 25-FEB-2000 (first entry)

XX Single chain Fv protein sequence shPM1-MCH4.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.

XX Synthetic.

XX MO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AA240309.

PT Efficient and selective isolation of a gene encoding membrane protein

XX with low or no antigenic binding activity, for diagnosis, study of, and
 XX production of drugs treating abnormal functions of the protein.

XX Example 7; Page 90-94; 120pp; Japanese.

CC This sequence represents a single chain Fv (scFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein

XX Sequence 381 AA;

Query Match 62.6%; Score 844; DB 3; Length 381;

Best Local Similarity 65.6%; Pred. No. 4.4e-49; Mismatches 46; Indels 12; Gaps 3;

Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKSGPTLVKPTQTLLTCTFGSGLRTTGEVGVWROPGKALEMLALYMDDDR 60
 DB 20 QVQLDSGSGVLRPSQTLLTCTVSGYSI-TSDHMSWVRQPRGLRWIGYISGITT 78
 QY 61 YPSLSKRLITTKDTSKQOVLTMTNVPADPATYCTHEQYVDTSGOPYDFDGGGT 120
 DB 79 YPSLSKRLITTKDTSKQOVLTMTNVPADPATYCTHEQYVDTSGOPYDFDGGGT 132
 QY 121 LVTVSSGGSG 180
 DB 133 LVTVSSGGSG 187
 QY 181 WTQOKRGKAPKVLIDASDLDTGIPSRFSGSGSGTDFITLISLQPEDIAATYCCQGS 240
 DB 188 WTQOKRGKAPKVLIDASDLDTGIPSRFSGSGSGTDFITLISLQPEDIAATYCCQGS 247
 QY 241 PLTFGGGTVDIK 253
 DB 248 PYTFGGGTVDIK 260

RESULT 5

AAVS5080 standard; protein; 519 AA.

XX AAVS5080;

XX 25-FEB-2000 (first entry)

XX Single chain Fv protein sequence shPM1(deltaEL)-BvGS3.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.

XX Synthetic.

XX MO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98UP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

XX N-PSDB; AAZ40312.

PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.

PS Example 7; Page 95-100; 120pp; Japanese.

CC This sequence represents a single chain Fv (scFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein

XX Sequence 519 AA;

SQ

Query Match Best Local Similarity 62.6%; Score 844; DB 3; Length 519;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

```

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRTTGEVGVWRPGKALEMLALTYWDDKR 60
DB 20 QVQLQESGPGLVPRSPGTLSTCTVSGYSL-TSDHAMSWKQPGKLEWIGIYSYGI 78
QY 61 YSPSLKSLRTLTNDSKQVLTMTNVPADATATYCTHEQYVYDSGQYFPDPMGQGT 120
DB 79 YNPSLKSRLVTLRLDTSKQFSLRLSSVTADTAAYVCAR-----SLARTTAMDYWGQS 132
QY 121 LVTVSSGGGSGGGGSGGGGSGGSGNIOVTPSSLSASVGRVTMTCRASQDIRKNLN 180
DB 133 LVTVS-----SGGGSGGGGSGGGGSGGSDIQMTQSPSSLSASVGRVTITCRASQDISSYLN 187
QY 181 WYQOKRGAAPKRLIYDASDLETGIPSRFSGSGGTDFTLTISLQPEDIATYVCOQSDYL 240
DB 188 WYQOKRGAAPKRLIYYSRLHSGVSPSRFSGSGGTDFTLTISLQPEDIATYVCOQNTL 247
QY 241 PLTFGGGTGVDIR 253
DB 248 PYTFGGGTGVDIR 260

```

RESULT 6

AAVS5074 ID AAV55074 standard; protein; 546 AA.

AC AAV55074;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence hPM1-BVGS3.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
XX antigen-binding cell; secretable functional protein; antigenic protein;
XX protein isolation; diagnosis; scFv.

OS Synthetic.

XX MO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98UP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Saito M, Ohtomo T;

XX WPI; 2000-039382/03.

XX N-PSDB; AAZ40303.

PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.

PS Example 5; Page 73-78; 120pp; Japanese.

CC This sequence represents a single chain Fv (scFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein

XX Sequence 546 AA;

SQ

Query Match Best Local Similarity 62.6%; Score 844; DB 3; Length 546;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

```

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRTTGEVGVWRPGKALEMLALTYWDDKR 60
DB 20 QVQLQESGPGVLPRSPGTLSTCTVSGYSL-TSDHAMSWKQPGKLEWIGIYSYGI 78
QY 61 YSPSLKSLRTLTNDSKQVLTMTNVPADATATYCTHEQYVYDSGQYFPDPMGQGT 120
DB 79 YNPSLKSRLVTLRLDTSKQFSLRLSSVTADTAAYVCAR-----SLARTTAMDYWGQS 132
QY 121 LVTVSSGGGSGGGGSGGGGSGGSGNIOVTPSSLSASVGRVTMTCRASQDIRKNLN 180
DB 133 LVTVS-----SGGGSGGGGSGGGGSGGSDIQMTQSPSSLSASVGRVTITCRASQDISSYLN 187
QY 181 WYQOKRGAAPKRLIYDASDLETGIPSRFSGSGGTDFTLTISLQPEDIATYVCOQSDYL 240
DB 188 WYQOKRGAAPKRLIYYSRLHSGVSPSRFSGSGGTDFTLTISLQPEDIATYVCOQNTL 247
QY 241 PLTFGGGTGVDIR 253
DB 248 PYTFGGGTGVDIR 260

```

RESULT 7

AAVS5081 ID AAV55081 standard; protein; 626 AA.

AC AAV55081;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1-kappa-BVGS3.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;

KM antigen-binding cell; secreted functional protein; antigenic protein;
 KM protein isolation; diagnosis; ScFv.
 XX
 OS Synthetic.
 XX
 XX MO960113-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-JP002341.
 XX
 XX 20-MAY-1998; 98JP-00138652.
 PR 01-OCT-1998; 98JP-00279876.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Saito M, Ohtomo T;
 DR MPI; 2000-039382/03.
 DR N-PSDB; AA240316.
 XX
 PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.
 XX
 PS Example 7; Page 103-109; 120pp; Japanese.
 XX
 CC This sequence represents a single chain Fv (ScFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secreted functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein
 XX
 SQ Sequence 626 AA;
 Query Match 62.6%; Score 844; DB 3; Length 626;
 Best Local Similarity 65.6%; Pred. No. 7, 4e-49;
 Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;
 QY 1 QVTLKESGPTLVKPTQTLTLCTFGSFLRTTGEVGVWRPGKALEWALITYMDDDR 60
 DB 20 QVQLOESGGLVRSQTLTLCTVSGYST-TSDHMSWVRQPGKLEWIGIYISGITT 78
 QY 61 YSPSLKSRITTKTISKQVLTMTNVPADATATYCTHEQYVYDTSGQPYFFDFWGQT 120
 DB 79 YNPSLSKRVMTLRDTSKQFSLRLSSVTAADTAAYYCAR-----SLARTTAMDYWGQS 132
 QY 121 LVTSSGG 180
 DB 133 LVTVS-----SGGG 187
 QY 181 WTQOKRGKAPKVLIVDASDLETGIPSRFGSGSGGTDFILTTISLQPEDATATYCCOOSDYL 240
 DB 188 WTQOKRGKAPKVLIVTSLRHSGVSPRFGSGSGGTDFITTTISLQPEDATATYCCOOSGNTL 247
 QY 241 PLTFGGGTGVNDIK 253
 DB 248 PYTFGGGTGVNDIK 260
 RESULT 8
 ID AAY55082 standard; protein; 640 AA.
 XX
 AC AAY55082;

XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Single chain Fv protein sequence sHPM1-MCH4-BVGS3.
 XX
 KM Gene isolation; membrane-bound protein; fusion protein; drug production;
 KM antigen-binding cell; secreted functional protein; antigenic protein;
 KM protein isolation; diagnosis; ScFv.
 XX
 OS Synthetic.
 XX
 XX MO960113-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-JP002341.
 XX
 XX 20-MAY-1998; 98JP-00138652.
 PR 01-OCT-1998; 98JP-00279876.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Saito M, Ohtomo T;
 DR MPI; 2000-039382/03.
 DR N-PSDB; AA240321.
 XX
 PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.
 XX
 PS Example 7; Page 111-117; 120pp; Japanese.
 XX
 CC This sequence represents a single chain Fv (ScFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secreted functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein
 XX
 SQ Sequence 640 AA;
 Query Match 62.6%; Score 844; DB 3; Length 640;
 Best Local Similarity 65.6%; Pred. No. 7, 6e-49;
 Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;
 QY 1 QVTLKESGPTLVKPTQTLTLCTFGSFLRTTGEVGVWRPGKALEWALITYMDDDR 60
 DB 20 QVQLOESGGLVRSQTLTLCTVSGYST-TSDHMSWVRQPGKLEWIGIYISGITT 78
 QY 61 YSPSLKSRITTKTISKQVLTMTNVPADATATYCTHEQYVYDTSGQPYFFDFWGQT 120
 DB 79 YNPSLSKRVMTLRDTSKQFSLRLSSVTAADTAAYYCAR-----SLARTTAMDYWGQS 132
 QY 121 LVTSSGG 180
 DB 133 LVTVS-----SGGG 187
 QY 181 WTQOKRGKAPKVLIVDASDLETGIPSRFGSGSGGTDFILTTISLQPEDATATYCCOOSDYL 240
 DB 188 WTQOKRGKAPKVLIVTSLRHSGVSPRFGSGSGGTDFITTTISLQPEDATATYCCOOSGNTL 247
 QY 241 PLTFGGGTGVNDIK 253
 DB 248 PYTFGGGTGVNDIK 260

Matches 156; Conservative 39; Mismatches 53; Indels 7; Gaps 2;

QY 1 QVTLKSGPTLVKPTQTLTCTFGSFLRTTGEVGVWRQPPGKALEWIALIYWDDDR 60
 DB 3 QVTLKSGGGLKPSGTLSTCTVSGGFLSRTSGVGMWRQPPGKALEWIALIYWDDDR 62
 QY 61 YSPSLKSLRTITKDTSKKQVLTMTNVPADPATYCTHGOYDTSGOPYTFDFWGQGT 120
 DB 63 YNPSLRSQTLISDTRNQVFLRTVDRADRTTYCAGYGNDBP-----PAYGQGT 117

QY 121 LVTSSGGGGSGGGSGGGSGG--GGSNIQVTPSPSLASVGDRTVMTGRASQDIRKN 178
 DB 118 LVTSSGAGPTSGSGKPGEGSTKGAPDIVLSQSPKFMSTVGDRTVITCKRASIYRTA 177

QY 179 LMMYQOKPKAPKVLVLDASDLETGIPSPSGSGSTDPILTTSSLOPEDIATYYCOQSD 238
 DB 178 VAMFQOKPGQSPKALVYLSNRHTGVDRPTSGSGSTDPILTTISNVOSEDLADYFLQHM 237

QY 239 YLPTFGGGTKVDIK 253
 DB 238 NYPTFGSGTKLEIK 252

RESULT 11
 ABP45038
 ID ABP45038 standard; protein; 251 AA.
 AC ABP45038;
 XX 19-AUG-2002 (first entry)
 DE Human Blys binding scfv seq ID 1049.

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.
 OS
 XX
 PN WO200202641-A1.
 PD 10-JAN-2002.
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 WPI; 2002-114799/15.
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 1654-1655; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 251 AA;
 XX
 QY Query Match 60.2%; Score 811.5; DB 5; Length 251;
 Best Local Similarity 63.0%; Pred. No. 4.7e-47;
 Matches 160; Conservative 31; Mismatches 58; Indels 5; Gaps 3;

QY 1 QVTLKSGPTLVKPTQTLTCTFGSFLRTTGEVGVWRQPPGKALEWIALIYWDDDR 60
 DB 1 QVTLKSGGGLKPSGTLSTCTVSGGFLSRTSGVGMWRQPPGKALEWIALIYWDDDR 60

QY 61 YSPSLKSLRTITKDTSKKQVLTMTNVPADPATYCTHGOYDTSGOPYTFDFWGQGT 120
 DB 61 YSPSLKSLRTITKDTSKKQVLTMTNVPADPATYCTHGOYDTSGOPYTFDFWGQGT 119

QY 121 LVTSSGGGGSGGGSGGGSGG--GGSNIQVTPSPSLASVGDRTVMTGRASQDIRKN 180
 DB 120 LVTSSGGGGSGGGSGGGSGG--ALEIVTQSPATLSLSPERATLSGRASQSSSYLA 176

QY 181 WYQOKPKAPKVLVLDASDLETGIPSPSGSGSTDPILTTSSLOPEDIATYYCOQSDYL 240
 DB 177 WYQOKPKAPKVLVLDASDLETGIPSPSGSGSTDPILTTSSLOPEDIATYYCOQSDYL 236

QY 241 P-LTFRGGGTKVDIK 253
 DB 237 PELTFRGGGTKVLEIK 250

RESULT 12
 AAR50092
 ID AAR50092 standard; protein; 909 AA.
 AC AAR50092;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-OCT-1994 (first entry)
 XX
 DE Humanised anti-CEA sFv fragment-human beta-glucuronidase fusion protein.
 XX
 KW Carcinoembryonic antigen; single chain variable region; sFv fragment;
 KW fusion gene; cancer treatment; targeted drug delivery; tumour.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein 20..909
 FT /label= fusion protein
 FT /note= "humanised anti-CEA sFv fragment fused to human
 FT beta-glucuronidase"
 XX
 PN EP590530-A2.
 XX
 PD 06-APR-1994.
 XX
 PF 24-SEP-1993; 93EP-00115418.
 PR 02-OCT-1992; 92DE-04233152.
 XX
 PA (BEHM) BEHRINGWERKE AG.
 XX
 PI Gehrman M, Seemann G, Boeslet K, Czech J;

XX WP1, 1994-111012/14.
DR N-PSDB; AAQ58896.

XX New fusion protein contg. enzyme for prodrug activation - coupled to
PT antigen binding component, esp. scFv antibody fragment, partic. for
XX treatment of tumours.

XX Claim 13; Page 12-15; 35pp; German.

XX The sequence AAR50092 comprises a humanised scFv-fragment against CEA
CC fused to a human beta-glucuronidase. The fusion protein is useful for
CC targeting beta-glucuronidase to cancer cells expressing CEA, where the
CC enzyme is able to convert a prodrug into its active form. Any fusion
CC protein not bound to tumour can be removed by internalisation via the
CC mannose-6-phosphate and galactose receptors. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 909 AA;

Query Match Best Local Similarity 60.2%; Score 811.5; DB 2; Length 909;
Matches 161; Conservative 30; Mismatches 49; Indels 13; Gaps 5;

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QY 1 QVTLKSGPTLVKPTQTLTLCTFSGFSRTTGGVGVWROPKALEMIALIYMDDKR 60
DB 20 QVQLQSGPGVLRPSQTLSTCTVSGFTI-SSGYSMHWVRQPPGLEGIEWIGYIGSGITN 78
QY 61 YSPSLKSRLLTITKDTSKQVVLMTNVPADATAYCTHEQYVYDTSQPYFPFMQGT 120
DB 79 YNPSLKSRYTLMVLTSSKNQFSLRLSSVYAAIDTAIVYICAREYDYH----WYFVWQGT 133
QY 121 LVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
DB 134 YTVTS-----SGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 187
QY 181 WTQOKPGKAPKVLIVASDLFTGIPSRFSGSGGDFILITSSLOPEDIAITYYCOQSDYL 240
DB 188 WYQOKPGKAPKVLIVASDLFTGIPSRFSGSGGDFILITSSLOPEDIAITYYCHOWMSY 247
QY 241 PLTFGGGTIVDIK 253
DB 248 P-TFGGTIKLEIK 259
```

RESULT 13

ABP45349 ID ABP45349 standard; protein; 248 AA.

AC ABP45349;

DT 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1360.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-024818P.

XX 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WP1, 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2025-2026; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantify the presence of Blys in
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the invention

XX Sequence 248 AA;

Query Match Best Local Similarity 59.6%; Score 803; DB 5; Length 248;
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

```
QY 1 QVTLKSGPTLVKPTQTLTLCTFSGFSRTTGGVGVWROPKALEMIALIYMDDKR 60
DB 1 QVQLQSGPGVLRPSQTLSTCTVSGFTI-SSGYSMHWVRQPPGLEGIEWIGYIGSGITN 78
QY 61 YSPSLKSRLLTITKDTSKQVVLMTNVPADATAYCTHEQYVYDTSQPYFPFMQGT 120
DB 59 YNPSLKSRYTLMVLTSSKNQFSLRLSSVYAAIDTAIVYICAREYDYH----WYFVWQGT 133
QY 121 LVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
DB 119 LVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 187
QY 181 WTQOKPGKAPKVLIVASDLFTGIPSRFSGSGGDFILITSSLOPEDIAITYYCOQSDYL 240
DB 176 WYQOKPGKAPKVLIVASDLFTGIPSRFSGSGGDFILITSSLOPEDIAITYYCHOWMSY 247
QY 241 PLTFGGGTIVDIK 253
DB 235 DPTFGGTIKLEIK 247
```

RESULT 14

ABP45592 ID ABP45592 standard; protein; 255 AA.

AC ABP45592;

DT 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1603.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;

Mon May 17 11:03:35 2004

us-10-072-301-23.rag

Page 10

```

QY      61  XSPSLKSLRLTTKDTSKKQVLLMTNVDPADTATYTCHEQYYVD-TSGOPY-YEDFWGQ 118
Db      59  YNPSLKRVTISVDTSKNCFSLTASVTMAADTAVVYCARGRPYIDILGIRYMFDEWGR 118
QY      119  GTLVTVSSGGGGSGGGSGGGSGGGSGGSIIOVYTGSPSLASVGDVRYMTCRASODIRKN 178
Db      119  GTLVTVS-----SGGGSGGGSGGGSGGSIIVWTOGSTSLASVDRVYITCRASQGISM 173
QY      179  LNWYQCKPFGAPVLYLYDASDLRTGTPSRFSGSGSGTDFILITISLQPELTATYYCGQSD 238
Db      174  LNWYQCKPFGAPVLYLYKASTLESQVPSRFSGSGGCTDFILITISLQPELPATYYCQGSY 233
QY      239  YLPLTFGGGKTVKIK 253
Db      234  STPMTFGGKLEIK 248

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Search completed: May 13, 2004, 15:00:58
Job time : 53.0738 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 13.8782 Seconds
(without alignments)
941.146 Million cell updates/sec

Title: US-10-072-301-23

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPPLFCGKTKVDIK 253

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	764	56.7	248	2	US-08-887-352B-22
2	764	56.7	248	3	US-09-109-207C-22
3	764	56.7	248	3	US-09-296-005-22
4	764	56.7	248	4	US-09-920-171-22
5	762	56.5	244	4	US-08-918-148-77
6	762	56.5	248	4	US-08-887-352B-23
7	762	56.5	248	3	US-09-109-207C-23
8	762	56.5	248	3	US-09-296-005-23
9	762	56.5	248	4	US-09-920-171-23
10	746.5	55.4	245	4	US-08-918-148-76
11	742	55.0	359	4	US-09-646-028-16
12	742	55.0	361	4	US-09-646-028-13
13	736	54.6	264	4	US-08-564-164A-4
14	734.5	54.5	240	1	US-08-488-113B-148
15	734.5	54.5	240	1	US-08-477-484B-148
16	734.5	54.5	240	2	US-08-646-360-148
17	734.5	54.5	240	3	US-08-839-765-148
18	734.5	54.5	240	3	US-09-136-389-148
19	734.5	54.5	240	4	US-09-610-838-148
20	734.5	54.5	240	4	US-09-711-485-148
21	730.5	53.4	245	4	US-08-918-148-78
22	720.5	53.4	235	2	US-08-190-199A-61
23	714.5	53.0	245	4	US-08-918-148-75
24	708.5	52.7	263	3	US-08-646-265A-75
25	708.5	52.6	263	4	US-08-752-844-66
26	708.5	52.6	263	4	US-09-293-533-66
27	707	52.4	301	2	US-08-661-052-14

28	707	52.4	301	3	US-09-188-082-14	Sequence 14, Appl
29	707	52.4	301	4	US-09-364-088-14	Sequence 14, Appl
30	707	52.4	301	4	US-09-102-716-14	Sequence 14, Appl
31	707	52.4	553	2	US-08-661-052-16	Sequence 16, Appl
32	707	52.4	553	3	US-09-188-082-16	Sequence 16, Appl
33	707	52.4	553	4	US-09-364-088-16	Sequence 16, Appl
34	707	52.4	553	4	US-09-102-716-16	Sequence 16, Appl
35	701.5	52.0	249	2	US-08-797-689-18	Sequence 18, Appl
36	701.5	52.0	249	4	US-09-984-186-18	Sequence 18, Appl
37	697.5	51.7	277	4	US-09-509-031-16	Sequence 16, Appl
38	685.5	50.9	277	2	US-08-256-790-2	Sequence 2, Appl
39	681.5	50.6	282	2	US-08-860-174A-10	Sequence 10, Appl
40	680.5	50.5	284	3	US-08-564-164A-2	Sequence 2, Appl
41	675	50.1	273	2	US-08-403-853-18	Sequence 18, Appl
42	672	49.9	243	1	US-07-958-140-2	Sequence 2, Appl
43	672	49.9	243	5	PCT-US93-09166-2	Sequence 2, Appl
44	664	49.3	240	4	US-10-092-246-36	Sequence 36, Appl
45	661	49.0	637	1	US-08-235-838-16	Sequence 16, Appl

ALIGNMENTS

```
RESULT 1
US-08-887-352B-22
; Sequence 22, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
; US-08-887-352B-22
;
Query Match      56.7%; Score 764; DB 2; Length 248;
Best Local Similarity 60.7%; Pred. No. 1.4e-53;
Matches 156; Conservative 30; Mismatches 57; Indels 14; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTPSGFSRTTGEVGVROPKALAEVIALIYMDDDR 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EQVLVESGGGLVQPGSSRLSCAVSGYSI-TGYSMMVTRQAPGKLEVAASITTYGSRN 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 YPSLSKSLRTITPKDTSKQGVLTMTNVDPADTATYYCTHEQYYDTSGQPYVDFWGGQT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 YNPSTVGRITTRDSDKNTFYLQMNLSLRADETAVVYVYCARSHYFG---HMFVAVWGQGT 115
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Db 60 YNPSVKGRIITISRDSDKNTFYLMNMSLRMEDTAIVYRGSGHYFG---HHHFAMVGGGT 115

Qy 121 LTVVSSGGGGSGGGGGSGGGGGSGGSGNIOVTQSPSSLSASGDRVTMTCRASDI----R 176

Db 116 LTVVS-----SEGGSGSGGGSGGGSDIOLTQSPSSLSASGDRVTITCRASKPVDEGD 170

Qy 177 KJLNMTYQOKPKGKAPKVLIVDASDLFTGIPSRFSGSGGSGTDILVLTSSLOPEDATYYCQ 236

Db 171 SYLNMTYQOKPKGKAPKVLIVAAAYLESQVPSRSGSGSGTDPLTLTSSLOPEDATYYCQ 230

Qy 237 SDYLPLTFGGGTQVDIK 253

Db 231 SHEDPYTFGGGTVEIK 247

US-08-918-77
 US-08-918-77
 Sequence 77, Application US/089181A8A
 Patent No. 6342220
 GENERAL INFORMATION:
 APPLICANT: Adams, Camella
 APPLICANT: W.
 APPLICANT: Carter, Paul J.
 APPLICANT: Fendly, Brian M.
 APPLICANT: Gurney, Austin L.
 TITLE OF INVENTION: Agonist Antibodies
 FILE REFERENCE: P0979
 CURRENT APPLICATION NUMBER: US/08/918,148A
 CURRENT FILING DATE: 1997-08-25
 NUMBER OF SEQ ID NOS: 79
 SEQ ID NO 77
 LENGTH: 244
 TYPE: ERT
 ORGANISM: artificial
 US-08-918-148-77

Query Match	56.5%	Score 762;	DB 4;	Length 244;
Best Local Similarity	60.6%;	Pred. No. 1.9e-53;		
Matches 154;	Conservative 33;	Mismatches 51;	Indels 16;	Gaps 4.

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QY 1 QVTLKSSGPIVYKPEOTLTLTCTFGSGFIPTTGEVGVNRQPPKALEMTLATLYMD-DK 59
Db 3 QVQLVVSGGGVLRPFGSLSLSCAVSGITLRT--YGMHVRKAPKGLFHWANGISFDRSE 60
QY 60 RYSPSLKSLRJTITKDTSKKQVVLTMVNDPADTATYYCTHEQYYDTSGQPYFDFWQOG 119
Db 61 YYADSVQGGFTISRDDSKNTLTYLQNNSLRAEDTAVYYCAR-----GAYHGFDIWGQG 112
QY 120 TLVTWSSGGGSGSGGSGGSGGSGSNITQVQSPSLSASVGRVMTTCRASQDTRKNTL 179
Db 113 TMTVTS-----SGGGGTGGGSGSGGSGSDIQMTQSPSTLSASITGRVITTCRASGITHML 167
QY 180 NMVQOKRGAAPKVLIVDASDLDTGLIPRPSGSGSTDEILITLISLOPEDIAATYYCQGS DY 239
Db 168 AMVQOKRGAAPKLLIYKASLSASGAPRPSGSGSTDEFTLITLISLQPDGFATYYCQGS YN 227
QY 240 LPLFGGSGTKVDIK 253
Db 228 YPLIFGGGTELEIK 241
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: RESULT 6
: US-08-887-352B-23
: Sequence 23. Application US/08887352B
: Patent No. 5994511
: GENERAL INFORMATION:
: APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
: TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of
: TITLE OF INVENTION: Improving Polypeptides
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way

```

1
2 CITY: South San Francisco
3 STATE: California
4
5 COUNTRY: USA
6
7 ZIP: 94080
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
11
12 COMPUTER: IBM PC compatible
13
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15
16 SOFTWARE: Winpatin (genentech)
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/887,352B
20
21 FILING DATE: 03-Jul-1997
22
23 CLASSIFICATION: 530
24
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Svoboda, Craig G.
27 REGISTRATION NUMBER: 39,044
28
29 REFERENCE/DOCKET NUMBER: P1123
30
31 TELECOMMUNICATION INFORMATION:
32
33 TELEPHONE: 650/225-1489
34
35 TELEFAX: 650/952-9881
36
37 INFORMATION FOR SEQ ID NO: 23:
38
39 SEQUENCE CHARACTERISTICS:
40
41 LENGTH: 248 amino acids
42
43 TYPE: Amino acid
44
45 TOPOLOGY: Linear
46
47 US-08-887-352B-23

Query March	56.5†	Score 762:	DB 2:	Length 248;
Best Local Similarity	60.3†	Pred. No. 2e-53;		
Marches 155: Conservative	32	Mismatches	56:	Indels 14:
		Gaps	4:	

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QY      1 OVLKESGGTLYKKPOTLITCTFSGFSRLRTTGSGVGNVRQPCKALEMLALTYMDDKR   60
Db      1 EVQLVESGGGLVQPGGSLRLSCAVGSYSI-TSGYSMMNIRAPCKGLEWVASIKYSGDEK   59

QY      61 YPSLSLKSLTIITKDISSKKQVULMTMNDVPATLTATYYTCHEGYYYDTSGGQYYIPDFMGQT  120
Db      60 YNSYVGGRITISRDSDSKPTFLQNMSLAEBTAAVYYCARSGSHYG---HMHFAVMGGGT  115

QY      121 LVTVSSGGGGSGGGSGGGSGGGGGINIQVTQSPSSLASVGVDRVTMTCRASODI-----R  176
Db      116 LVTVS-----SFGGGSBEGGSGGGGSGSDIQLVQSPSSLASVGDRAVTTITCRASKPVDSBGD  170

QY      177 KNLINMTQQKPKGAAPVYLIDASDLDTGIPISRFSGSGSGSTDFILTISSLQPEDPATYYCQG  236
Db      171 SYLNMTQQKPKGAAPKLLIYAASYLESGVPSRFSGSGSGSTDFTLTISSLQPEDPATYYCQG  230

QY      237 SDYLPILTGGGGRHKVDIK 253
Db      231 SHEDPTTFGGGTKVEIK 247
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RESULT 7
US-09-109-207C-23
; Sequence 23, Application US/09109207C

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1  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
2  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
3  FILE REFERENCE: P1123R1
4  CURRENT APPLICATION NUMBER: US/09/109,207C
5  CURRENT FILING DATE: 1998-06-30
6  PRIOR APPLICATION NUMBER: US 60/051,554
7  PRIOR FILING DATE: 1997-07-03
8  NUMBER OF SEQ ID NOS: 44
9  SEQ ID NO 23
10 LENGTH: 248
11 TYPE: PRT
12 ORGANISM: Artificial
13 FEATURE:
14 NAME/KEY: Artificial
15 LOCATION: 1-248
16 OTHER INFORMATION: sFv sequence derived from MAE11

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,164A
FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00714
FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/07241
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST93030-US
TELEPHONE: (610)454-3816
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-564-164A-4

Query Match 54.6%; Score 736; DB 3; Length 264;
Best Local Similarity 57.7%; Pred. No. 2.5e-51;
Matches 146; Conservative 32; Mismatches 61; Indels 14; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLTLCTFGSGFSRTTGBGVGWRRPGKALEMLALYWDGDK 60
DB 11 QVLOESGPGGLQPAQASISITCTVSGFSL--STGVHWKRSFGKLEMLGVIRGGGTD 68
QY 61 YSPSLKSRLLTKDKSKQVULMTNVDPADTATYCTHEQYVDTSGQPYFDFMGQGT 120
DB 69 YNAAMSRISITKDKSKQVFFKNSLQPPDDTAMYYCAKR-----GGGYFDWVGQGT 121
QY 121 LVTVSSGGGGGGGGGGGGGGGSGNSIOVTPSPSLSASVGDRTVMTCAASODIRKNT 180
DB 122 TVTVS-----SGGGGGGGGGGGGGGSDIELTQSPASVSGTVMTCRASINISNTA 176
QY 181 WYQOKRGAAPKRVLYDASDLFTGIPSPSGSGGTDFILTTSSLOPEDIAATYCCQGSQDY 240
DB 177 WYQOKRGAAPKRVLYDASDLFTGIPSPSGSGGTDFILTTSSLOPEDIAATYCCQGSQDY 240
QY 241 PLTFGGGATKVDIK 253
DB 237 PYRGGGATKLETK 249

RESULT 14
US-08-488-113B-148
Sequence 148, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.B3.CZA
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-148

Query Match 54.5%; Score 734.5; DB 1; Length 240;
Best Local Similarity 57.9%; Pred. No. 2.9e-51;
Matches 147; Conservative 31; Mismatches 61; Indels 15; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLTLCTFGSGFSRTTGBGVGWRRPGKALEMLALYWDGDK 59
DB 1 EIQVDSGGGLVPRGSGVRISCAAGYTF--ITVGMNWRQAPGKLEMGWINTHTGEP 58
QY 60 RYSPSLKSRLLTKDKSKQVULMTNVDPADTATYCTHEQYVDTSGQPYFDFMGQGT 119
DB 59 TVADSRKGRFTSLDSDKNTAYIQNSLRAEDTAVYFCTRR-----GYDWYFDWVGQ 111
QY 120 LVTVSSGGGGGGGGGGGGGGGSGNSIOVTPSPSLSASVGDRTVMTCAASODIRKNT 179
DB 112 TVTVS-----SGGGGGGGGGGGGGGSDIQMTQSPSLSASVGDRTVMTCAASODIRKNT 166
QY 180 WYQOKRGAAPKRVLYDASDLFTGIPSPSGSGGTDFILTTSSLOPEDIAATYCCQGSQDY 239
DB 167 WYQOKRGAAPKRVLYDASDLFTGIPSPSGSGGTDFILTTSSLOPEDIAATYCCQGSQDY 226
QY 240 PLTFGGGATKVDIK 253
DB 227 SPWTFGGGATKLEMK 240

RESULT 15
US-08-477-484B-148
Sequence 148, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ. ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-148

Query Match 54.5%; Score 734.5; DB 1; Length 240;
Best Local Similarity 57.9%; Pred. No. 2.9e-51;
Matches 147; Conservative 31; Mismatches 61; Indels 15; Gaps 4;

QY 1 QVTLKSSGPTLVKPTOTLTCTFSGFSRLTTGEGVGVWRQPPGKALEWIALI-YWDDK 59
DB 1 EIQLVQSGGGLVPGGSVRISCAASGYTF-TVYGMWVRQAPGKLEWGMWINTHTGP 58
QY 60 RYSPSLKSLRTITTKDTSKKQVVLTMNTVDPADATATYCTHEQYYDTSQPYFDFWGG 119
DB 59 TYADSKRGKFTPSLDISKATAYLQINSLAEDTAYVFCRR-----GYDWYFDWGG 111
QY 120 TLVTYSSGG 179
DB 112 TTVTVS-----SGGG 166
QY 180 NMYQOKPGAKPKLITDASDLDTGIRSRSGSGSGTDFILITISLQPEDATATYCCQSDY 239
DB 167 SWFQKPGAKPKLITRANRLBSGVPSRSGSGSGTDFILITISLQYEDFGIYCCQYDE 226
QY 240 LPLTFGGGTRVDIX 253
DB 227 SPWTFGGGTRVDIX 240

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.4587 Seconds
(without alignments)
1879.405 Million cell updates/sec

Title: US-10-072-301-23

Perfect score: 1348
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPITFGGKTKVDIK 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1348	100.0	253	14	US-10-072-301-23 Sequence 23, Appl
2	1348	100.0	253	14	US-10-072-301-31 Sequence 31, Appl
3	1348	100.0	253	14	US-10-071-866-23 Sequence 23, Appl
4	1348	100.0	253	14	US-10-071-866-31 Sequence 31, Appl
5	1348	100.0	253	15	US-10-360-828-23 Sequence 23, Appl
6	1348	100.0	253	15	US-10-360-828-31 Sequence 31, Appl
7	821.5	60.9	286	12	US-10-406-830-8 Sequence 8, Appl
8	821.5	60.9	286	10	US-09-880-748-1049 Sequence 1049, Ap
9	811.5	60.2	251	12	US-10-293-418-1049 Sequence 1049, Ap
10	803	59.6	248	10	US-09-880-748-1360 Sequence 1360, Ap
11	803	59.6	248	12	US-10-293-418-1360 Sequence 1360, Ap
12	801.5	59.5	255	10	US-09-880-748-1603 Sequence 1603, Ap
13	801.5	59.5	255	12	US-10-293-418-1603 Sequence 1603, Ap
14	800.5	59.4	249	10	US-09-880-748-1321 Sequence 1321, Ap
15	800.5	59.4	249	12	US-10-293-418-1321 Sequence 1321, Ap

16	794	58.9	253	14	US-10-072-301-17	Sequence 17, Appl
17	794	58.9	253	14	US-10-072-301-25	Sequence 25, Appl
18	794	58.9	253	14	US-10-071-866-17	Sequence 17, Appl
19	794	58.9	253	14	US-10-071-866-25	Sequence 25, Appl
20	794	58.9	253	15	US-10-360-828-17	Sequence 17, Appl
21	794	58.9	253	15	US-10-360-828-25	Sequence 25, Appl
22	789	58.5	248	10	US-09-880-748-1876	Sequence 1876, Ap
23	789	58.5	248	12	US-10-293-418-1876	Sequence 1876, Ap
24	787	58.4	248	10	US-09-880-748-1421	Sequence 1421, Ap
25	787	58.4	248	12	US-10-293-418-1421	Sequence 1421, Ap
26	781.5	58.0	243	10	US-09-880-748-1935	Sequence 1935, Ap
27	781.5	58.0	243	12	US-10-293-418-1935	Sequence 1935, Ap
28	781.5	58.0	249	10	US-09-880-748-1188	Sequence 1188, Ap
29	781.5	58.0	249	12	US-10-293-418-1188	Sequence 1188, Ap
30	777	57.6	250	10	US-09-880-748-1174	Sequence 1174, Ap
31	777	57.6	250	12	US-10-293-418-1174	Sequence 1174, Ap
32	777	57.6	287	12	US-10-406-830-5	Sequence 5, Appl
33	769	57.0	266	12	US-10-257-864A-108	Sequence 108, App
34	769	57.0	291	12	US-10-423-847-10	Sequence 10, Appl
35	765	56.8	250	15	US-10-423-847-12	Sequence 12, Appl
36	764.5	56.7	333	14	US-10-059-261-61	Sequence 61, Appl
37	764	56.7	248	9	US-09-920-171-22	Sequence 22, Appl
38	764	56.7	248	14	US-10-113-996-22	Sequence 22, Appl
39	762	56.5	248	9	US-09-920-171-23	Sequence 23, Appl
40	762	56.5	248	10	US-09-880-748-1004	Sequence 1004, Ap
41	762	56.5	248	12	US-10-293-418-1004	Sequence 1004, Ap
42	762	56.5	248	14	US-10-113-996-23	Sequence 23, Appl
43	761	56.5	240	9	US-09-192-854-2	Sequence 2, Appl
44	761	56.5	240	9	US-09-968-561A-2	Sequence 2, Appl
45	761	56.5	240	10	US-09-968-744A-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-10-072-301-23
Sequence 23, Application US/10072301
Publication NO. US20030152913A1
GENERAL INFORMATION:
APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 25636-718
CURRENT APPLICATION NUMBER: US/10/072.301
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 253
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Clone 15.150.24
US-10-072-301-23
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Query Match	100.0%	Score 1348;	DB 14;	Length 253;
Best Local Similarity	100.0%	Pred. No. 2e-87;		
Matches	253;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	QVTLKESGPTLVKPTQTTLTCTFSGFSIRTTGEGVWROPGRALLETALIIYDDDKR	60	
DB	1	QVTLKESGPTLVKPTQTTLTCTFSGFSIRTTGEGVWROPGRALLETALIIYDDDKR	60	
QY	61	YSPSLKSLTITTKDSSKQVLTMTNVDPADATATTCHEOYVYDTSQGPYFEDFMGGST	120	
DB	61	YSPSLKSLTITTKDSSKQVLTMTNVDPADATATTCHEOYVYDTSQGPYFEDFMGGST	120	
QY	121	LVTYSSGGGSGGGGSGGGGSGGGSNTQVTPSSLSASVGDRTVMTCRASQDIRKNLN	180	
DB	121	LVTYSSGGGSGGGGSGGGGSGGGSNTQVTPSSLSASVGDRTVMTCRASQDIRKNLN	180	

QY 181 WYQKPKGAPKVLIVDASDLTGIPSRFSGSGGSDTDFILITISLQPEDIAITYYCCQSDYL 240
DB 181 WYQKPKGAPKVLIVDASDLTGIPSRFSGSGGSDTDFILITISLQPEDIAITYYCCQSDYL 240
QY 241 PLTFGGGTAKVDIK 253
DB 241 PLTFGGGTAKVDIK 253

RESULT 2
US-10-072-301-31
; Sequence 31, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-31

Query Match 100.0%; Score 1348; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGGVGVWVQPGKALEMLALTYMDDDKR 60
DB 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGGVGVWVQPGKALEMLALTYMDDDKR 60
QY 61 YSPSLKSRLLITTKDTSKQVVLMTNVPADATATYCTHBOYYDDTSQGPYYDFDFWGQGT 120
DB 61 YSPSLKSRLLITTKDTSKQVVLMTNVPADATATYCTHBOYYDDTSQGPYYDFDFWGQGT 120
QY 121 LVTYSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
DB 121 LVTYSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
QY 181 WYQKPKGAPKVLIVDASDLTGIPSRFSGSGGSDTDFILITISLQPEDIAITYYCCQSDYL 240
DB 181 WYQKPKGAPKVLIVDASDLTGIPSRFSGSGGSDTDFILITISLQPEDIAITYYCCQSDYL 240
QY 241 PLTFGGGTAKVDIK 253
DB 241 PLTFGGGTAKVDIK 253

RESULT 3
US-10-071-866-23
; Sequence 23, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23

Query Match 100.0%; Score 1348; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGGVGVWVQPGKALEMLALTYMDDDKR 60
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DB 61 YSPSLKSRLLITTKDTSKQVVLMTNVPADATATYCTHBOYYDDTSQGPYYDFDFWGQGT 120
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DB 121 LVTYSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
QY 181 WYQKPKGAPKVLIVDASDLTGIPSRFSGSGGSDTDFILITISLQPEDIAITYYCCQSDYL 240
DB 181 WYQKPKGAPKVLIVDASDLTGIPSRFSGSGGSDTDFILITISLQPEDIAITYYCCQSDYL 240
QY 241 PLTFGGGTAKVDIK 253
DB 241 PLTFGGGTAKVDIK 253

RESULT 4
US-10-071-866-31
; Sequence 31, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-071-866-31

Query Match 100.0%; Score 1348; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGGVGVWVQPGKALEMLALTYMDDDKR 60
DB 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGGVGVWVQPGKALEMLALTYMDDDKR 60
QY 61 YSPSLKSRLLITTKDTSKQVVLMTNVPADATATYCTHBOYYDDTSQGPYYDFDFWGQGT 120
DB 61 YSPSLKSRLLITTKDTSKQVVLMTNVPADATATYCTHBOYYDDTSQGPYYDFDFWGQGT 120
QY 121 LVTYSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
DB 121 LVTYSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
QY 181 WYQKPKGAPKVLIVDASDLTGIPSRFSGSGGSDTDFILITISLQPEDIAITYYCCQSDYL 240

Db 181 WTQOKRGKAPKVLIVDASDLETGIPSRFSGSGGTDFILITISLQEPEDIAIYYCCQSDYL 240
QY 241 PLTFGGGTVDIK 253
Db 241 PLTFGGGTVDIK 253

RESULT 5

US-10-360-828-23
Sequence 23, Application US/10360828
Publication No. US20030206909A1
GENERAL INFORMATION:
APPLICANT: Hua, Shaobing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133,978
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 253
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Clone 15.150.24
US-10-360-828-23

Query Match 100.0%; Score 1348; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPKALEWLAIIYWDNR 60
Db 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPKALEWLAIIYWDNR 60
QY 61 YPSLSKSRLLITIKDTSKQVLTMTNVPADTAIYYCTHEQYYDTSGQPYFDFWGGCT 120
Db 61 YPSLSKSRLLITIKDTSKQVLTMTNVPADTAIYYCTHEQYYDTSGQPYFDFWGGCT 120
QY 121 LVTSSGGGSGGSGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASODIRKXNL 180
Db 121 LVTSSGGGSGGSGGSGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASODIRKXNL 180
QY 181 WTQOKRGKAPKVLIVDASDLETGIPSRFSGSGGTDFILITISLQEPEDIAIYYCCQSDYL 240
Db 181 WTQOKRGKAPKVLIVDASDLETGIPSRFSGSGGTDFILITISLQEPEDIAIYYCCQSDYL 240
QY 241 PLTFGGGTVDIK 253
Db 241 PLTFGGGTVDIK 253

RESULT 6

US-10-360-828-31
Sequence 31, Application US/10360828
Publication No. US20030206909A1
GENERAL INFORMATION:
APPLICANT: Hua, Shaobing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727
CURRENT APPLICATION NUMBER: US/10/360,828
CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133,978
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 253
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Clone 15.150.24 Variant
US-10-360-828-31

Query Match 100.0%; Score 1348; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPKALEWLAIIYWDNR 60
Db 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPKALEWLAIIYWDNR 60
QY 61 YPSLSKSRLLITIKDTSKQVLTMTNVPADTAIYYCTHEQYYDTSGQPYFDFWGGCT 120
Db 61 YPSLSKSRLLITIKDTSKQVLTMTNVPADTAIYYCTHEQYYDTSGQPYFDFWGGCT 120
QY 121 LVTSSGGGSGGSGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASODIRKXNL 180
Db 121 LVTSSGGGSGGSGGSGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASODIRKXNL 180
QY 181 WTQOKRGKAPKVLIVDASDLETGIPSRFSGSGGTDFILITISLQEPEDIAIYYCCQSDYL 240
Db 181 WTQOKRGKAPKVLIVDASDLETGIPSRFSGSGGTDFILITISLQEPEDIAIYYCCQSDYL 240
QY 241 PLTFGGGTVDIK 253
Db 241 PLTFGGGTVDIK 253

RESULT 7

US-10-406-830-8
Sequence 8, Application US/10406830
Publication No. US20040071696A1
GENERAL INFORMATION:
APPLICANT: ADAMS, GREGORY P.
APPLICANT: WEINER, LOUIS M.
APPLICANT: JAMES, MARKS D.
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
FILE REFERENCE: 4077-000410US
CURRENT APPLICATION NUMBER: US/10/406,830
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/370,276
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic antibody.
US-10-406-830-8

Query Match 60.9%; Score 821.5; DB 12; Length 286;
Best Local Similarity 66.1%; Pred. No. 2.7e-50;
Matches 168; Conservative 28; Mismatches 43; Indels 15; Gaps 6;
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPKALEWLAIIYWDNR 60
Db 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPKALEWLAIIYWDNR 60

Db 23 QVQLQESGPGLVKPSSETLSLTCTVSGGSRFS--YTWGKIR-PEKGLIEWIGIFYSGSTN 79
QY YSPSLKSRLLTTKQSKQVVLMTNNDPADTATYYCTHROYVDTSGPPYFDPMGGGT 120
Db 80 YNPSLKSRTVITISVDTSKQSLKLSLTADTAVYYCARGHL-----GELGWDPFGQGT 134
QY 121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTSPPSSLSASVGRVMTTCRASQDTRKLN 180
Db 135 LVTVS-----SSGGSGGGGSGGGGSDIQWTSPPSSLSASVGRVMTTCRASQDTRKLN 189
QY 181 WYQKPKGKAPKVLIDASDLFTGIPSRFSGSGGTDFILITSSLOPEDATATYYC-QQSDY 239
Db 190 WYQKPKGKAPKVLIDASDLFTGIPSRFSGSGGTDFILITSSLOPEDATATYYC-QQSDY 249
QY 240 LPLTFGGGTAKVDIK 253
Db 250 -PLTFGGGTAKVEIK 262

RESULT 8

US-09-880-748-1049
/ Sequence 1049, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS23
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1049
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1049

Query Match 60.2%; Score 811.5; DB 10; Length 251;
Best Local Similarity 63.0%; Pred. No. 1,2e-49;
Matches 160; Conservative 31; Mismatches 58; Indels 5; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGPSLRTTGSGVWVROPKALFWLALYYDDDKR 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSRFSRWGWRPFGKAPFENIGIYYTGKTY 60
QY YSPSLKSRLLTTKQSKQVVLMTNNDPADTATYYCTHROYVDTSGPPYFDPMGGGT 120
Db 61 YSPSLKSRVITISVDTSKQSLKLSLTADTAVYYCARAGYDLT-GVPYFDPMGGGT 119
QY 121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTSPPSSLSASVGRVMTTCRASQDTRKLN 180
Db 120 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTSPPSSLSASVGRVMTTCRASQDTRKLN 180
QY 181 WYQKPKGKAPKVLIDASDLFTGIPSRFSGSGGTDFILITSSLOPEDATATYYC-QQSDY 240
Db 177 WYQKPKGKAPKVLIDASDLFTGIPSRFSGSGGTDFILITSSLOPEDATATYYC-QQSDY 240
QY 241 P-LTFGGGTAKVDIK 253
Db 237 P-LTFGGGTAKVEIK 250

RESULT 9

US-10-293-418-1049
/ Sequence 1049, Application US/10293418
/ Publication No. US2003022396A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS23P2
/ CURRENT APPLICATION NUMBER: US/10/293,418
/ CURRENT FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-16
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1049
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-1049

Query Match 60.2%; Score 811.5; DB 12; Length 251;
Best Local Similarity 63.0%; Pred. No. 1,2e-49;
Matches 160; Conservative 31; Mismatches 58; Indels 5; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGPSLRTTGSGVWVROPKALFWLALYYDDDKR 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSRFSRWGWRPFGKAPFENIGIYYTGKTY 60
QY YSPSLKSRLLTTKQSKQVVLMTNNDPADTATYYCTHROYVDTSGPPYFDPMGGGT 120
Db 61 YSPSLKSRVITISVDTSKQSLKLSLTADTAVYYCARAGYDLT-GVPYFDPMGGGT 119
QY 121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTSPPSSLSASVGRVMTTCRASQDTRKLN 180
Db 120 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTSPPSSLSASVGRVMTTCRASQDTRKLN 180
QY 181 WYQKPKGKAPKVLIDASDLFTGIPSRFSGSGGTDFILITSSLOPEDATATYYC-QQSDY 240
Db 177 WYQKPKGKAPKVLIDASDLFTGIPSRFSGSGGTDFILITSSLOPEDATATYYC-QQSDY 240
QY 241 P-LTFGGGTAKVDIK 253
Db 237 P-LTFGGGTAKVEIK 250

RESULT 10
US-09-880-748-1360
/ Sequence 1360, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS23
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1360
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1360

Query Match 59.6%; Score 803; DB 10; Length 248;
Best Local Similarity 63.2%; Pred. No. 4,6e-49;
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTGEGVWVRQPGKALEWIALIYMDDDR 60
1 QVQLQESGPGLVKPSFTLSLCTVSGGSIRS--YWSWIRQSPGRLGHWIYHSGSTD 58
DB 61 YSPSLKSLRTITKDTSKQVLTMTNVPADATATYCTHEQYVYDTSQPYFDFWGQGT 120
59 YNPSLRSRVMTSIDTSKQFSLNTSVTAADTAIVYVCARDHYDVLGSLYLAQFVWGQGT 118
QY 121 LVTSSGGGSGGSGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASQDRIKLN 180
119 LVTSSGGGSGGSGGSGGSGGSGGSG--ALDIQLTQSPSSLSASVGDRTVTCRASQISGRYLN 175
QY 181 WYQKPKGAPKYLIDASDLDTGIPSRFSGSGGTDFILITISLQPEDATATYCCQSDYL 240
176 WYQKPKGAPKRLIFVTSSLSHSDVSRFRSGSGGTDFSLITISLQPEDATATYCCQSDYL 234
DB 241 PLTFGGGTGVKDIK 253
QY 235 DPTFGGTGRLLEIK 247

RESULT 11
US-10-293-418-1360
Sequence 1360, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1360
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1360

Query Match 59.6%; Score 803; DB 12; Length 248;
Best Local Similarity 63.2%; Pred. No. 4,6e-49;
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTGEGVWVRQPGKALEWIALIYMDDDR 60
1 QVQLQESGPGLVKPSFTLSLCTVSGGSIRS--YWSWIRQSPGRLGHWIYHSGSTD 58
DB 61 YSPSLKSLRTITKDTSKQVLTMTNVPADATATYCTHEQYVYDTSQPYFDFWGQGT 120
59 YNPSLRSRVMTSIDTSKQFSLNTSVTAADTAIVYVCARDHYDVLGSLYLAQFVWGQGT 118
QY 121 LVTSSGGGSGGSGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASQDRIKLN 180
119 LVTSSGGGSGGSGGSGGSGGSGGSG--ALDIQLTQSPSSLSASVGDRTVTCRASQISGRYLN 175
QY 181 WYQKPKGAPKYLIDASDLDTGIPSRFSGSGGTDFILITISLQPEDATATYCCQSDYL 240
176 WYQKPKGAPKRLIFVTSSLSHSDVSRFRSGSGGTDFSLITISLQPEDATATYCCQSDYL 234
DB 241 PLTFGGGTGVKDIK 253
QY 235 DPTFGGTGRLLEIK 247

RESULT 12
US-09-880-748-1603
Sequence 1603, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1603
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1603

Query Match 59.5%; Score 801.5; DB 10; Length 255;
Best Local Similarity 62.0%; Pred. No. 6,1e-49;
Matches 163; Conservative 27; Mismatches 54; Indels 19; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTGEGVWVRQPGKALEWIALIYMDDDR 56
1 QVQLQESGPGLVKPSFTLSLCTVSGGSIRS--YWSWIRQSPGRLGHWIYHSGSTD 60
DB 57 DPKRSPSLKSLRTITKDTSKQVLTMTNVPADATATYCTHEQYVYDTSQPYFDFWGQGT 112
61 SD--YGASVRSRITITNADTSKQFSLNTSVTAADTAIVYVCARDHYDVLGSLYLAQFVWGQGT 116
QY 113 --FDFWGQGTIVTVSSGGGSGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCR 170
117 GGDVWGRGTIVTVS-----SGGSGGSGGSGGSGGSGDIDMTQSPSSLSASIGRVTTCR 171
DB 171 ASQDRIKLNWYQKPKGAPKYLIDASDLDTGIPSRFSGSGGTDFILITISLQPEDAT 230
172 ASBGIVHWLAWYQKPKGAPKYLIFVTSSLSHSDVSRFRSGSGGTDFSLITISLQPEDAT 231
QY 231 TYCCQSDYLPLTFGGGTGVKDIK 253
DB 232 TYCCQSDYVPLTFGGGTGRLLEIK 254

```

Query Match Similarity      59.5% Score 801.5; DB 12; Length 255;
Best Local Similarity      62.0%; Pred. No. 6,1e-49;
Matches      163; Conservative      27; Mismatches      54; Indels      19; Gaps      6;

Qy      1 QVTLKESGPTLVKPYQTTLTCTFSGFSRLTTGEGVGVWROPGRKALEMLALTY----WD      56
Db      1 QVQLQQSGSPGLVKKPFGQTLSTLSCAISGDSVSGAAMNVIQGPSRGLFEMLGRTYRSGQWY      60

Qy      57 DDKRISPLKSRLLTTKDTSTKKQVVLMTNNDPALTATYYCHGEQYYD--TSQOPYY---      112
Db      61 SD--GGAIVRSKRTTNADTISKQFSLQLNSVTPEDVTAYYCARSGRDILTG--YSGG      116

Qy      113 --FDPMQGTTLVTVSSGGGGSGGGSGGGSGGGSNIVQVTSPPSLASVADRYVMTCR      170
Db      117 GGMVDVWGSGTLTVTS-----SGGGSGGGSGGGSGGSDIQMGWSPSTLSASIGDRYITLCR      171

Qy      171 ASQDIRKRLNMYQKPGKAPKYLITDASDLEFGIRSPRSGSGGTFDPLTTTSSLOPEDIA      230
Db      172 ASSEGIVHWLAWYQKPGKAPKLLIYKASLSAGAPSRFSGGSGGTFDPLTTTSSLOPDDFA      231

Qy      231 TTYCQGSNDYLLPLTFGGGTTKVDIK      253
Db      232 TTYCQQYSNYPPLTFGGGTLKIK      254

RESULT 14
US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816

```

Query Match	59.4%;	Score 800.5;	DB 10;	Length 249;
Best Local Similarity	64.3%;	Pred. No. 76-49;		
Matches	164;	Conservative	27;	Mismatches 55; Indels 9; Gaps 4
Qy	1	QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGSGVMTROPFGKALEMLAIYYDDDKR	60	
Db	1	QVQLQQMAGAGILKSEETLSLTCVAYGGSF--SGYYMSWIRPPGPGLEIMEIHNSGATN	58	
Qy	61	YSPSLKSRRLTTKTSKKQVLLMTNVPADATATYYCTHEQYVD--TGQPY-YEPFMQO	118	
Db	59	YNPSLKRVTISVDTSKNQPSLKLSSVTAADTAIYYCARGRYVDILGRYNNMDFPMGR	118	
Qy	119	GLTVTVSSGGGGSGGGSGGGSGGGSNIQVTSPPSLASVGDVMTTCRASGDIDKN	178	
Db	119	GLTVTVS-----SGGGSGGGSGGGSGSDIMYTSPTSLASVGDVMTTCRASGIGISW	173	
Qy	179	LNMYQKRPKAPKYLIDASDLRTGIPSRFSGSGSGTFILITSLQPEDIATYYCQOQSD	238	
Db	174	LNMYQKRPKAPKYLIIKASTLBSGVSRFSGSGSGDTFTLITSSLQPEDPATYYCQOQSY	233	
Qy	239	YLPITFGGSGTKVDIK	253	
Db	234	STPMTFGGSGTKLEIK	248	

RESULT 15
US-10-293-418-1321
Sequence 1321, Application US/10293418
Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bvys
FILE REFERENCE: PE523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIORITY APPLICATION NUMBER: 60/331,469
PRIORITY FILING DATE: 2001-11-16
PRIORITY APPLICATION NUMBER: 60/340,817
PRIORITY FILING DATE: 2001-12-19
PRIORITY APPLICATION NUMBER: 09/880,748
PRIORITY FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/293,499
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: 60/277,319
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/276,248
PRIORITY FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: 60/240,816
PRIORITY FILING DATE: 2000-10-17
PRIORITY APPLICATION NUMBER: 60/212,210
PRIORITY FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1321
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1321

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.4218 seconds

(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-23

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTLLT.....CQGSVDYLPITFGGTRKVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	45.3	268	2 A56446	Ig heavy chain V r
2	578.5	42.9	249	2 S41374	single chain Fv an
3	551	40.9	124	2 A49002	Ig heavy chain V r
4	538.5	39.9	138	2 S31513	Ig heavy chain - h
5	534.5	39.7	374	2 S69339	Ig heavy chain V r
6	533.5	39.6	233	2 UCS322	p53 specific singl
7	487	36.1	119	2 S18555	Ig heavy chain V r
8	485.5	36.0	125	1 MHHMOC	Ig heavy chain V-I
9	474.5	35.2	121	1 G1H0HE	Ig heavy chain V-I
10	470.5	34.9	118	2 S18556	Ig heavy chain V r
11	469.5	34.8	121	2 A36005	Ig heavy chain V r
12	468	34.7	108	1 K1H0RY	Ig kappa chain V-I
13	468	34.7	129	2 S52789	Ig kappa chain V r
14	462	34.3	110	2 S44118	Ig kappa chain V-I
15	456	33.8	108	1 K1H0AU	Ig kappa chain V-I
16	456	33.8	108	2 B49047	Ig kappa chain V-I
17	456	33.8	125	2 S40349	Ig kappa chain V-J
18	449	33.3	107	2 S36264	Ig lambda chain V
19	448	33.2	108	1 K1H0SW	Ig kappa chain V-I
20	447	33.2	107	2 S36269	Ig lambda chain V
21	445	33.0	122	2 S11740	Ig heavy chain pre
22	445	33.0	123	2 S40331	Ig kappa chain - h
23	443	32.9	108	2 S19674	Ig kappa chain V r
24	443	32.9	129	2 S52793	Ig kappa chain V r
25	442	32.8	108	1 K1H0AG	Ig kappa chain V-I
26	442	32.8	124	2 S40348	Ig kappa chain V-J
27	441	32.7	125	2 S40316	Ig kappa chain - h
28	441	32.7	127	2 S40367	Ig kappa chain V-J
29	440	32.6	107	2 S36262	Ig lambda chain V

30	439	32.6	129	2 S40317	Ig kappa chain - h
31	437	32.4	139	2 S40365	Ig kappa chain - h
32	435	32.3	108	1 K1H0RE	Ig kappa chain V-I
33	435	32.3	108	1 K1H0WS	Ig kappa chain V-I
34	435	32.3	120	1 G1H0CO	Ig heavy chain V-I
35	434	32.2	108	2 S31954	Ig kappa chain (BR
36	432	32.0	109	2 S31981	Ig kappa chain - h
37	431	32.0	105	2 S36266	Ig lambda chain V
38	431	32.0	129	2 S52792	Ig kappa chain V r
39	430	31.9	117	2 S46376	Ig kappa chain V-J
40	429	31.8	125	2 S40350	Ig kappa chain - h
41	429	31.8	143	2 PT0174	Ig heavy chain pre
42	428	31.8	109	2 S31998	Ig heavy chain - h
43	427	31.7	108	2 S36279	Ig lambda chain V
44	427	31.7	117	2 S43528	Ig kappa chain V r
45	427	31.7	117	2 S42263	Ig kappa chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #ext_change 16-Aug-1996

C/Accession: A56446
R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident:

A/Reference number: A56446; WUID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 45.3%; Score 611; DB 2; Length 268;
Best Local Similarity 49.6%; Pred. No. 1.3e-34;
Matches 126; Conservative 42; Mismatches 70; Indels 16; Gaps 6;

QY	1	QVTLKESGPTLVKPTQTLLTCTPSGFSRTTGEVGVROPKALFWLALITY-WDDX	59
DB	3	QVTLKESGPTLVKPTQTLLTCTPSGFSRTTGEVGVROPKALFWLALITY-WDDX	60
QY	60	RYSPLSKRLTITTKDTSKKQVLTMTNVDPADATATYCTHGYDYDTSGOPYFDFWGG	119
DB	61	KYDPKFGKATITADITSSNTAVLQLSLTSEDTAVYCAS---YVLT---YENYWGQ	113
QY	120	TLVTVSSGGGGSGGGSGGGSGGGSGGNSIQVTPSSLASVGDRTYMTCRASQDIRKL	179
DB	114	TLVTVSS---SGGGSGGGSGGGSGGGSDIELTQSPALMSASIGEKVMSCRASSSV-NP	167
QY	180	NMVQKPKGAPVLYLSDLETGTPSPRSSGSGDFLTITSSLOPEDATATYTCQGSY	239
DB	168	YVYQKSDASPLWLYTSHLPVGPAPRSSGSGNSYSLTISMEGDAATYTCQQFTS	227
QY	240	LPITFGGTRKVDIK 253	
DB	228	SPITFGGTRKVDIK 241	

RESULT 2

S41374
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 06-Jan-1995

C/Accession: S41374

R/Artzenko, O.; Weiler, B.W.; Wuentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374

A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <Ara>
A:Cross-references: EMBL:Z29480

Query Match 42.9%; Score 578.5; DB 2; Length 249;
Best Local Similarity 44.8%; Pred. No. 1.9e-32;
Matches 116; Conservative 50; Mismatches 74; Indels 19; Gaps 5;

```
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 59
DB 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 59
QY 60 YSPSLKSLRLITTKDTSKKQVVLTMNVDPADPATATYCTHGEQYYDTSQPYFPDPMQGT 119
DB 59 KYVPRFQDKATITADSSNTAVLLSLTSSEDTAVYCCARRDTLYTSIG-----YMGQG 112
QY 120 TLTVTSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 178
DB 113 STTVTSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 178
QY 179 ----LWYQOKPKAKVLYDASPLETSGIPRFSGSGGTDFTLTSLQPEDATATYCC 234
DB 168 GDSYLFWFLQRPQSPQLIYMSVLASGVPRFSGSGGTSFTLRISRVAEDVGYVYC 227
QY 235 QGSDVPLTFPGGTATVDK 253
DB 228 MOHREYPLTFGAGTLELK 246
```

RESULT 3

A:Accession: A49002
Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49002
R:Studer, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.
Arthritis Rheum. 35, 900-904, 1992
A:Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene
A:Reference number: A49002; MUID:92352481; PMID:11322670
A:Accession: A49002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-124 <STU>
A:Cross-references: GB:M90808; NID:G185515; PIDN:AA52989.1; PID:G567176
A:Experimental source: BBV-transformed lymphoblastoid cell line SSH23
A>Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBI:110262)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 40.9%; Score 551; DB 2; Length 124;
Best Local Similarity 81.7%; Pred. No. 6.9e-31;
Matches 103; Conservative 10; Mismatches 11; Indels 2; Gaps 1;

```
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 60
DB 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 60
QY 61 YSPSLKSLRLITTKDTSKKQVVLTMNVDPADPATATYCTHGEQYYDTSQPYFPDPMQGT 120
DB 61 YSPSLKSLRLITTKDTSKKQVVLTMNVDPADPATATYCTHGEQYYDTSQPYFPDPMQGT 120
QY 121 LVTWSS 126
DB 119 LVTWSS 124
```

RESULT 4

S31513
Ig heavy chain - human
C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31513
R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31513
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <CHA>
A:Cross-references: EMBL:X69861; NID:G33084; PIDN:CAA49495.1; PID:G33085
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-114/Domain: immunoglobulin homology <IMM>

Query Match 39.9%; Score 538.5; DB 2; Length 138;
Best Local Similarity 80.8%; Pred. No. 5.4e-30;
Matches 101; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

```
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 60
DB 16 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 75
QY 61 YSPSLKSLRLITTKDTSKKQVVLTMNVDPADPATATYCTHGEQYYDTSQPYFPDPMQGT 120
DB 76 YSPSLKSLRLITTKDTSKKQVVLTMNVDPADPATATYCTHGEQYYDTSQPYFPDPMQGT 132
QY 121 LVTWSS 125
DB 133 LVTWSS 137
```

RESULT 5

S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
R:Khmelich, A.A.; Auncutier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khmelich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 'C', 142-374 <KH2>
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 39.7%; Score 534.5; DB 2; Length 374;
Best Local Similarity 81.0%; Pred. No. 2.8e-29;
Matches 102; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

```
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 60
DB 20 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTTGEGVGVWVROPKALFMTALTYWDDDKR 79
QY 61 YSPSLKSLRLITTKDTSKKQVVLTMNVDPADPATATYCTHGEQYYDTSQPYFPDPMQGT 120
DB 80 YSPSLKSLRLITTKDTSKKQVVLTMNVDPADPATATYCTHGEQYYDTSQPYFPDPMQGT 136
QY 121 LVTWSS 126
DB 137 LVTWSS 142
```


Db 1 QVTLKNGEPTLVKPTETLLTCTLSGLSLTDDGVAVGKIRGPGRALEMLALIMLYDDDK 60
 QY 60 RPSPLKSRLLTITKDTSKQVYVLTMTNDPADIAITYYCTHEQYVYDTSQPYFDFPMGOG 119
 Db 61 RPSPLKSRLLTITKDTSKQVYVLTMTNDPADIAITYYCTHEQYVYDTSQPYFDFPMGOG 114
 QY 120 LTVVSS 126
 Db 115 TKVAVSS 121

RESULT 10
 S18556
 Ig heavy chain V region precursor (VII-5b) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
 C/Accession: S18556
 R/Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Seeda, E.; H
 EMO J. 10, 3641-3645, 1991
 A/Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
 A/Reference number: S18551; MUID:92037524; PMID:1935893
 A/Accession: S18556
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-118 <SH1>
 A/Cross-references: EMBL:X62108; NID:937840; PIDN:CAA44018.1; PID:937841
 C/Genetics: 16/1
 C/Superfamily: immunoglobulin V region, immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.10-118/Product: Ig heavy chain V region (VII-5b) #status predicted <MAT>
 F.14-116/Domain: immunoglobulin homology <IMV>

Query Match 34.9% Score 470.5; DB 2; Length 118;
 Best Local Similarity 88.9% Pred. No. 1.9e-25;
 Matches 88; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
 QY 1 QVTLKNGEPTLVKPTETLLTCTLSGLSLTDDGVAVGKIRGPGRALEMLALIMLYDDDK 60
 Db 20 QVTLKNGEPTLVKPTETLLTCTLSGLSLTDDGVAVGKIRGPGRALEMLALIMLYDDDK 78
 QY 61 YSPSLKSRLLTITKDTSKQVYVLTMTNDPADIAITYYCTH 99
 Db 79 YSPSLKSRLLTITKDTSKQVYVLTMTNDPADIAITYYCAH 117

RESULT 11
 A36005
 Ig heavy chain V region (M60) - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1990 #sequence_revision 13-Sep-1991 #text_change 16-Dec-1998
 C/Accession: A36005
 R/Schroeder, J.T.; H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A/Reference number: A36005; MUID:90349571; PMID:21117273
 A/Accession: A36005
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-121 <SCH>
 A/Cross-references: GB:M34027
 C/Genetics:
 A/Gene: GDB:IGH@; IGHV1
 A/Cross-references: GDB:118731; OMIM:146910
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region, immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F.15-99/Domain: immunoglobulin homology <IMV>

Query Match 34.8% Score 469.5; DB 2; Length 121;
 Best Local Similarity 72.2% Pred. No. 2.3e-25;
 Matches 91; Conservative 10; Mismatches 20; Indels 5; Gaps 1;

QY 1 QVTLKNGEPTLVKPTETLLTCTLSGLSLTDDGVAVGKIRGPGRALEMLALIMLYDDDK 60
 Db 1 EVTLKNGEPTLVKPTETLLTCTLSGLSLTDDGVAVGKIRGPGRALEMLALIMLYDDDK 60
 QY 61 YSPSLKSRLLTITKDTSKQVYVLTMTNDPADIAITYYCTHEQYVYDTSQPYFDFPMGOG 120
 Db 61 YSPSLKSRLLTITKDTSKQVYVLTMTNDPADIAITYYCTHEQYVYDTSQPYFDFPMGOG 115
 QY 121 LTVVSS 126
 Db 116 LTVVSS 121

RESULT 12
 K1HURY
 Ig kappa chain V-I region (Roy) - human (tentative sequence)
 C/Species: Homo sapiens (man)
 C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 31-Mar-2000
 C/Accession: A91638; B94417; A01874; S02575
 R/Hilchmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 348, 1077-1080, 1967
 A/Title: Die chemische Struktur von zwei Bence-Jones-Proteinen (Roy und Cum.) vom kappa
 A/Reference number: A91638; MUID:68362076; PMID:5595110
 A/Accession: A91638
 A/Molecule type: protein
 A/Residues: 1-38; GPK, 42-108 <HIL>
 A/Note: the sequence of the C region, which has the Inv (1,2) marker, is also given
 R/Hilchmann, N.; Barrikol, H.U.; Hesse, M.; Langer, B.; Ponatig, H.; Steimetz-Kayne,
 In Gamma Globulin: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
 A/Reference number: A94417
 A/Contents: revisions to residues 39 and 41
 A/Accession: B94417
 A/Molecule type: protein
 A/Residues: 39;41 <HIL2>
 R/Steiner, V.; Chang, J.Y.
 FBS Lett. 222, 6-10, 1987
 A/Title: Chemical modification of the carboxyl groups of protein subunits enhances th
 A/Reference number: S02572; MUID:88005152; PMID:3115831
 A/Contents: annotation
 C/Comment: This is a Bence Jones protein.
 C/Genetics:
 A/Gene: GDB:IGKV1
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12
 C/Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kappa
 hain disulfide bonds; in some cases, such as Iga and Igm, the subunits associate into 1a
 C/Superfamily: immunoglobulin V region, immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F.16-90/Domain: immunoglobulin homology <IMV>
 F.23-88/Disulfide bonds: #status predicted

Query Match 34.7% Score 468; DB 1; Length 108;
 Best Local Similarity 84.1% Pred. No. 2.6e-25;
 Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 QY 147 NIQTQSPSSLSASVGRVMTCTCRASODIRKNTLNTWYQXGKAPKULIYASLFGIRG 206
 Db 1 DIQMTQSPSSLSASVGRVMTCTCRASODIRKNTLNTWYQXGKAPKULIYASLFGIRG 206
 QY 207 RPSGSGSTDFLITSLQPEPDIAITYYCOQSDYLPITFGGTVYDIK 253
 Db 61 RPSGSGSTDFLITSLQPEPDIAITYYCOQSDYLPITFGGTVYDIK 107

RESULT 13
 S52789
 Ig kappa chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C/Accession: S52789
 R/Rocca, A.; Khamilichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,
 submitted to the EMBL Data Library, March 1995

A:Description: light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52789
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KOC>
A:Cross-references: EMBL:X85995; NID:G758588; PIDN:CAA59987.1; PID:G758589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 34.7%; Score 468; DB 2; Length 129;
Best Local Similarity 81.1%; Pred. No. 3.1e-25;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 143 GGGSNIQVQSPSSLSASVGDRTVMTCRASQDIRKNLMYQOKPGKAPKLYIDASDLFT 202
DB 19 GARCDIQMTQSPSSLSASVGDRTVITTCQASQDISNYLMYQOKPGKAPKLYIDASDLFT 78

QY 203 GTPSRSGSGGTDFTLTITSSLOPEDIAITYCCQSDYLPFTFGGTRKVDIK 253
DB 79 GTPSRSGSGGTDFTLTITSSLOPEDIAITYCCQSDYLPFTFGGTRKVEIK 129

RESULT 14
S4418
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S4418
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A:Reference number: S44105
A:Accession: S4418
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <HAW>
A:Cross-references: EMBL:231395; NID:G472972; PIDN:CAA83270.1; PID:G940529
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 34.3%; Score 462; DB 2; Length 110;
Best Local Similarity 83.5%; Pred. No. 6.6e-25;
Matches 91; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 147 NIQVQSPSSLSASVGDRTVMTCRASQDIRKNLMYQOKPGKAPKLYIDASDLFTGIPS 206
DB 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLMYQOKPGKAPKLYIDASDLFTGIPS 60

QY 207 RFGSGSGGTDFTLTITSSLOPEDIAITYCCQSDYLPFTFGGTRKVDIK 253
DB 61 RFGSGSGGTDFTLTITSSLOPEDIAITYCCQSDYLPFTFGGTRKVDIK 109

RESULT 15
KIHUAD
Ig kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C:Accession: A91653; A01862; S02573
R:Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A:Title: Die primärstrukturalen monoklonalen Immunglobulin-V-Kette vom kappa-Typ, Sub
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653
A:Molecule type: protein
A:Residues: 1-108 <SCH>
A>Note: the C region of this chain has the Inv (3) marker
R:Fehlhammer, H.; Schliffer, M.; Bpp, O.; Colman, P.M.; Latman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A:Title: The structure determination of the variable portion of the Bence-Jones protein

A:Reference number: A90729; MUID:77022433; PMID:1234024
A:Contents: annotation; X-ray crystallography
A>Note: the structure of the V region was determined by molecular replacement methods ut
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substructures enhances the
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Comment: This is a Bence Jones protein.
C:Genetic: GDB:IGKV1
A:Gene: GDB:136264
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kai
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 16
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 33.8%; Score 456; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.7e-24;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 147 NIQVQSPSSLSASVGDRTVMTCRASQDIRKNLMYQOKPGKAPKLYIDASDLFTGIPS 206
DB 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLMYQOKPGKAPKLYIDASDLFTGIPS 60

QY 207 RFGSGSGGTDFTLTITSSLOPEDIAITYCCQSDYLPFTFGGTRKVDIK 253
DB 61 RFGSGSGGTDFTLTITSSLOPEDIAITYCCQSDYLPFTFGGTRKVEIK 107

Search completed: May 13, 2004, 15:08:43
Job time : 12.4218 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.1233 Seconds

(without alignments)
1849.388 Million cell updates/sec

Title: US-10-072-301-23

Sequence: 1 QVTLKESGPTLVKPTQTLLT.....CQSPDYLPVTFGGGTFKVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485.5	36.0	125	1 HV2D_HUMAN	P01817 homo sapien
2	474.5	35.2	121	1 HV2E_HUMAN	P01818 homo sapien
3	468	34.7	108	1 KVIJ_HUMAN	P01608 homo sapien
4	468	34.7	108	1 KVIJ_HUMAN	P01608 homo sapien
5	456	33.8	108	1 KVIJ_HUMAN	P01594 homo sapien
6	448	33.2	108	1 KVIJ_HUMAN	P01609 homo sapien
7	442	32.8	108	1 KVIJ_HUMAN	P01593 homo sapien
8	435	32.3	108	1 KVIJ_HUMAN	P01607 homo sapien
9	435	32.3	108	1 KVIJ_HUMAN	P01611 homo sapien
10	435	32.3	120	1 HV2B_HUMAN	P01815 homo sapien
11	425	31.5	108	1 KVIJ_HUMAN	P01595 homo sapien
12	425	31.5	108	1 KVIJ_HUMAN	P01600 homo sapien
13	423	31.4	108	1 KVIJ_HUMAN	P01597 homo sapien
14	423	31.4	108	1 KVIJ_HUMAN	P01607 homo sapien
15	423	31.4	129	1 KVIJ_HUMAN	P04431 homo sapien
16	418	31.0	108	1 KVIJ_HUMAN	P01599 homo sapien
17	418	31.0	108	1 KVIJ_HUMAN	P01605 homo sapien
18	415	30.8	108	1 KVIJ_HUMAN	P01610 homo sapien
19	413	30.6	108	1 KVIJ_HUMAN	P01603 homo sapien
20	411	30.5	147	1 HV2H_HUMAN	P04438 homo sapien
21	408.5	30.3	107	1 KVIJ_HUMAN	P01596 homo sapien
22	408.5	30.3	109	1 KVIJ_HUMAN	P01612 homo sapien
23	406	30.1	129	1 KVIJ_HUMAN	P04432 homo sapien
24	405	30.0	108	1 KVIJ_HUMAN	P01632 mus musculu
25	404	30.0	108	1 KVIJ_HUMAN	P01604 homo sapien
26	403	29.9	108	1 KVIJ_HUMAN	P01606 homo sapien
27	402.5	29.9	119	1 HV2C_HUMAN	P01650 homo sapien
28	401	29.7	108	1 KVIJ_HUMAN	P01650 mus musculu
29	401	29.7	108	1 KVIJ_HUMAN	P01653 mus musculu
30	397	29.5	108	1 KVIJ_HUMAN	P01598 homo sapien
31	391	29.0	108	1 KVIJ_HUMAN	P01651 mus musculu
32	389	28.9	126	1 HV2A_HUMAN	P01814 homo sapien
33	388	28.8	108	1 KVIJ_HUMAN	P01648 mus musculu

34	387	28.7	108	1 KVIJ_MOUSE	P01645 mus musculu
35	387	28.7	117	1 KVIJ_HUMAN	P01602 homo sapien
36	386	28.6	108	1 KVIJ_MOUSE	P01644 mus musculu
37	386	28.6	108	1 KVIJ_MOUSE	P01646 mus musculu
38	385	28.6	108	1 KVIJ_MOUSE	P01647 mus musculu
39	382	28.3	112	1 KVIJ_HUMAN	P01613 homo sapien
40	381	28.3	108	1 KVIJ_MOUSE	P01649 mus musculu
41	378	28.0	108	1 KVIJ_MOUSE	P01649 mus musculu
42	373.5	27.7	144	1 HV4J_MOUSE	P01819 mus musculu
43	372	27.6	117	1 KVIJ_HUMAN	P01601 homo sapien
44	367	27.2	128	1 KVIJ_MOUSE	P01637 mus musculu
45	363.5	27.0	133	1 KVIJ_HUMAN	P06313 homo sapien

ALIGNMENTS

RESULT 1	ID	HV2D_HUMAN	STANDARD;	PRT;	125 AA.
AC	P01817;				
DT	21-UTL-1986 (Rel. 01, Created)				
DT	21-UTL-1986 (Rel. 01, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Ig heavy chain V-II region MCB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE-81118242; PubMed-6780622;				
RA	Gerber-Venson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,				
RA	Litman G.W.;				
RT	"Molecular basis for the temperature-dependent insolubility of				
RT	cryoglobulins. X. The amino acid sequence of the heavy chain variable				
RT	region of MCB."				
RL	J. Immunol. 126:1212-1216 (1981).				
CC	-1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM				
CC	CRYOIMMUNOGLOBULIN.				
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A02092; MEHDMC.				
DR	HSSP; P01825; 7FAB.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGY; 1.				
DR	PROSITE; PS00835; Ig_LIKE; 1.				
KW	Immunoglobulin V region; Pyroglutamate carboxylic acid.				
FT	DOMAIN 1 113				
FT	MOD RES 1 1				
FT	MOD RES 1 1				
FT	NON_TER 125 125				
SO	SEQUENCE 125 AA; 13783 MW; 7A1ADP4C40F4B5 CRC64;				
Query Match	36.0%; Score 485.5; DB 1; Length 125;				
Best Local Similarity	73.8%; Pred. No. 1.4e-31;				
Matches	93; Conservative 11; Mismatches 21; Indels 1; Gaps 1;				
QY	1 QVTLKESGPTLVKPTQTLLTCTFGSFSRTGEGVGWVRPPGKLEWLLALTYMDDR 60				
DB	1 QVTLKESGPTLVKPTQTLLTCTFGSFSRTGEGVGWVRPPGKLEWLLALTYMDDR 60				
QY	61 YPSLSKRLITIKDTSKQVLTMTNVDPADATATYCTHEQYVYDTSQPYDFDNGGCT 120				
DB	61 YPSLSKRLITIKDTSKQVLTMTNVDPADATATYCTHEQYVYDTSQPYDFDNGGCT 119				
QY	121 LVTVSS 126				
DB	120 LVTVSS 125				

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RESULT 2
ID HY2E HUMAN STANDARD; PRT; 121 AA.
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains."
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003 (1969).
CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02093; GIHURH.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Pyrrrolidone carboxylic acid.
KW DOMAIN 1 120
KW MOD_RES 1 121
KW NON_TER 1 121
KW PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match.
Best Local Similarity 71.7%; Pred. No. 1e-30; Length 121;
Matches 91; Conservative 10; Mismatches 19; Indels 7; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLLTCTPFGSFLRTGEGVMVQPPGKALEMLA-LIYDDDK 59
DB 1 QVTLKESGPTLVKPTQTLLTCTPFGSFLRTGEGVMVQPPGKALEMLA-LIYDDDK 59
QY 60 RYSPSLKRLTITDTSKQVLTMTNVDPADTATYTCHEQYYDTSGQPYFPFGQG 119
DB 61 RYSPSLKRLTITDTSKQVLTMTNVDPADTATYTCHEQYYDTSGQPYFPFGQG 119
QY 120 TLTVVSS 126
DB 115 TKVAVSS 121

RESULT 3
ID KVIY HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=68362076; PubMed=5595110;
RA Hillemann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and

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RT Cum.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080 (1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hillemann N., Barikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Ster L., Matsubae S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulin: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23
KW DOMAIN 2 34
KW DOMAIN 3 49
KW DOMAIN 4 56
KW DOMAIN 5 57
KW DOMAIN 6 88
KW DOMAIN 7 97
KW DOMAIN 8 98
KW DOMAIN 9 107
KW DISULFID 23 88
KW NON_TER 108 108
KW BY SIMILARITY.
SQ SEQUENCE 108 AA; 11782 MW; F5ACDE5A313DF3A CRC64;

Query Match.
Best Local Similarity 84.1%; Pred. No. 2.8e-30; Length 108;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 147 NIQVTPSPSLASVGDVMTTCRASQDIRKMLNMYQKPGKAPKLYIDASDLETGIPS 206
DB 1 DIQVTPSPSLASVGDVMTTCRASQDIRKMLNMYQKPGKAPKLYIDASDLETGIPS 206
QY 207 RFGSGSGDFTLITSLSPEDTATYCCOQSYLPLTRGGGTVKDIK 253
DB 61 RFGSGSGDFTLITSLSPEDTATYCCOQSYLPLTRGGGTVKDIK 253

RESULT 4
ID KVIY HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RA MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers."
RL Biochemistry 33:14648-14657 (1994).
RN [2]
RP SEQUENCE OF 1-35.
RA MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;

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RT "Characterization and preliminary crystallographic data on the VL-related fragment of the human KI Bence Jones protein Mat.",
 RL J. Mol. Biol. 147:185-193 (1981).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB: 1MTL; 01-NOV-94.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; P:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KM DOMAIN 1 23
 FT 1 23
 FT 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT 107 88
 FT DISULFID 23 31
 FT CONFLICT 30 31
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT TURN 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT STRAND 80 82
 FT HELIX 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
 Query Match 34.7%; Score 468; DB 1; Length 108;
 Best Local Similarity 84.1%; Pred. No. 2.8e-30;
 Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 147 NIQTQSPSSLSASVGDRTVMTCTRASODIRKILNMYQOKRGKAPKYLITDASDLFTGIFS 206
 DB 1 DIQMTQSPSSLSASVGDRTVITCTRASQDITNYVMFQQRPGAPKYLITGASILETVGPS 60
 QY 207 RFGSGSGGDFILITISLQPEDIAITYCCQSDYLPPLTFGGGTRKVDIK 253
 DB 61 RFGSGSGGDFITFTTISLQPEDIAITYCCQYDILPLTFGGGTRKVDIK 107
 RESULT 5
 KVIQ_HUMAN STANDARD; PRT; 108 AA.
 AC P01554;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IG kappa chain V-1 region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN 11
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;

RA Schlecht H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
 RN 12
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlhämmer H., Schiffer M., Epp O., Coleman P.M., Lattman E.E.,
 RA Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146 (1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC PIR: A91653; KIHUAV.
 DR PDB: 1JVS; 30-JAN-02.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; P:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KM DOMAIN 1 23
 FT 1 23
 FT 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT DISULFID 23 31
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6F89 CRC64;
 Query Match 33.8%; Score 456; DB 1; Length 108;
 Best Local Similarity 81.3%; Pred. No. 2.5e-29;
 Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 147 NIQTQSPSSLSASVGDRTVMTCTRASODIRKILNMYQOKRGKAPKYLITDASDLFTGIFS 206
 DB 1 DIQMTQSPSSLSASVGDRTVITCTRASQDITNYVMFQQRPGAPKYLITGASILETVGPS 60
 QY 207 RFGSGSGGDFILITISLQPEDIAITYCCQSDYLPPLTFGGGTRKVDIK 253
 DB 61 RFGSGSGGDFITFTTISLQPEDIAITYCCQYDILPLTFGGGTRKVDIK 107
 RESULT 6
 KVIQ_HUMAN STANDARD; PRT; 108 AA.
 AC P01609;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-1 region scw.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN 11
 RP SEQUENCE.
 RX MEDLINE=75059271; PubMed=4435756;
 RA Eulitz M., Hilschmann N.;
 RT "The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein scw).";
 RT and the complete amino acid sequence.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866 (1974).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR: A01875; KIHUSW.

DR HSSP: P01607; IREI.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; P:antigen binding; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003596; IG_v.

DR Pfam: PF00047; Ig_v.

DR SMART: SM00406; IGV_1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108

SEQUENCE 108 AA; 11764 MW; 32CECDDP9644414 CRC64;

Query Match Best Local Similarity 33.2%; Score 448; DB 1; Length 108; Matches 84; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 147 NIQVTPSSLSASVDRVTMTCRASODIRKULNMYOQKPKAPVLIYDASDLETGIPS 206
1 DIQMTQSPSSLSASVDRVTITCOASQDIRKULNMYDQPKAPRLLIYGASTLETGIPS 60

DB 207 RFGSGSGTDFLTITSSLOPEDIAITYCOQSDYLPRTFGGKTVDIK 253
61 RFGSGSGTDFLTITSSLOPEDIAITYCOQSDYLPRTFGGKTVDIK 107

RESULT 7

KVLA_HUMAN

ID KVLA_HUMAN STANDARD; PRT; 108 AA.

AC P01593;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG kappa chain V-I region AG.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE.

RA MEDLINE=69234734; PubMed=4893682;

RA Titani K., Shinoda T., Putnam F.W.;

RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The

RT complete sequence and the location of the disulfide bridges.";

RL J. Biol. Chem. 244:3550-3560(1969).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC PIR: A01861; KIHUAG.

DR HSSP: P01607; IREI.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; P:antigen binding; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003596; IG_v.

DR Pfam: PF00047; IGV_1.

DR SMART: SM00406; IGV_1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 23 88 FRAMEWORK-4.

FT NON_TER 108 108

SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match Best Local Similarity 32.8%; Score 442; DB 1; Length 108; Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 147 NIQVTPSSLSASVDRVTMTCRASODIRKULNMYOQKPKAPVLIYDASDLETGIPS 206
1 DIQMTQSPSSLSASVDRVTITCOASQDIRKULNMYDQPKAPRLLIYGASTLETGIPS 60

DB 207 RFGSGSGTDFLTITSSLOPEDIAITYCOQSDYLPRTFGGKTVDIK 253
61 RFGSGSGTDFLTITSSLOPEDIAITYCOQSDYLPRTFGGKTVDIK 107

RESULT 8

KVLO_HUMAN

ID KVLO_HUMAN STANDARD; PRT; 108 AA.

AC P01607;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE IG kappa chain V-I region Rel.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE.

RA MEDLINE=76023758; PubMed=809329;

RA Palm W., Hilschmann N.;

RT "The primary structure of a crystalline monoclonal immunoglobulin

RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation

RT and characterization of the tryptic peptides; the complete amino acid

RT sequence of the protein; a contribution to the elucidation of the

RT three-dimensional structure of antibodies, in particular their

RT combining site.";

RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).

[2]

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RA MEDLINE=76039968; PubMed=182131;

RA Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions

RT of the Bence-Jones protein REI refined at 2.0-A resolution.";

RL Biochemistry 14:4943-4952(1975).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

CC PIR: A91663; KIHURE.

DR PDB: IREI; 17-FEB-84.

DR PDB: IAR2; 12-NOV-97.

DR PDB: 1BWV; 29-DEC-99.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; P:antigen binding; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003596; IG_v.

DR Pfam: PF00047; IGV_1.

DR SMART: SM00406; IGV_1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT STRAND 40 41
 FT STRAND 44 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT STRAND 56 57
 FT STRAND 60 61
 FT STRAND 62 67
 FT STRAND 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON TER 108
 SQ SEQUENCE 108 AA, 11902 MW, 9E8143E1188BCE2A CRC64;

Query Match 32.3%; Score 435; DB 1; Length 108;
 Best Local Similarity 78.3%; Pred. No. 1.1e-27;
 Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 147 NIQTQSPSSLSASVGDRTVMTCRASQDIRKINLMWYQKPGKAPKYLIDASDLGTGIPS 206
 DB 1 DIQTQSPSSLSASVGDRTVMTCRASQDIRKINLMWYQKPGKAPKYLIDASDLGTGIPS 60
 QY 207 RFGSGSGTDFLTITISLQPEDPATYCCQSDYLPFTFGGCTKVDI 252
 DB 61 RFGSGSGTDFLTITISLQPEDPATYCCQSDYLPFTFGGCTKVDI 106

RESULT 9
 KY1S_HUMAN
 ID KY1S_HUMAN STANDARD; PRT; 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DS Ig kappa chain V-I region Mes.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81092279; PubMed=6778806;
 RA Kretzlin H., Yang C., Krusche J.U., Hilschmann N.,
 RT "Preparative separation of the tryptic hydrolyzate of a protein by
 RT high-pressure liquid chromatography. I. The primary structure of a
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
 RT Mes)."
 CC Hope-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR: A01877; K1HWS.
 DR HSSP: P80352; 1MTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGv; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 98 107 FRAMEWORK-4.
 FT NON TER 108 BY SIMILARITY.
 SQ SEQUENCE 108 AA, 11608 MW, 782B14A649A60E45 CRC64;

Query Match 32.3%; Score 435; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 1.1e-27;
 Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 147 NIQTQSPSSLSASVGDRTVMTCRASQDIRKINLMWYQKPGKAPKYLIDASDLGTGIPS 206
 DB 1 DIQTQSPSSLSASVGDRTVMTCRASQDIRKINLMWYQKPGKAPKYLIDASDLGTGIPS 60
 QY 207 RFGSGSGTDFLTITISLQPEDPATYCCQSDYLPFTFGGCTKVDI 253
 DB 61 RFGSGSGTDFLTITISLQPEDPATYCCQSDYLPFTFGGCTKVDI 107

RESULT 10
 HV2B_HUMAN
 ID HV2B_HUMAN STANDARD; PRT; 120 AA.
 AC P01815;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region COR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 RT heavy chains."
 RT Biochem. J. 117:641-660 (1970).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02089; G1HUCO.
 DR HSSP: P01825; 7PAB.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGv; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 110 IG-LIKE
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 94
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).
 FT NON TER 120
 SQ SEQUENCE 120 AA, 13226 MW, 158A8B29AE7EBE98 CRC64;

Query Match 32.3%; Score 435; DB 1; Length 120;
 Best Local Similarity 69.0%; Pred. No. 1.2e-27;
 Matches 87; Conservative 10; Mismatches 23; Indels 6; Gaps 2;

QY 1 QVTLKSGPGLVKKPQTLLTCTFSGFSLSRTGEGVGMWROPKALBWLALTYMDDDR 60
 DB 1 QVTLKSGPGLVKKPQTLLTCTFSGFSLSRTGEGVGMWROPKALBWLALTYMDDDR 60
 QY 61 YPSLSKSLRTTKDTSKQVNLTMNVDPADATATYCTHEQYVYDTSQGVYDFPWGCT 120
 DB 61 YPSLSKSLRTTKDTSKQVNLTMNVDPADATATYCTHEQYVYDTSQGVYDFPWGCT 114

QY 121 LVTSS 126
DB 115 PVTSS 120

RESULT 11

KVIC_HUMAN
ID KVIC_HUMAN STANDARD; PRT; 108 AA.
AC P01595;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]

RP SEQUENCE.
RX MEDLINE=7029807; PubMed=4561064;
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT "Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT B1). 3. The complete amino acid sequence and the genetic
RT significance of the variability principles for the mechanism of
RT antibody formation."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01863; KIHU01.
DR HSSP; P01607; IRET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; I9_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SO SEQUENCE

Query Match 31.5%; Score 425; DB 1; Length 108;
Best Local Similarity 76.6%; Pred. No. 6.7e-27;
Matches 82; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 147 NIVTSPSSLSASVGDRTYMTCRASODIRKUNMYOQPKAPAVLYIDASDIETGIPS 206
DB 1 DIOMTSPSSLSASVGDRTYMTCRASODIRKUNMYOQPKAPAVLYIDASDIETGIPS 206
QY 207 RFGSGSGDFLTITSLQPEPIATYYCOQSDYPLTFGGGTXYDIK 253
DB 61 RRGSGSGDFLTITSLQPEPIATYYCOQSDYPLTFGGGTXYDIK 107

RESULT 12
KVLH_HUMAN
ID KVLH_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]

RP SEQUENCE.
RX MEDLINE=7053133; PubMed=5124396;
RA Milstein C.P., Deveron E.V.;
RT "The amino acid sequence of a human kappa light chain."
RT Biochem. J. 123:945-958(1971).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01865; KIHU01.
DR HSSP; P01607; IRET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]

RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Han): subdivision within
RT subgroupa."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01868; KIHU01.
DR HSSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; I9_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SO SEQUENCE

Query Match 31.5%; Score 425; DB 1; Length 108;
Best Local Similarity 76.6%; Pred. No. 6.7e-27;
Matches 82; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
QY 147 NIVTSPSSLSASVGDRTYMTCRASODIRKUNMYOQPKAPAVLYIDASDIETGIPS 206
DB 1 DIOMTSPSSLSASVGDRTYMTCRASODIRKUNMYOQPKAPAVLYIDASDIETGIPS 206
QY 207 RFGSGSGDFLTITSLQPEPIATYYCOQSDYPLTFGGGTXYDIK 253
DB 61 RRGSGSGDFLTITSLQPEPIATYYCOQSDYPLTFGGGTXYDIK 107

RESULT 13
KVLH_HUMAN
ID KVLH_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]

RP SEQUENCE.
RX MEDLINE=7053133; PubMed=5124396;
RA Milstein C.P., Deveron E.V.;
RT "The amino acid sequence of a human kappa light chain."
RT Biochem. J. 123:945-958(1971).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01865; KIHU01.
DR HSSP; P01607; IRET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

QY 147 NIVTSPSSLSASVGDRTYMTCRASODIRKUNMYOQPKAPAVLYIDASDIETGIPS 206
DB 1 DIOMTSPSSLSASVGDRTYMTCRASODIRKUNMYOQPKAPAVLYIDASDIETGIPS 206
QY 207 RFGSGSGDFLTITSLQPEPIATYYCOQSDYPLTFGGGTXYDIK 253
DB 61 RRGSGSGDFLTITSLQPEPIATYYCOQSDYPLTFGGGTXYDIK 107

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 147 NIQVTPSSLSASVGDRTVMTCRASQDIRKNIWMYQOKRGPAPKVLIDASDLFTGIPS 206
DB 1 BIZMTQSPSSLSASVGDRTVITCRAGSYNKYIMYQOKRGPAPKVLIFASSLSKGVPS 60
QY 207 RFGSGSGTDFILTTISLQPEDIAITYCCQSDVLPFTFGGTRKVDI 252
DB 61 RFGSGSGTDFILTTISLQPEDFATYYCCQSYTTPFTFGGTRKVM 106

RESULT 14
KVIV HUMAN STANDARD; PRT; 108 AA.
AC P04430.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=86174817; PubMed=3083240;
RT Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL MOL. Immunol. 23:73-78(1986).
DR PIR: A01878; KIHUBN.
DR HSSP: P80362; IMTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944F936FD37 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

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QY 147 NIQVTPSSLSASVGDRTVMTCRASQDIRKNIWMYQOKRGPAPKVLIDASDLFTGIPS 206
DB 1 DIQVTPSSLSASVGDRTVITCRASQSYNVVAMFQOKRGPAPKVLIDASLSQGVPS 60
QY 207 RFGSGSGTDFILTTISLQPEDIAITYCCQSDVLPFTFGGTRKVDI 253
DB 61 RFGSGSGTDFILTTISLQPEDFATYYCCQNSYPTFTFGGTRVQIK 107

RESULT 15
KVIV HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=85014148; PubMed=6091049;
RX Klobeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; KIHOMK.
DR HSSP: P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 FRAMEWORK-3.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AF2F9 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 129;
Matches 83; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 143 GGGNIQVTPSSLSASVGDRTVMTCRASQDIRKNIWMYQOKRGPAPKVLIDASDLFT 202
DB 19 GARCDIQVTPSSLSASVGDRTVITCRASQISNVLMYQOKRGPAPKVLIDASSLSQ 78
QY 203 GIPRFGSGSGTDFILTTISLQPEDIAITYCCQSDVLPFTFGGTRKVDI 253
DB 61 GIPRFGSGSGTDFILTTISLQPEDFATYYCCQSDVLPFTFGGTRKVDI 107

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Db 79 GVTSRFSGSGSTDFLLISLQPEDSATYCCQSYSTLITFGQTRLEIK 129

Search completed: May 13, 2004, 15:02:05
Job time : 8.1233 secs

DR HSPF, P01825; 7EAB.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 FT NON_TER 1 121
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 40.8%; Score 549.5; DB 4; Length 121;
 Best Local Similarity 82.5%; Pred. No. 1e-39;
 Matches 104; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY 1 QVTLKESGPTLVKPTOTLTCTFSGFSRTTGEVGVWROPKALEMLALTYWDDK 60
 DB 1 QVTLKESGPTLVKPTOTLTCTFSGFSRTTGEVGVWROPKALEMLALTYWDDK 60
 QY 61 YSPSLKSRLLTKDTSKKQVLTMTNVPADPATYCTHBOYYDTSGQPYFDFWGGGT 120
 DB 61 YSPSLKSRLLTKDTSKKQVLTMTNVPADPATYCTHBOYYDTSGQPYFDFWGGGT 115
 QY 121 LVTWSS 126
 DB 116 LVTWSS 121

RESULT 5

Q925S1 PRELIMINARY; PRT; 218 AA.
 AC 0925S1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MRP5 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Ren D., Zhao T., Li X.,
 RA Su C.;
 RA "Mechanism of exogenous nucleic acids and their precursors improving
 RT the repair of intestinal epithelium after irradiation in mice.";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain.";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL: AF240168; AAK43733.1; -.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PR00047; Ig; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 FT NON_TER 218
 FT NON_TER 218
 SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 36.8%; Score 496.5; DB 11; Length 218;
 Best Local Similarity 44.8%; Pred. No. 7.8e-35;
 Matches 103; Conservative 42; Mismatches 66; Indels 19; Gaps 6;
 QY 1 QVTLKESGPTLVKPTOTLTCTFSGFSRTTGEVGVWROPKALEMLALTYWDD-K 59
 DB 3 QVTLKESGPTLVKPTOTLTCTFSGFSRTTGEVGVWROPKALEMLALTYWDD-K 60

QY 60 RYPSLSKSRLLTKDTSKKQVLTMTNVPADPATYCTHBOYYDTSGQPYFDFWGGG 119
 DB 61 KYAEFPKGFARFASLETSAITLQISNLKNEITATYFCM--RWDIDG-----FAWGGG 113
 QY 120 TLVTWSSGGGGGGGGGGGGGGGSGNSIQVTSFSSLSASVGDRTVMTCRASQDIR--- 176
 DB 114 TLVTWSS-----SGGGGGGGGGGGGGGSDIVLTQSPASLAVSICQRTATISCRASESVNDIG 168
 QY 177 -KNLWYQQKPGKARKVLIYDASDETGPSPFSSGSGSTDPILRTISSIQ 225
 DB 169 ISFMWVPOKPGQPPRLIYVASSKQSGVPAGILASGSDTDFSLNLYPME 218

RESULT 6

Q811U5 PRELIMINARY; PRT; 118 AA.
 AC 0811U5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-human Fc gamma receptor III 368 gamma heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Bruenke J., Valerius T., Repp R., Fey G.H.;
 RL Submitted (NOV-2002) to the EMBL/Genbank/DDA databases.
 DR EMBL: AY173025; ANO18227.1; -.
 DR GO: GO:004872; F:receptor activity; IEA.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PR00047; Ig; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR Receptor.
 FT NON_TER 1
 FT NON_TER 118
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12979 MW; F57BB07033742B99 CRC64;

Query Match 33.4%; Score 450; DB 11; Length 118;
 Best Local Similarity 66.7%; Pred. No. 3.6e-31;
 Matches 84; Conservative 17; Mismatches 17; Indels 8; Gaps 1;

QY 1 QVTLKESGPTLVKPTOTLTCTFSGFSRTTGEVGVWROPKALEMLALTYWDDK 60
 DB 1 QVTLKESGPTLVKPTOTLTCTFSGFSRTTGEVGVWROPKALEMLALTYWDDK 60
 QY 61 YSPSLKSRLLTKDTSKKQVLTMTNVPADPATYCTHBOYYDTSGQPYFDFWGGGT 120
 DB 61 YSPSLKSRLLTKDTSKKQVLTMTNVPADPATYCTHBOYYDTSGQPYFDFWGGGT 112
 QY 121 LVTWSS 126
 DB 113 LVTWSS 118

RESULT 7

Q96SA9 PRELIMINARY; PRT; 107 AA.
 AC 096SA9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
  rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
  antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL: U96396; AA68785.1; -.
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR InterPro: IPR007110; Ig_1like.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER
FT
SQ SEQUENCE 107 AA; 11520 MW; 4B843B9C5B577F16 CRC64;

Query Match
Best Local Similarity 82.2%; Score 448.5; DB 4; Length 107;
Matches 88; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 147 NIQVTPSSLSASVGDRTVMTCRASODIRKLNMYQKPGKAPVLYDASDLETGIPS 206
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNMYQKPGKAPVLYDASDLETGIPS 60
Qy 207 RFSGSGGTDFLTITSLQPEDIATYYCOQSDYLPFTFGGTGYDIR 253
Db 61 RFSGSGGTDFLTITSLQPEDPATYYCOQSYSTLTFGGGTGYEIK 106

RESULT 8
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
  (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AA056273.1; -.
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR HSP: P01607; IREI.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER
FT
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 78.5%; Score 429; DB 4; Length 108;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=1468171;
RA Covenno R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:

Qy 147 NIQVTPSSLSASVGDRTVMTCRASODIRKLNMYQKPGKAPVLYDASDLETGIPS 206
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNMYQKPGKAPVLYDASDLETGIPS 60
Qy 207 RFSGSGGTDFLTITSLQPEDIATYYCOQSDYLPFTFGGTGYDIR 253
Db 61 RFSGSGGTDFLTITSLQPEDPATYYCOQSYSTLTFGGGTGYEIK 107

RESULT 9
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
  (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035033; AA056269.1; -.
DR HSP: P01607; IREI.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER
FT
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 78.5%; Score 424.5; DB 4; Length 107;
Matches 84; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 147 NIQVTPSSLSASVGDRTVMTCRASODIRKLNMYQKPGKAPVLYDASDLETGIPS 206
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNMYQKPGKAPVLYDASDLETGIPS 60
Qy 207 RFSGSGGTDFLTITSLQPEDIATYYCOQSDYLPFTFGGTGYDIR 253
Db 61 RFSGSGGTDFLTITSLQPEDPATYYCOQSYSTLTFGGGTGYEIK 106

RESULT 10
Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=1468171;
RA Covenno R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
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RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.
RL Blood 98:714-720(2001).
DR EMBL: AF361758; AAK51465.1; -.
DR InterPro: IPR007110; Ig_V.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFC57 CRC64;

Query Match
Best Local Similarity 74.8%; Score 423; DB 4; Length 116;
Matches 80; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 147 NIQVTPSSLSASVGDVMTTCRASQDIRKINLMWYQOKPGKAPKLYIDASDLRTGIPS 206
DB 1 DIQMTQSPSSLSASVGDVMTTCRASQDIRKINLMWYQOKPGKAPKLYIDGSLTKGVPS 60
QY 207 RSSGSGSGTDFLTITSSLOPEDVATYYCOQSDYLPITFGGKTVNDIK 253
DB 61 RSSGSGSATNFTVITSSLOPEDVATYYCOQYHMLPTFGPGTKVDFK 107

RESULT 11
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR PIR: PH0863; PH0863.
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; Ig_V-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match
Best Local Similarity 75.7%; Score 419; DB 4; Length 108;
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 147 NIQVTPSSLSASVGDVMTTCRASQDIRKINLMWYQOKPGKAPKLYIDASDLRTGIPS 206
DB 1 DIQMTQSPSSLSASVGDVMTTCRASQDIRKINLMWYQOKPGKAPKLYIDGSLTKGVPS 60
QY 207 RSSGSGSGTDFLTITSSLOPEDVATYYCOQSDYLPITFGGKTVNDIK 253
DB 61 RSSGSGSGTDFLTITSSLOPEDVATYYCOQYHMLPTFGPGTKVDFK 107

RESULT 12

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Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
ID Q7Z3Y4;
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R., Sanchez A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Trimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RX MEDLINE=12477932; PubMed=12477932;
RA Strausberg R.,
RA Submitter (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC005332; AAH05332.1; -.
DE Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match
Best Local Similarity 73.0%; Score 416; DB 4; Length 236;
Matches 81; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 143 GGSNINQVTPSSLSASVGDVMTTCRASQDIRKINLMWYQOKPGKAPKLYIDASDLRT 202
DB 19 GARCIDIQMTQSPSSLSASVGDVMTTCRASQDIRKINLMWYQOKPGKAPKLYIDGSLTK 78
QY 203 GIPSRFSGSGSGTDFLTITSSLOPEDVATYYCOQSDYLPITFGGKTVNDIK 253
DB 79 GVQSKFSGSGSGTDFLTITSSLOPEDVATYYCOQYHMLPTFGPGTKVDFK 129

RESULT 13
Q91WS9 PRELIMINARY; PRT; 233 AA.
ID Q91WS9;
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=10090;
RA Strausberg R.,

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RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC013496; AAH13496.1.
 DR InterPro: IPR007110; IG_1ike.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00406; IGv. 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match
 Best Local Similarity 28.9%; Score 390; DB 11; Length 233;
 Matches 75; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 143 GGGSNIGVTPSSLSASVGDRTYMTGRASQDIRKRLNMYQKPGKAPVLYDASDLET 202
 DB 16 GSRCDIOMTVTSLASIGDRVTYISGSGSGCIAYLWYQKPGVTKLIITYTSLHS 75
 QY 203 GTPSRFSGSGGTDFLTITSLQPEDYATYCCQSDYLPITFGGTXDK 253
 DB 76 GTPSRFSGSGGTDFLTITSLQPEDYATYCCQYRILPMTFGGTXDK 126

RESULT 14
 ID 072473 PRELIMINARY; PRT; 234 AA.
 AC 072473;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DS Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Reinhold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh N.K.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonalyuk S., Carninci P., Prange C.,
 RA Brownstein M.J., Udell T.B., Toshyuk S., Abramson R.D., Mullany S.J.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.C.,
 RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Mitra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC056256; AAH56256.1;
 KM Hypothetical protein.
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BCOF CRC64;

Query Match
 Best Local Similarity 28.7%; Score 387; DB 4; Length 234;
 Matches 69.4%; Pred. No. 2.3e-25;

Matches 77; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 143 GGGSNIGVTPSSLSASVGDRTYMTGRASQDIRKRLNMYQKPGKAPVLYDASDLET 202
 DB 17 GARCALRMQSPSSPFSASQDRVTYITCRASQSGSYLWYQKPGKAPVLYDASDLET 76
 QY 203 GTPSRFSGSGGTDFLTITSLQPEDYATYCCQSDYLPITFGGTXDK 253
 DB 77 GTPSRFSGSGGTDFLTITSLQPEDYATYCCQYRILPMTFGGTXDK 127

RESULT 15
 ID 043234 PRELIMINARY; PRT; 97 AA.
 AC 043234;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DS Rheumatoid factor RF-ET13 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borreszen M., Natvig J.B., Thompson K.M.;
 RT "Heterogenous RF structures between and within healthy individuals are
 RT not related to HLA DRB1*0401.";
 RL Mol. Immunol. 0:0-0(1997).
 DR EMBL: AF035802; AAB88534.1;
 DR HSP; P01789; IMCP.
 DR InterPro: IPR007110; IG_1ike.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IGv. 1.
 DR SMART: SM00406; IGv. 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9A812D CRC64;

Query Match
 Best Local Similarity 28.5%; Score 384; DB 4; Length 97;
 Matches 73; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
 QY 3 TLKSGPTLVKPGQTLITCTSGSRLRTTGGVGVWVQPPGKALEWLYTMDDDKYS 62
 DB 1 TLKSGPALVKPELTITCTVSGFSLSNRMGVSWINQPPGKAVEMLAHIFANDKSY 60
 QY 63 PSIKSLRTTKDTSKKQVLTWTVNDPADTATYTC 97
 DB 61 TSIKSLRTISKOTSKSQVLTWTVNDPADTATYTC 95

Search completed: May 13, 2004, 15:06:58
 Job time : 35.0199 secs

Query Match 58.4%; Score 768.5; DB 4; Length 245;
 Best Local Similarity 62.4%; Pred. No. 2.9e-45;
 Matches 159; Conservative 30; Mismatches 53; Indels 13; Gaps 4;

QY 1 QVTLKSGPTLVKPKQTTLTCTLSGFSLSSTGVSVGMIRPPGKALEMILASIMNDDKC 60
 Db 1 EVQLVDSGGGLVQPGGSLRLSCAASGFTFSYAMS--WVQAPQKGLMWSAISGSGSGST 58
 QY 61 -YSPSLKSRLLITTDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPOSFASDVMGP 119
 Db 59 YIASVVKRFTISIDNSKNTLYLQMSLRADTAVYYCA-----RYSFSPVPMWQ 109
 QY 120 GTMTVSSGGGSGGSGGSGGSGGSGSYELMQLPSVSVSPQGTASITCSGDNLAGDKYA 179
 Db 110 GTLVTVSSAGGSGGSGGSGGSGGSDIELQPSVSAPEQTAIRISCGDALGDYKA 169
 QY 180 CMYQKPKRSPVLYVYGDNRPGGIPRFRSGNSGNTATLTISGTQAMDEADYCOAMD 239
 Db 170 SMYQKPGQAPVLYVYDDSDRPSGIPRFRSGNSGNTATLTISGTQADEADYCOASTDN 229
 QY 240 -STAVFGTGTKLTVL 253
 Db 230 FDSPVFGGGLTVL 244

RESULT 2
 ABP45537
 ID ABP45537 standard; protein; 250 AA.
 AC ABP45537;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Bly's binding scFv SEQ ID 1548.
 XX
 KM Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antitumoric;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 BN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 PS Claim 1; Page 2250-2251; 3148pp; English.
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Bly's) super family and induces B cell
 CC tumour necrosis factor (TNF) proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antitumoric and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Bly's. The antibodies bind to Bly's
 CC and so may be used to detect and quantitate the presence of Bly's in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Bly's. They may also be
 CC administered to treat diseases associated with aberrant Bly's expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 250 AA;

Query Match 58.0%; Score 783; DB 5; Length 250;
 Best Local Similarity 63.5%; Pred. No. 6.8e-45;
 Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

QY 1 QVTLKSGPTLVKPKQTTLTCTLSGFSLSSTGVSVGMIRPPGKALEMILASIMNDDKC 60
 Db 1 QVQLDSGPGLVKPSSETLTCAVSGYSIS--SGYWGIRPPGKGLMGLSTIHSSTY 59
 QY 61 YSPSLKSRLLITTDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPOSFASDVMGP 120
 Db 60 YNPSLKSRVLTISVDISKQPSLKSSVTAADTAVYYCA--RVHYDILVGYLAFDIMGQ 117
 QY 121 TMVTVSSGGGSGGSGGSGGSGGSGSYELMQLPSVSVSPQGTASITCSGDNLAGDKYC 180
 Db 118 TMVTVSSGGGSGGSGGSGGSGGSDIELQPSVSAPEQTAIRISCGDALGDYKA 174
 QY 181 WYQKPKRSPVLYVYGDNRPGGIPRFRSGNSGNTATLTISGTQAMDEADYCOAMD 240
 Db 175 WYQKPGQAPVLYVYDDSDRPSGIPRFRSGNSGNTATLTISGTQADEADYCOASTDN 234
 QY 241 --TVFRTGTGTKLTVL 253
 Db 235 GNVHVFGGGLTVL 249

RESULT 3
 ABP45640
 ID ABP45640 standard; protein; 247 AA.
 AC ABP45640;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Bly's binding scFv SEQ ID 1651.
 XX
 KM Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antitumoric;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 BN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

(CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PA Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX MPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2373-2374; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antitumoric and anti-AIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABA43990-ABA47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX Sequence 247 AA;

XX Query Match 57.7%; Score 779.5; DB 5; Length 247;

XX Best Local Similarity 60.5%; Pred. No. 1.2e-44; Mismatches 44; Indels 33; Gaps 5;

XX Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;

XX 1 QVTLKSGPTLVPTOTLTCTLTSGFSLTSGSVGMIRQPPKALEMLASINMDDKC 60

XX 1 QVQLQSGPGPLVAPSETSLTCTVSNYSIS-SCGYNCMIQPPKALEMLASINMDDKC 59

XX 61 YSPSLKSLTITTDTPRQNVLAISMNDPADTATYSCA-----LDMPPHDSGPQ 109

XX 60 YNPSLKSRLVITSDTSKNGFSLKLSVTADTAIVYCARFRYDILNGYYDM----- 111

XX 110 SPFASDVWGPGTWTWTSSSGGSGSGSGSGSGSGSGSSSTELMOLSVSVSPQOTASITC 169

XX 112 -----YWGKGLVTVYSSGGSGSGSGSGSGSGSS-----ELTQDPAVSVLAQQTIVRTIC 160

XX 170 SGDNLDKRCACWYQQRGRSPVAVIYGDNRKPSGIPERFSGNSGNTATLTISGTOAMDE 229

XX 161 QGDSLNSYASWYQQRGAPVAVIYGNKRPISGIPDRFSGSSGNTASLTITGAQADE 220

XX 230 ADYVQAMDTST--TAVFGTGTCLTVL 253

XX 221 ADYVQAMDTST--TAVFGTGTCLTVL 246

XX 230 ADYVQAMDTST--TAVFGTGTCLTVL 253

XX 221 ADYVQAMDTST--TAVFGTGTCLTVL 246

XX 230 ADYVQAMDTST--TAVFGTGTCLTVL 253

XX 221 ADYVQAMDTST--TAVFGTGTCLTVL 246

XX 230 ADYVQAMDTST--TAVFGTGTCLTVL 253

XX 221 ADYVQAMDTST--TAVFGTGTCLTVL 246

XX 230 ADYVQAMDTST--TAVFGTGTCLTVL 253

XX 221 ADYVQAMDTST--TAVFGTGTCLTVL 246

XX 230 ADYVQAMDTST--TAVFGTGTCLTVL 253

XX 221 ADYVQAMDTST--TAVFGTGTCLTVL 246

KM polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;
KM infectious disease; acquired immunodeficiency syndrome; viral infection;
KM AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;
KM ischaemic injury; myocardial infarction; reperfusion injury; cachexia;
KM anorexia; stroke; cardiovascular disorder; peripheral artery disease;
KM limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;
KM ocular disorder; wound healing; angiogenesis; transplantation.

XX Unidentified.

XX Key Location/Qualifiers

XX Domain 1..125

XX Region 25..35

XX Region 50..66

XX Region 99..114

XX Region 142..249

XX Region 164..174

XX Region 190..196

XX Region 229..238

XX Region 255..264

XX Region 281..290

XX Region 307..316

XX Region 323..332

XX Region 349..358

XX Region 375..384

XX Region 391..400

XX Region 417..426

XX Region 443..452

XX Region 469..478

XX Region 495..504

XX Region 521..530

XX Region 547..556

XX Region 573..582

XX Region 599..608

XX Region 625..634

XX Region 651..660

XX Region 677..686

XX Region 703..712

XX Region 729..738

XX Region 755..764

XX Region 781..790

XX Region 807..816

XX Region 833..842

Accession	Protein	Gene	Organism	Source	Accession	Protein	Gene	Organism	Source
1	26-AUG-1999,	99EP-00116691.			1	26-AUG-1999,	99EP-00116691.		
2	28-AUG-2000,	2000WC-EP008388.			2	28-AUG-2000,	2000WC-EP008388.		
3	01-MAR-2001.				3	01-MAR-2001.			
4	WO200114558-A1.				4	WO200114558-A1.			
5	Homo sapiens.				5	Homo sapiens.			
6	Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_5.				6	Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_5.			
7	Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;				7	Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;			
8	miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.				8	miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.			
9	29-MAY-2001 (first entry)				9	29-MAY-2001 (first entry)			
10	AAB67621,				10	AAB67621,			
11	AAB67621 standard; protein; 245 AA.				11	AAB67621 standard; protein; 245 AA.			
12	RESULT 5				12	RESULT 5			

25-AUG-1999. 988D-00116601
 28-AUG-2000, 2000MO-EP008388.
 01-MAR-2001.
 WO200114558-A1.
 Homo sapiens.
 Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing; miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
 Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_6.
 29-MAY-2001 (first entry)
 AAB67622;
 AAB67622 standard; protein; 245 AA.

```

XX (MORP-) MORPHOSYS AG.
PA Kretschmar T, Tesar M, Marget M, Kroenke M;
PI MPI; 2001-218451/22.
XX
XX Novel isolated human immunoglobulin or functional immunoglobulin fragment
PT specific for human leukocyte antigen Cw6, useful for treatment of humans
PT and for human leukocyte antigen phenotyping.
XX
XX Claim 3; Fig 1; 23pp; English.
XX
CC AAB6717-23 represent single chain antibody (scFv) fragments which are
CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
CC from a synthetic human combinatorial antibody library based on molecular
CC consensus frameworks and CDRs randomised with trinnucleotides. The
CC specification describes a human immunoglobulin fragments specific for HLA
CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
CC natural killer cell silencing as well as miscarriages. HLA-Cw6
CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may
CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
CC useful for the preparation of a pharmaceutical for the treatment of
CC humans. They are also useful for HLA phenotyping
XX
SQ Sequence 245 AA;
Query Match 55.8%; Score 753.5; DB 4; Length 245;
Best Local Similarity 60.3%; Pred. No. 6.3e-43;
Matches 155; Conservative 29; Mismatches 56; Indels 17; Gaps 5;
QY 1 OYTLKSGPTLVKPKQTLLTCTLSGFSISTSVSGWIRPPKALWLASINMND-DK 59
DB 1 EVQLVDSGAEVKKPGESLKISCKSGSYFTS--YWGWRQMPKGLWMMGIYPSDST 58
QY 60 CYSPLSKRLITTKDTPKQVVLAMSNMPPADATATSCALDMPHDSGQSPD--ASDV 117
DB 59 RSPSPFGQVITISADKSISTAYIQWSLSASDPMATYCA-----RDMFPIIDY 107
QY 118 GPGTMTVSSGGGSGGGSGGGSGGGSSYELWQLPSVSVSPGQTASITSCGDLGDK 177
DB 108 GGTITLVTSAGSGSGGGSGGGSGGGSDIELTQPPSVSVAPGQTARISCSGDALGDK 167
QY 178 YACWYQKRGSRVLYVYGDNKRPSGIPRFGSGNSGNATLTISTGQAMDEADYVCOAM 237
DB 168 YASWYQKRGQAPVLYVYDSDRPSGIPRFGSGNSGNATLTISTGQADEADYVCOAY 227
QY 238 DTST-AVFGNGTKLTVL 253
DB 228 DSDSYLVFPGGKTLTVL 244

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FT FT /label= VH_FR2
FT FT 50. .65
FT FT /label= VH_CDR2
FT FT 67. .97
FT FT /label= VH_FR3
FT FT 98. .104
FT FT /label= VH_CDR3
FT FT 106. .116
FT FT /label= VH_FR4
FT FT 117. .131
FT FT /label= Linker
FT FT 132. .152
FT FT /label= VL_FR1
FT FT 154. .164
FT FT /label= VL_CDR1
FT FT 165. .178
FT FT /label= VL_FR2
FT FT 180. .186
FT FT /label= VL_CDR2
FT FT 187. .218
FT FT /label= VL_FR3
FT FT Misc-difference 209
FT FT /note= "Encoded by ACG"
FT FT Region 219. .226
FT FT /label= VL_CDR3
FT FT 228. .237
FT FT /label= VL_FR4
FT FT Misc-difference 234
FT FT /note= "Encoded by GTC"
XX
XX WO2003048337-A2.
XX
XX 12-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US038849.
XX
XX 04-DEC-2001; 2001US-037294P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Marasco WA, Gennari F;
XX
XX MPI; 2003-482710/45.
XX
XX N-PSDB; ACC84103.
XX
XX Novel antibody to extracellular epitopes of Epstein Barr Virus latent
XX membrane protein, useful for prevention and treatment of diseases caused
XX by Epstein-Barr Virus, e.g. malignancies and lymphoproliferative
XX diseases.
XX
XX Disclosure; Page 20; 52pp; English.
XX
XX The present sequence is the protein sequence of anti-Epstein-Barr virus
XX (EBV) latent membrane protein (LMP) scFv FG-1. The scFv was isolated from
XX a human antibody phage display library. It comprises a DP-88/hv1051K VH
XX germline and 3r.9C5/DP123 VL germline. It is an example of antibodies of
XX the invention directed against EBV LMP proteins (LMP1, LMP2A or LMP2B).
XX Claimed methods of generating an immune reaction comprise administering
XX an antibody with specificity for EBV LMP, or an immune cell endowed with
XX antibody specificity for an EBV LMP by transformation, to an individual
XX having an EBV-associated disease such as malignancy, Hodgkin's disease,
XX chronic EBV syndrome or oral hairy cell leukoplakia. The malignancy is
XX especially Burkitt's lymphoma, lymphoproliferative disease, B-
XX lymphoproliferative disease, non-Hodgkin's lymphoma (NHL), T-NHL, NK-NHL,
XX lymphomasopharyngeal carcinoma or gastric carcinoma. Alternatively, the
XX lymphocytes of an individual having an EBV associated malignancy are
XX transformed with a chimeric gene encoding e.g. a single chain antibody as
XX a means of treatment
XX
XX Sequence 237 AA;
Query Match 55.7%; Score 753; DB 6; Length 237;
Best Local Similarity 59.2%; Pred. No. 6.6e-43;

```

Matches 154; Conservative 25; Mismatches 51; Indels 30; Gaps 5;
 QY 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSGVSVMIRPQKALEWLASI----- 53
 Db 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSGVSVMIRPQKALEWLASI----- 53
 QY 54 NMDNDKCYSPSLKRLTITKDTKPNQVVLAMSNMADPADTATYSCALDMPHDSGPFDA 113
 Db 59 N-----YAKFGQRTVITADKSTAYMELSLREBDIAVYCA-----KRGDG 102
 QY 114 SDVWPGMTVTVSSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 173
 Db 103 MDVWGGQTLTVTVSSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 157
 QY 174 LGDKYACWYQKRGSPVLVIYGDNRPSGIPERFSGNSGNTATLTISGQAMDEADY 233
 Db 158 LGNRVYMWYQKRGSGPVLVIYQDRKRPSGIPERFSGNSGNTATLTISGQAMDEADY 217
 QY 234 QAMDTSTAVFGTGTCLTVL 253
 Db 218 QAMASGTGVFGTGTCLTVL 237

RESULT 8
 AAB67623
 ID AAB67623 standard; protein, 245 AA.
 AC AAB67623;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_7.
 XX
 KW Human leukocyte antigen, HLA; HLA-Cw6; natural killer cell silencing;
 XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
 OS Homo sapiens.
 XX
 FN WO200114558-A1.
 XX
 PD 01-MAR-2001.
 XX
 PF 28-AUG-2000; 2000WO-EP008388.
 XX
 PR 26-AUG-1999; 99EP-00116691.
 XX
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Kretzschmar T, Teasar M, Marget M, Kroenke M;
 XX WPI; 2001-218451/22.
 DR
 XX
 PT Novel isolated human immunoglobulin or functional immunoglobulin fragment
 PT specific for human leukocyte antigen Cw6, useful for treatment of humans
 PT and for human leukocyte antigen phenotyping.
 XX
 PS Claim 3; Fig 1; 23pp; English.
 XX
 CC AAB67617-23 represent single chain antibody (scFv) fragments which are
 CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
 CC from a synthetic human combinatorial antibody library based on molecular
 CC consensus frameworks and CDRs randomised with trinucleotides. The
 CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
 CC natural killer cell silencing as well as miscarriages. HLA-Cw6
 CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may
 CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
 CC useful for the preparation of a pharmaceutical for the treatment of
 CC humans. They are also useful for HLA phenotyping
 CC
 SQ Sequence 245 AA;

Query Match 55.7%; Score 752.5; DB 4; Length 245;

Best Local Similarity 60.0%; Pred. No. 7.4e-43;
 Matches 153; Conservative 31; Mismatches 58; Indels 13; Gaps 4;
 QY 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSGVSVMIRPQKALEWLASI----- 53
 Db 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSGVSVMIRPQKALEWLASI----- 53
 QY 60 CYSPSLKRLTITKDTKPNQVVLAMSNMADPADTATYSCALDMPHDSGPFDA 119
 Db 59 RYPSFGQVITADKSTAYMELSLREBDIAVYCA-----MDNMG 109
 QY 120 GTWTVTVSSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 179
 Db 110 GTLVTVSSAGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 169
 QY 180 CWYQKRGSPVLVIYGDNRPSGIPERFSGNSGNTATLTISGQAMDEADY 238
 Db 170 SWYQKRGSPVLVIYQDRKRPSGIPERFSGNSGNTATLTISGQAMDEADY 229
 QY 239 TSTAVFGTGTCLTVL 253
 Db 230 FRDVVFGGTGTCLTVL 244

RESULT 9
 AAB02186
 ID AAB02186 standard; protein, 280 AA.
 AC AAB02186;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE PAM2 single chain variable region (scFv) antibody.
 XX
 KW Pectin; PAM1 antibody; single chain variable region; scFv; food; jam;
 XX yogurt; gel; homogalacturonan; HG; plant cell wall.
 XX
 OS Unidentified.
 XX
 FN
 XX
 PD Key Location/Qualifiers
 FT 1..22 /label=pe1B_leader_sequence
 FT 23..138 /label=Heavy_chain_fragment
 FT 139..154 /label=Linker
 FT 155..275 /label=Light_chain_fragment
 FT 265..275 /label=Myc_epitope
 FT Misc-difference 279..80 /note="Encoded by TAGACT"
 FT
 XX
 FN US6228599-B1.
 XX
 PD 08-MAY-2001.
 XX
 PF 26-FEB-1999; 99US-00260527.
 XX
 PR 24-DEC-1998; 98GB-00028700.
 XX
 PA (DANI-) DANISCO AS.
 XX
 PI Knox JP, Willats WGT, Mikkelsen JD;
 XX WPI; 2001-342672/36.
 DR N-PADB; AAD06194.
 DR
 XX
 PT New PAM1 and PAM2 antibodies capable of binding de-esterified
 PT homogalacturonan, useful for identifying a pectin moiety, for quantifying
 PT the amount of pectin in a sample or for extracting pectin from a sample.
 XX
 PS Claim 2; Fig 4B; 21pp; English.

PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMS-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI, 2002-114799/15.
 DR
 XX
 XX

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 XX

PS Claim 1, Page 2746-2747, 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC acquired immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC

SQ Sequence 254 AA;

Query Match 55.3%; Score 747; DB 5; Length 254;
 Best Local Similarity 59.8%; Pred. No. 1.8e-42;
 Matches 155; Conservative 34; Mismatches 58; Indels 12; Gaps 5;

QY 1 QVTLKESGPTLVKPNQTLTLCTLSGSLSTGVSVMIRPPKALMLASINMNDKC 60
 DB 1 QVQLQESGPGLVESGTLISLTCAVSGASISSNNL-MSWVQPPGKGLMIGELIYSGS 59
 QY 61 YSPSLKRLITTKDTPKQVVLAMSNMDDPDATYSCALDMPHDSGPOS---FDASDV 116
 DB 60 YNPSLRGRVITISVSKSTNPSLKLITVTDLTIVYICADY--YDSSSYSSGDYYIMDV 117
 QY 117 WGPRTMTVSSGGGSGGGSGGGSGGGSGGGSYELMQLPSVSVPQQTASITCSGDNIGD 176
 DB 118 WGGITVTVSSGGGSGGGSGGGSGGGSGGG---ALSYELTQPPSVSPQQTATITCSGDALPK 174
 QY 177 KVACWYQOKPRSPVLVIYGNKRPSGIPERFSGNSGNTATLTISGQAMDEADYCOA 236
 DB 175 QNAYWYQOKRQGAFLVIYRDSERRSGIPERFSGSGTATLTISGVADEADYCOA 234
 QY 237 WDTSTA--VPGTGTKLTVL 253
 DB 235 ADSTSYIVFGGKTIVL 253

RESULT 12
 ABP45469
 ID ABP45469 standard; protein; 250 AA.
 XX
 AC ABP45469;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 XX Human BLyS binding scFv SEQ ID 1480.
 DE BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS
 XX Homo sapiens.
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX

PR 16-MAR-2001; 2001US-0293499P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMS-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI, 2002-114799/15.
 XX

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1, Page 2169-2170, 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC acquired immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC

SQ Sequence 250 AA;

Query Match 54.9%; Score 742; DB 5; Length 250;
 Best Local Similarity 56.9%; Pred. No. 3.8e-42;
 Matches 152; Conservative 30; Mismatches 53; Indels 32; Gaps 6;

QY 1 QVTLKESGPTLVKPNQTLTLCTLSGSLSTGVSVMIRPPKALMLASINMNDKC 59
 DB 1 QVQLQESGPGLVESGTLISLTCAVSGASISSNNL-MSWVQPPGKGLMIGELIYSGS 58
 QY 60 YSPSLKRLITTKDTPKQVVLAMSNMDDPDATYSCALDMPHDSGPOSFDASDV 116
 DB 59 YNPSLRGRVITISVSKSTNPSLKLITVTDLTIVYICADY--YDSSSYSSGDYYIMDV 116
 QY 117 WGPRTMTVSSGGGSGGGSGGGSGGGSGGGSYELMQLPSVSVPQQTASITCSGDNIGD 168
 DB 117 WGGITVTVSSGGGSGGGSGGGSGGGSGGG---ALSYELTQPPSVSPQQTATITCSGDALPK 166
 QY 107 YLEFYQHMGRKGLTVTVSSGGGSGGGSGGGSGGGSGGGSYELMQLPSVSVPQQTASIT 162
 DB 107 YLEFYQHMGRKGLTVTVSSGGGSGGGSGGGSGGGSGGG---ALSYELTQPPSVSPQQTASIT 162
 QY 169 CSGNLDGKXACWYQOKPRSPVLVIYGNKRPSGIPERFSGNSGNTATLTISGQAMD 228
 DB 163 CSGNLDGKXACWYQOKPRSPVLVIYGNKRPSGIPERFSGNSGNTATLTISGQAMD 222
 QY 229 EADYCOAMD--ISTAVFGTGTKLTVL 253
 DB 229 EADYCOAMD--ISTAVFGTGTKLTVL 253

Db 223 EADYSCQTDGSGTSSVFFGGGKTLTVL 249

RESULT 13

ABP45596

ID ABP45596 standard; protein; 256 AA.

AC

XX ABP45596;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human BlyS binding scFv SEQ ID 1607.

XX

KM BlyS; B lymphocyte stimulator; TNF superfamily; human; cytosolic;

KM tumour necrosis factor; B cell proliferation; B cell differentiation;

KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 2320-2321; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS

CC and so may be used to detect and quantitate the presence of BlyS in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BlyS. They may also be

CC administered to treat diseases associated with aberrant BlyS expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of

CC the invention

XX

SQ Sequence 256 AA;

XX

Query Match 54.5%; Score 736; DB 5; Length 256;

Best Local Similarity 58.5%; Pred. No. 9.8e-42;

Matches 152; Conservative 33; Mismatches 63; Indels 12; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLVLTCTLSGSLTSGSVSGWIRQPKALEWLASINWDDKC 60

1 QVQLQSSGSLVHPGQSLTSLTCAVSGSGSISSGYSWIRQPKGLEWIGVYHSGSTV 60

QY 61 YSPSLKRLTITKDTPEKNQVLAISNMDDPATYSCA-LDMPPHD--SGPQSFDAADW 117

Db 61 YNPSLKSRTTISVDRKNOFSLKLSVTADTVVYCAKQRQSDYILITCYQAGYAFDIW 120

QY 118 GPCTWTVSSGGGGSGGGSGGGSGGGSSYLEMQLPSVSVSPGQTASTTCSG--DNIG 175

Db 121 GRGTPTVTS-----SGGGSGGGSGGGSGGSGVLTQPPSVSAPAGQKVTISCGSTSNIG 175

QY 176 DKYACWYQOKPGRSPVLVLYGDNKRPSGIPEPRTSGNSGNTATLITSGQAMDEADYCYC 235

Db 176 NNVSVWYQHPGKAPPLMIYDVSKRPSGVDRPSGSKGNSASLDISGLQSEDEADYCA 235

QY 236 AMDTSTA--VFGTGTLTVL 253

Db 236 AMDSLSEFLFGTGTLTVL 255

RESULT 14

ABP44979

ID ABP44979 standard; protein; 251 AA.

XX

AC ABP44979;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human BlyS binding scFv SEQ ID 990.

XX

KM BlyS; B lymphocyte stimulator; TNF superfamily; human; cytosolic;

KM tumour necrosis factor; B cell proliferation; B cell differentiation;

KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 1583-1584; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS

CC and so may be used to detect and quantitate the presence of BlyS in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BlyS. They may also be

CC administered to treat diseases associated with aberrant BlyS expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
XX the invention
SQ Sequence 251 AA;

Query Match 54.4%; Score 734.5; DB 5; Length 251;
Best Local Similarity 59.9%; Pred. No. 1.2e-41;
Matches 154; Conservative 30; Mismatches 62; Indels 11; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMNDKC 60
DB 1 QVQLQESGPGILVKPSETLSLTCTVSGGSISSSYVMIRPPGKALEWIGSIYSGSTY 60
QY 61 YSPSLKSRLLTITKDTTPNQVVLAMSNMNDPADTATYSICALDMPHDSGQSPFASDVMG 120
DB 61 YNPSLKSRLVITISVDTISKNQPSLKLSSVTADVAIVYCAFR--YILISYYGMVWGRG 118
QY 121 TMTTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 177
DB 119 TMTTVS-----SGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 173
QY 178 YACMYOQKPRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYCOAW 237
DB 174 YVSMYQOHQKAPKMLITYGSKRPISGVNRFSGSKSGNTASLTISGLQAEDEADYCSY 233
QY 238 DT-STAVFGTGTGKLTVL 253
DB 234 TTRSTVFGGTGKLTVL 250

RESULT 15
ABP45318
ID ABP45318 standard; protein; 252 AA.
XX
AC ABP45318;
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1329.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX
PN MO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001MO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 1989-1990; 3148pp; English.
PS
XX

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
XX the invention
SQ Sequence 252 AA;

Query Match 54.3%; Score 733; DB 5; Length 252;
Best Local Similarity 58.0%; Pred. No. 1.5e-41;
Matches 153; Conservative 31; Mismatches 56; Indels 24; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMNDKC 60
DB 1 QVQLQESGPGILVKPSETLSLTCTVSGGSISSSYVMIRPPGKALEWIGSIYSGSTY 60
QY 61 YSPSLKSRLLTITKDTTPNQVVLAMSNMNDPADTATYSICALDMPHDSGQSPFASDVMG 113
DB 61 YNPSLKSRLVITISVDTISKNQPSLKLSSVTADVAIVYCAFGDYILITGYPLH-----A 112
QY 114 SDVWGPGTMTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 173
DB 113 FDIWKGKTLVTS-----SGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 167
QY 174 L---GKTYACMYOQKPRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEA 227
DB 168 SAVGYNVYVSWYQOHQKAPKMLITYGSKRPISGVNRFSGSKSGNTASLTISGLQAEDEA 230
QY 231 DYVCOAMD--STAVFGTGTGKLTVL 253
DB 228 DYVCSYTRSTVFGGTGKLTVL 251

Search completed: May 13, 2004, 15:00:59
Job time : 53.0738 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 13.8782 Seconds
(without alignments)
941.146 Million cell updates/sec

Title: US-10-072-301-25

Perfect score: 1351

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....COAMDSTAVFGTGTKLTVL 253

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6C_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771.5	57.1	249	4	US-10-039-785-53 Sequence 53, Appl
2	752.5	55.7	278	3	US-09-260-527-3 Sequence 3, Appl
3	717	53.1	244	4	US-08-918-148-79 Sequence 79, Appl
4	694	51.4	250	4	US-10-039-785-50 Sequence 50, Appl
5	692	51.2	309	4	US-09-079-023-9 Sequence 9, Appl
6	688.5	51.0	312	4	US-09-079-023-10 Sequence 10, Appl
7	684	50.6	244	4	US-10-039-785-44 Sequence 44, Appl
8	668.5	49.5	280	4	US-09-260-527-1 Sequence 1, Appl
9	630.5	46.7	310	4	US-09-079-023-11 Sequence 11, Appl
10	617.5	45.7	258	2	US-08-665-202-5 Sequence 5, Appl
11	617.5	45.7	258	2	US-09-313-574-5 Sequence 5, Appl
12	607.5	45.0	235	2	US-08-190-199A-61 Sequence 61, Appl
13	606.5	44.9	249	4	US-08-918-148-74 Sequence 74, Appl
14	592.5	43.9	263	2	US-08-752-844-66 Sequence 66, Appl
15	592.5	43.9	263	2	US-09-293-533-66 Sequence 66, Appl
16	587.5	43.5	281	4	US-09-025-769B-178 Sequence 178, App
17	584.5	43.3	334	4	US-09-646-028-53 Sequence 53, Appl
18	584.5	43.3	339	4	US-09-646-028-55 Sequence 55, Appl
19	584.5	43.3	348	4	US-09-646-028-51 Sequence 51, Appl
20	574.5	42.5	245	4	US-10-039-785-42 Sequence 42, Appl
21	565.5	41.9	245	4	US-10-039-785-47 Sequence 47, Appl
22	565	41.8	248	2	US-08-887-352B-23 Sequence 23, Appl
23	565	41.8	248	2	US-09-109-207C-23 Sequence 23, Appl
24	565	41.8	248	3	US-09-296-005-23 Sequence 23, Appl
25	565	41.8	248	4	US-09-920-171-23 Sequence 23, Appl
26	563	41.7	248	2	US-08-887-352B-22 Sequence 22, Appl
27	563	41.7	248	3	US-09-109-207C-22 Sequence 22, Appl

28	563	41.7	248	3	US-09-296-005-22 Sequence 22, Appl
29	563	41.7	248	4	US-09-920-171-22 Sequence 22, Appl
30	561	41.5	264	3	US-08-564-164A-4 Sequence 4, Appl
31	552.5	40.9	245	4	US-08-918-148-76 Sequence 76, Appl
32	552.5	40.9	245	4	US-10-039-785-46 Sequence 46, Appl
33	549.5	40.7	482	4	US-09-509-031-16 Sequence 16, Appl
34	549	40.6	255	4	US-09-553-498-8 Sequence 8, Appl
35	549	40.6	255	4	US-09-618-869-8 Sequence 8, Appl
36	547.5	40.5	245	4	US-10-039-785-49 Sequence 49, Appl
37	546.5	40.5	245	4	US-08-918-148-78 Sequence 78, Appl
38	546.5	40.5	284	3	US-08-564-164A-2 Sequence 2, Appl
39	542.5	40.2	245	4	US-10-039-785-51 Sequence 51, Appl
40	541.5	40.1	245	4	US-10-039-785-48 Sequence 48, Appl
41	541.5	40.1	249	2	US-08-797-689-18 Sequence 18, Appl
42	541.5	40.1	249	4	US-09-984-186-18 Sequence 18, Appl
43	541.5	40.1	282	2	US-08-860-174A-10 Sequence 10, Appl
44	538.5	39.9	245	4	US-10-039-785-45 Sequence 45, Appl
45	537.5	39.8	245	4	US-08-918-148-75 Sequence 75, Appl

ALIGNMENTS

RESULT 1	US-10-039-785-53
Sequence 53, Application US/10039785	
Patent No. 6538938	
GENERAL INFORMATION:	
APPLICANT: Salcedo et al.	
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL	
FILE REFERENCE: PFS50	
CURRENT APPLICATION NUMBER: US/10/039,785	
CURRENT FILING DATE: 2002-05-07	
PRIOR APPLICATION NUMBER: 60/369,860	
PRIOR FILING DATE: 2002-04-05	
PRIOR APPLICATION NUMBER: 60/341,237	
PRIOR FILING DATE: 2001-12-20	
PRIOR APPLICATION NUMBER: 60/331,310	
PRIOR FILING DATE: 2001-11-14	
PRIOR APPLICATION NUMBER: 60/331,044	
PRIOR FILING DATE: 2001-11-07	
PRIOR APPLICATION NUMBER: 60/327,364	
PRIOR FILING DATE: 2001-10-09	
PRIOR APPLICATION NUMBER: 60/323,807	
PRIOR FILING DATE: 2001-09-21	
PRIOR APPLICATION NUMBER: 60/309,176	
PRIOR FILING DATE: 2001-08-02	
PRIOR APPLICATION NUMBER: 60/294,981	
PRIOR FILING DATE: 2001-06-04	
PRIOR APPLICATION NUMBER: 60/293,473	
PRIOR FILING DATE: 2001-05-25	
NUMBER OF SEQ ID NOS: 66	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 53	
LENGTH: 249	
TYPE: PRT	
ORGANISM: Artificial sequence	
FEATURE:	
OTHER INFORMATION: T1006F07 scFv	
US-10-039-785-53	
Query Match	57.1%; Score 771.5; DB 4; Length 249;
Best Local Similarity	62.4%; Pred. No. 1.1e-50;
Matches	159; Conservative 28; Mismatches 59; Indels 9; Gaps 5;
QY	1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSGCVGWTRPPGRALRWLASINWDDK 60
DB	1 EVQLVESGGGLVQPGSLRLSCAASGFTFSITAMS-WRQAPGKLEWVASISGSGST 58
QY	61 -YSPSLKSLRLITTKDTPKQVVLAMSNDDPADTATYSCALDMPPHDSGQSFSDASDVWCP 119
DB	59 YVADSVKRFITSRNSKNITLYLQWNSLRADETAVYYCARBPSFOQWGHYSY-GMDVWQ 117

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599

```

1  GENERAL INFORMATION:
2  APPLICANT: Knox, J.P.
3  APPLICANT: Mikkelsen, J.D.
4  APPLICANT: Willats, W. G.
5  TITLE OF INVENTION: ANTIBODY
6  FILE REFERENCE: DVOU19.001AUS
7  CURRENT APPLICATION NUMBER: US/09/260,527A
8  CURRENT FILING DATE: 1999-02-26
9  NUMBER OF SEQ ID NOS: 7
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 3
12 LENGTH: 278
13 TYPE: PRT
14 ORGANISM: UNKNOWN
15 FEATURES:
16 OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
17 OTHER INFORMATION: from a naive phage display library known as the
18 OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
19 OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
20 US-09-260-527-3

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Best Local Similarity	60.4%;	Pred. No. 3.4e-49;	Score 132.5;	DB 3;	Length 278;
Matches 154;	Conservative 31;	Mismatches 19;			

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QY      1 QVTLKESGPTLVKPTQVLLTLTLCTLSGFSLSSTGVSVMIRPPGKALEMLTASINMDDKC 60
Db      23 QVQLQESPGIYKESDSTLSLTCAVSQYISISSN-NWGMIRPPGKLEMLTGYIYSGSTY 81
QY      61 YSPISKSRLLITTKDTPNQVFLAMSNMDDPADTATYSCALMDPPHDSGPGSFSDSDVWGFG 120
Db      82 YNPSIKSRVTMSVDTSKQPSLTSLTASVTAVDITAYYCA-----RHPKRYD----WGQG 131
QY      121 TMVTVSSGGGSGSGGGSGGGSGGGSSSELMQLPVSYSVSPGQTASITTCGMDLADPYAC 180
Db      132 TLVTVSRGGGSGSGGGSGGGGSS-----ELTQDPASVALGQTVRITTCGDSLSRYAS 185
QY      181 WYQOKRPSRVLYITYGDMKPSGIGPERFSGNSGNTALTITSGTQAMDSDADYYCAQMTS 240
Db      186 WYQOKRQDAVLVIYKKNRPSGIGIDRFSGSSGNTASLITTAQAEDEADYYCNSRDS 245
QY      241 --TAVFQGTGKLTVL 253
Db      246 GNRHVFQGGTKLTVL 260

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US-08-918-148-79
; Sequence 79, Application US/08918148A
; Patent No. 6342220

```

; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M

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? APPLICANT: Garney, Austin L.
? TITLE OF INVENTION: Acoustic Antibodies
? FILE REFERENCE: P0979
? CURRENT APPLICATION NUMBER: US/08/918,148A
? CURRENT FILING DATE: 1997-08-25
? NUMBER OF SEQ ID NOS: 79
? SEQ ID NO 79
? LENGTH: 244
? TYPE: PRT
? ORGANISM: artificial
US-08-918-148-79

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best local similarity 59.1%; Pred. No. 1.3e-46;
Matches 152; Conservative 30; Mismatches 53; Indels

QY 1 QVTLKESGPTLYMPOTITLLTCTSGFSLSTSGVSGVMGIQPPKALEWLASINWMDKC 60

Db 3 QVQLQSGPGLVAPSRFTLSLTCTVSGDSISITYS--MIQPPGKGLIEWIGIYYSGSTN 60

QY 61 YSPSLKRLTIITMDPPKXNVLAISNMDPADTATYSCALDMPHDSGPSPASDVWGCG 120

Db 61 YNPILKSRITLIQVDTSKQPSFLKLSVLAADTAVYTCARG-----YFDVWGCG 109

QY 121 TMTVTSGGGGGGGGGGGGGGGGGGSGSYELMQLPSVSYPCQGTASITCSG---DNLDDK 177

Db 110 TMTVTS-----SGGGGGGGGGGGGGGGGGSYVLTPPSVSGSPCGQSTISCTGSSSDVGYN 164

QY 178 YACWQQRKGRSPVLYITGDKRPSGIPERFSGSNSGNATATLTISGTQAMDEADYICQAW 237

Db 165 YYSWVQDHPGAKPKMLMITEGSKRPSGVNRFSGSKSGNTASTLTISGLQAMDEADYICGSY 224

QY 238 DT--STNIVGTGTKLTVL 253

Db 225 TTRSTRVFGGKTKLTVL 241

US-10-039-785-50
Sequence 50, Application US/10039785

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1 patent NO. 6538938
1 GENERAL INFORMATION:
1 APPLICANT: Salcedo et al.
1 TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
1 FILE REFERENCE: p5550
1 CURRENT APPLICATION NUMBER: US/0/039,785
1 PRIORITY FILING DATE: 2002-05-07
1 PRIOR APPLICATION NUMBER: 60/369,860
1 PRIOR FILING DATE: 2002-04-05
1 PRIOR APPLICATION NUMBER: 60/341,237
1 PRIOR FILING DATE: 2001-12-20
1 PRIOR APPLICATION NUMBER: 60/331,310
1 PRIOR FILING DATE: 2001-11-14
1 PRIOR APPLICATION NUMBER: 60/331,044
1 PRIOR FILING DATE: 2001-11-07
1 PRIOR APPLICATION NUMBER: 60/327,364
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1 PRIOR APPLICATION NUMBER: 60/323,807
1 PRIOR FILING DATE: 2001-09-21
1 PRIOR APPLICATION NUMBER: 60/309,176
1 PRIOR FILING DATE: 2001-08-02
1 PRIOR APPLICATION NUMBER: 60/294,981
1 PRIOR FILING DATE: 2001-06-04
1 PRIOR APPLICATION NUMBER: 60/293,473
1 PRIOR FILING DATE: 2001-05-25
1 NUMBER OF SEQ ID NOS: 66
1 SOFTWARE: PatentIn Ver. 2.1
1 SEQ ID NO 50
1 LENGTH: 250
1 TYPE: PRT
1 ORGANISM: Artificial sequence
1 FEATURE:

```

OTHER INFORMATION: T1015A02 scfv
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (250)
 OTHER INFORMATION: Xaa equals either Gly or Ser
 US-10-039-785-50

Query Match 51.4%; Score 694; DB 4; Length 250;

Best Local Similarity 54.5%; Pred. No. 7.3e-45;

Matches 140; Conservative 36; Mismatches 69; Indels 12; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMNDKX 60
 1 QVQLQESGPGLVKPSQTLSLKCNVSGSIGTGYYVMIRPPGKLEWIGYIHSGSTY 60
 DB 61 YSPSLKSLRTTKDTPKQNVLAISMNDPADTATYSCALDMPHDSGQSPDASDVWGP 120
 61 YPSPSLKSLRTLVMDISRNQFSLSKLTSTVADTALYYCVREMANGD---HMSAFDLWGQ 116
 QY 121 TWVTYSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPQGTASITCSG--DNLGDKY 178
 117 TLVTYSSGGGSGGGSGGGSGGGSS---AQAVLTQPSASGTPQGRVITPSSGSSNIGMT 172
 DB 179 ACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYTCQAMD 238
 173 VMWYQQLPETAPEKLTLYGNDQRPQGVDRPFGSKSGTASLAITGLQSDPADYTCAMD 232
 QY 239 TSTA--VRETGKTLTVL 253
 DB 233 DSLIGYVFGTGTQTLTVL 249

RESULT 5

US-09-079-029-9

Sequence 9, Application US/09079029

Patent No. 6342369

GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.

APPLICANT: Aehkenazi, Avi J.

APPLICANT: Chuncharapai, Anan

APPLICANT: Kim, Kyung J.

TITLE OF INVENTION: Apo-2 Receptor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079,029

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1101R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

Query Match 51.2%; Score 692; DB 4; Length 309;
 Best Local Similarity 55.9%; Pred. No. 1.3e-44;
 Matches 143; Conservative 33; Mismatches 64; Indels 16; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMNDKX 60
 40 EVQLVQSGGVERPQGSRLTSCASGFTFDDYGM--WVROAPGKLEWVSGINWNGST 97
 DB 61 -YSPSLKSLRTTKDTPKQNVLAISMNDPADTATYSCALDMPHDSGQSPDASDVWGP 119
 98 GTADSVKGVITSRDANKNSLYLQMSLAEDTAYYCAKIL-----GAGRGYFDLMK 152
 QY 120 GTWTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPQGTASITCSGDNLDKXA 179
 153 GTTVTVSSGGGSGGGSGGGSGGGSS-----ELTPDAVSVALGQTVRITCGQDSLRSYYA 206
 DB 180 CWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYTCQAMT 239
 207 SWYQOKPQAPVLVIYGNKRRPSGIPDRPSGSSGNTASLTITGAQAEDEADYTCNSRDS 266
 QY 240 S--TAVFGTKTLTVL 253
 DB 267 SGNHVPFGGKTLTVL 282

RESULT 6

US-09-079-029-10

Sequence 10, Application US/09079029

Patent No. 6342369

GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.

APPLICANT: Aehkenazi, Avi J.

APPLICANT: Chuncharapai, Anan

APPLICANT: Kim, Kyung J.

TITLE OF INVENTION: Apo-2 Receptor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079,029

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1101R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 312 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-079-029-10

Query Match 51.0%; Score 688.5; DB 4; Length 312;

Best Local Similarity 56.9%; Pred. No. 2.4e-44;

Matches 145; Conservative 31; Mismatches 66; Indels 13; Gaps 5;

QY 2 VTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMNDKX 60
 41 VQLVESGGGLVQPGSLRLSKCAASGFTFSYMS--WVROAPGKLEWVAINIKQGSSEK 98
 DB

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11

Query Match 46.7%; Score 630.5; DB 4; Length 310;
Best Local Similarity 51.4%; Pred. No. 5,4e-40;
Matches 133; Conservative 42; Mismatches 63; Indels 21; Gaps 7;

QY 1 QVTLKESGPTLVKPTOTLTCTLSGFSLSGVSVMWIRPPGKALEWLASINMW-DDK 59
DB 40 QVQLVQSGGCVQVQPGSRSLTSCAASCFITSSYGMH--WRQAPGKLEWVAGIFIDGSK 97
QY 60 CYSPLSKRLITTKTPKNQVVLAMSNMADPATATYSCALDMPPHDSGPOSFDPASDVWCP 119
DB 98 YVADSVKGFITISRDNSKNTIVLQWNSLAEEDTAVYYCARD-----RGYYMDVWVK 149
QY 120 GTMTVTVSSGGSGSGSGSGSGSGSSSEYELMQLPVSVSFQQTASITCSG--DNLGDK 177
DB 150 GTTVTVS-----SGGGSGSGSGSGSGSGSVLTQPPSVSGAPQQRVTISCTGRSSNIGAG 204
QY 178 Y-ACWYQOKRGRSPVLVIYGDNRPSGIERPFGSGNSGNTATLTISGTMDEADYVCCA 236
DB 205 HDVHYVQQLPGLTAPKLLIYDSDNRPSGVPDRFSGSRSGTSASLALITGLDAEDADYVCCS 264
QY 237 WDTST--AVFGTGTKLTVL 253
DB 265 YDSLRGVSFGGCTKTVTL 283

RESULT 10
US-08-665-202-5
Sequence 5, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-202-5

Query Match 45.7%; Score 617.5; DB 2; Length 258;
Best Local Similarity 49.3%; Pred. No. 4,1e-39;
Matches 132; Conservative 39; Mismatches 68; Indels 29; Gaps 8;

QY 1 QVTLKESGPTLVKPTOTLTCTLSGFSLSGVSVMWIRPPGKALEWLASINMW-DK 59
DB 1 QVQLVQSGGCVQVQPGSRSLTSCAASCFITSSYGMH--WRQAPGKLEWVAGIFIDGSK 58
QY 60 CYSPLSKRLITTKTPKNQVVLAMSNMADPATATYSCALDMPPHDSG-----PQ 109
DB 59 KTSFPGQGVITISVDKSVSTAVILQWNSLKPDSAVYFCA----RHDVGYCSSNCAKWP 114
QY 110 SPDADWCPGTMVTVSSGGSGSGSGSGSGSSSEYELMQLPVSVSFQQTASITC 169
DB 115 YFOH--WQGTLLTVS-----SGGGSGSGSGSGSGSVLTQPPSVSAAPQKVTIIC 166
QY 170 SG--DNLGDKYACWQOKRGRSPVLVIYGDNRPSGIERPFGSGNSGNTATLTISGTM 227
DB 167 SSSSSNIGNNIVSWVQQLPGLTAPKLLIYGTNRPGVDPDRFSGSRSGTSASLALISGRSB 226
QY 228 DEADYVCCAMDTSTA--VFGTGTKLTVL 253
DB 227 DEADYVCCAMDDSLSGWVFGGCTKTVTL 254

RESULT 11
US-09-315-574-5
Sequence 5, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSES: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-315-574-5

Query Match 45.7%; Score 617.5; DB 4; Length 258;
Best Local Similarity 49.3%; Pred. No. 4,1e-39;
Matches 132; Conservative 39; Mismatches 68; Indels 29; Gaps 8;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSSTGVSVMIRPPGKALEMLASINMND-DK 59
DB 1 QVQLQSGAELEKPKESLKISCKSGYSFTSYWIA--WVRQMPGKLEWLVGIMAGSTN 58
QY 60 CYSPSLKRLITTKDTPTKQVVLAMSNNDPADTATYSCALDMPPHSG-----PQ 109
DB 59 KTSPPFOQVITISVDKSVSTAVLQMSLKPSDSAVIFCA-----RHVGVCSSSNCAKME 114
QY 110 SFADADVNGPTMTVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPQQTASINIC 169
DB 115 YFQH---WGQITLVTS-----SGGGSGGGSGGGSGGGSGGLVLPSPVSAAPQKVTISC 166
QY 170 SG--DNIGDKYACVYQKPKGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTOAM 227
DB 167 SGSSSNIGNNYVSVYQQLPGTAPRLILGHTNRPAGVPPRFSGSKSGTASIALISGRSE 226
QY 228 DEADYYCOAMDTSRA--VPFGTGTKLTVL 253
DB 227 DEADYYCAAMDLSLGMVFGGGTKLTVL 254

RESULT 12

US-08-190-199A-61
Sequence 61, Application US/08190199A
Patent No. 5830663
GENERAL INFORMATION:
APPLICANT: EMBLETON, Michael J.
APPLICANT: GOROCIOV, Guy
APPLICANT: JONES, Peter T.
APPLICANT: WINTER, Gregory P.
TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,199A
FILING DATE: 13-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01483
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9212419.7
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9117352.6
FILING DATE: 10-AUG-1991
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-190-199A-61

Query Match 45.0%; Score 607.5; DB 2; Length 235;
Best Local Similarity 51.0%; Pred. No. 2,1e-38;
Matches 128; Conservative 31; Mismatches 71; Indels 21; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSSTGVSVMIRPPGKALEMLASINMNDKC 60
DB 1 QVQLKESGPTLVKPSQSLISITCTVSGFSLTSYGVH--WVRQMPGKLEWLVGIMAGSTN 58
QY 61 YSPSLKRLITTKDTPTKQVVLAMSNNDPADTATYSCALDMPPHSGPQSPFADVWGPG 120
DB 59 YNSALMRLISTKDNKSGVFLKMSLSLQTDITAMYYCARDRGAY-----WGQG 106
QY 121 TMTVTVSSGGGSGGGSGGGSGGGSGGGSSYELMQLPSV--SVSPQQTASITCGDNIGDKTA 179
DB 107 TLTVTVS-----AGGGSGGGSGGGSGGGSGGLVLPSPVSAAPQKVTISC 166
QY 180 CWTQOKPKGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTOAMDEADYYCOAMD 239
DB 161 HMTQOKSGTSPKMTITDTSKLASGVPARPSGSGATSYSLTISWEADATYVCOQMS 220
QY 240 STAVPFGTKL 250
DB 221 NPVTFGAGTKL 231

RESULT 13

US-08-918-148-74
Sequence 74, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Rendly, Brian M.
APPLICANT: Guiney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 74
LENGTH: 249
TYPE: PRT
ORGANISM: artificial
US-08-918-148-74

Query Match 44.9%; Score 606.5; DB 4; Length 249;
Best Local Similarity 49.6%; Pred. No. 2,6e-38;
Matches 128; Conservative 41; Mismatches 70; Indels 19; Gaps 6;

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Oy      61 -YSPLSKSLRTTKOTPKNOVLAMSNNDPADTATYSGCALDMPHDSGPOSFDASDVWGP    119
         :|::||:::||::||::||::||::||::||::||::||::||::||::||::||
Db       77 NTHSALISLSTLSKONSKSQFLKLAKNSTQTDTRATTYYCA-----KLGNYDALDYWGQ   128

Oy      120 GTMVTVSSGGGGSGCGGSGGGGSSEYELMDLP-SVSVPQCQTASITCSGD----N    173
Db      129 GTSVTVS-----SGGGSGGGGGSGGGSDVMTGTCPILSLPVSLADQAHSICRSQSIVHS  183A

Oy      174 LGDKXACWCQQOKRPGSPVLVIYGDMKRPSGIPEPFGSNSGNNTALTLTISGQAMDADRY  233
Db      184 NGMTYLLEWLTLQRPGOSPMLLIYPFVSNRRSGVDPRSGSGSDTFDLKI SRVEADELVGY  243

Oy      234 CQAMDSTAVFGNGTKLFY  252
Db      244 CFQGSHVPWTFCGGTKLERI  262

RESULT 15
US-09-293-533-66
; Sequence 66, Application US/09293533
; Date Nov 1980

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1          RESULT 15
2          US-09-293-533-66
3          : Sequence 66, Application US/09293533
4          : Patent No. 6509016
5          :
6          : GENERAL INFORMATION:
7          :   APPLICANT: Chatterjee, Malaya
8          :   APPLICANT: Poon, Kenneth A.
9          :   APPLICANT: Chatterjee, Sunil K.
10         :   TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
11         :   TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
12         :   NUMBER OF SEQUENCES: 66
13         :   CORRESPONDENCE ADDRESSES:
14         :     ADDRESSEE: MORRISON & FOERSTER
15         :     STREET: 755 PAGE MILL ROAD
16         :     CITY: PALO ALTO
17         :     STATE: CA
18         :     COUNTRY: USA
19         :     ZIP: 94304-1018
20         :   COMPUTER READABLE FORM:
21         :     MEDIUM TYPE: Floppy disk
22         :     COMPUTER: IBM PC compatible
23         :     OPERATING SYSTEM: PC-DOS/MS-DOS
24         :     SOFTWARE: PatentIn Release #1.0, Version #1.30
25         :   CURRENT APPLICATION DATA:
26         :     APPLICATION NUMBER: US/09/293,533
27         :     FILING DATE:
28         :     CLASSIFICATION:
29         :     PRIOR APPLICATION DATA:
30         :       APPLICATION NUMBER: US/08/752,844
31         :       FILING DATE:
32         :       ATTORNEY/AGENT INFORMATION:
33         :         NAME: Schiff, J. Michael
34         :         REGISTRATION NUMBER: 40,253
35         :         REFERENCE/DOCKET NUMBER: 30414-20002.21
36         :       TELECOMMUNICATION INFORMATION:
37         :         TELEPHONE: (415) 813-5600
38         :         TELEFAX: (415) 494-0792
39         :         TELEX: 706141
40         :       INFORMATION FOR SEQ. ID NO: 66:
41         :         SEQUENCE CHARACTERISTICS:
42         :           LENGTH: 263 amino acids
43         :           TYPE: amino acid
44         :           TOPOLOGY: linear
45         :         MOLECULE TYPE: protein
46         :
47         :   US-09-293-533-66
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Db      77  NYHSLISRLISKDNKSQVFLKNSIQTDPTATYCA-----KLGNVDALDYMGO 128
QY      120  GIMVTVSSGGGGGGGGGGGGGGGGGGSSYELMQLP-SVSVSPQOTASITCSGD-----N 173
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QY      174  LQDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGSGNSGNTATLTI SGTQAMDEADYY 233
Db      184  NGNTYLEWYLOKPGQSPNLLIYFVSNRFGVDPDRFSGSGSGTDPFTLKISRVEAEDLGVIY 243
QY      234  QQAMDTSTAVFSGTKLTV 252
Db      244  CFQSHVPMWTFGGGTKEI 262

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Search completed: May 13, 2004, 15:10:48
 Job time : 13.8782 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.4587 Seconds
(without alignments)
1879.405 Million cell updates/sec

Title: US-10-072-301-25

Perfect score: 1351

Sequence: 1 QVTLKESGPTLVKPTQTLTL.....CQAMPSTAVFGNGTKLTVL 253

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1351	100.0	253	14	US-10-072-301-17 Sequence 17, Appl
2	1351	100.0	253	14	US-10-072-301-25 Sequence 17, Appl
3	1351	100.0	253	14	US-10-071-866-17 Sequence 25, Appl
4	1351	100.0	253	14	US-10-071-866-25 Sequence 25, Appl
5	1351	100.0	253	15	US-10-360-828-17 Sequence 17, Appl
6	1351	100.0	253	15	US-10-360-828-25 Sequence 25, Appl
7	794	58.8	253	14	US-10-072-301-23 Sequence 23, Appl
8	794	58.8	253	14	US-10-071-866-23 Sequence 23, Appl
9	794	58.8	253	14	US-10-071-866-23 Sequence 23, Appl
10	794	58.8	253	14	US-10-071-866-23 Sequence 23, Appl
11	794	58.8	253	15	US-10-360-828-23 Sequence 23, Appl
12	794	58.8	253	15	US-10-360-828-31 Sequence 31, Appl
13	794	58.8	250	10	US-09-880-748-1548 Sequence 1548, Ap
14	783	58.0	250	12	US-10-293-418-1548 Sequence 1548, Ap
15	779.5	57.7	247	10	US-09-880-748-1651 Sequence 1651, Ap

16	779.5	57.7	247	12	US-10-293-418-1651 Sequence 1651, Ap
17	771.5	57.1	249	13	US-10-039-785-53 Sequence 53, Appl
18	771.5	57.1	249	14	US-10-139-785-53 Sequence 53, Appl
19	747	55.3	254	10	US-09-880-748-1966 Sequence 1966, Ap
20	747	55.3	254	12	US-10-293-418-1966 Sequence 1966, Ap
21	742	54.9	250	10	US-09-880-748-1480 Sequence 1480, Ap
22	742	54.9	250	12	US-10-293-418-1480 Sequence 1480, Ap
23	739.5	54.7	258	14	US-10-072-301-27 Sequence 27, Appl
24	739.5	54.7	258	14	US-10-071-866-27 Sequence 27, Appl
25	739.5	54.7	258	15	US-10-360-828-27 Sequence 27, Appl
26	736	54.5	256	10	US-09-880-748-1607 Sequence 1607, Ap
27	736	54.5	256	12	US-10-293-418-1607 Sequence 1607, Ap
28	734.5	54.4	251	10	US-09-880-748-990 Sequence 990, Ap
29	734.5	54.4	251	12	US-10-293-418-990 Sequence 990, Ap
30	733	54.3	252	10	US-09-880-748-1329 Sequence 1329, Ap
31	733	54.3	252	12	US-10-293-418-1329 Sequence 1329, Ap
32	731	54.1	254	10	US-09-880-748-844 Sequence 844, Ap
33	731	54.1	254	12	US-10-293-418-844 Sequence 844, Ap
34	730	54.0	252	14	US-10-120-414-73 Sequence 73, Appl
35	728.5	53.9	247	10	US-09-880-748-1018 Sequence 1018, Ap
36	728.5	53.9	247	12	US-10-293-418-1018 Sequence 1018, Ap
37	723.5	53.6	251	10	US-09-880-748-1316 Sequence 1316, Ap
38	723.5	53.6	251	12	US-10-293-418-1316 Sequence 1316, Ap
39	723.5	53.6	253	10	US-09-880-748-1619 Sequence 1619, Ap
40	723.5	53.6	253	12	US-10-293-418-1619 Sequence 1619, Ap
41	722.5	53.5	251	10	US-09-880-748-952 Sequence 952, Ap
42	722.5	53.5	251	12	US-10-293-418-952 Sequence 952, Ap
43	721.5	53.4	255	10	US-09-880-748-841 Sequence 841, Ap
44	721.5	53.4	255	12	US-10-293-418-841 Sequence 841, Ap
45	721	53.4	248	10	US-09-880-748-1995 Sequence 1995, Ap

ALIGNMENTS

RESULT 1
US-10-072-301-17
; Sequence 17, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODE.
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35
US-10-072-301-17

Query Match	100.0%	Score 1351;	DB 14;	Length 253;
Best local Similarity	100.0%	Pred. No. 2.8e-87;		
Matches 253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVTLKESGPTLVKPTQTLTLTCTLSGFSSTGVSIGWIRPPGKALBWLASINMNDK 60		
DB	1	QVTLKESGPTLVKPTQTLTLTCTLSGFSSTGVSIGWIRPPGKALBWLASINMNDK 60		
QY	61	YSPSLKSRLLTIKDPKNOVLAMSNMADPADATYSCALDMPHDSGPOSFDSVWGR 120		
DB	61	YSPSLKSRLLTIKDPKNOVLAMSNMADPADATYSCALDMPHDSGPOSFDSVWGR 120		
QY	121	TWVTYSSGGGSGGGGSGGGGSGGGGSGYELMQLPSVSVSPQGTASITCSGDNLDGRKYAC 180		
DB	121	TWVTYSSGGGSGGGGSGGGGSGGGGSGYELMQLPSVSVSPQGTASITCSGDNLDGRKYAC 180		

Qy	181	MYQOKPERSVLYIYGDNRKPSGIPERRSGNSGNTATLITLISGTOAMDEADYCYQAMDTS	240
Db	181	MYQOKRERSVLYIYGDNRKPSGIPERRSGNSGNTATLITLISGTOAMDEADYCYQAMDTS	240
Qy	241	TAVFGTGTKLTVL	253
Db	241	TAVFGTGTKLTVL	253

```

RESULT 2
US-10-072-301-25
/ Sequence 25, Application US/10072301
/ Publication No. US20030152913A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Yi
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORCEPTORS FOR HUMAN IMMUNODEF
/ TITLE OF INVENTION: VIRUS
/ FILE REFERENCE: 25636-718
/ CURRENT APPLICATION NUMBER: US/10/072,301
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 25
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.186.35 Variant
US-10-072-301-25

```

```

RESULT 3
US-10-071-866-17
/ Sequence 17, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST E
/ TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35
US-10-071-866-17

```

```

RESULT 4
US-10-071-866-25
: Sequence 25, Application US/10071866
: Publication No. US20030165988A1
GENERAL INFORMATION:
: APPLICANT: Hua, Shao-bing
: APPLICANT: Pauling, Michelle H.
: APPLICANT: Zhu, Li
: TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
: TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
: FILE REFERENCE: 25636-717
: CURRENT APPLICATION NUMBER: US/10/071,866
: CURRENT FILING DATE: 2002-02-08
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 25
: LENGTH: 253
: TYPE: PRT
: ORGANISM: Artificial Sequence
FEATURES:
: OTHER INFORMATION: Clone 15.186.35 Variant
US-10-071-866-25

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Db 181 WTQOKRGRSPVLVYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMDTS 240
QY 241 TAVFGTGTGTLTVL 253
Db 241 TAVFGTGTGTLTVL 253

RESULT 5

US-10-360-828-17
; Sequence 17, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Clone 15.186.35
US-10-360-828-17

Query Match 100.0%; Score 1351; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
QY 61 YSPSLKSRLLTIKDPKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFDSADVWGPG 120
Db 61 YSPSLKSRLLTIKDPKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFDSADVWGPG 120
QY 121 TWVTSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITSGDNLGDKYAC 180
Db 121 TWVTSSGGGGSGGGGGGGGGGGSSYELMQLPSVSVSPGQTASITSGDNLGDKYAC 180
QY 181 WTQOKRGRSPVLVYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMDTS 240
Db 181 WTQOKRGRSPVLVYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMDTS 240
QY 241 TAVFGTGTGTLTVL 253
Db 241 TAVFGTGTGTLTVL 253

RESULT 6

US-10-360-828-25
; Sequence 25, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-360-828-25

Query Match 100.0%; Score 1351; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
QY 61 YSPSLKSRLLTIKDPKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFDSADVWGPG 120
Db 61 YSPSLKSRLLTIKDPKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFDSADVWGPG 120
QY 121 TWVTSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITSGDNLGDKYAC 180
Db 121 TWVTSSGGGGSGGGGGGGGGGGSSYELMQLPSVSVSPGQTASITSGDNLGDKYAC 180
QY 181 WTQOKRGRSPVLVYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMDTS 240
Db 181 WTQOKRGRSPVLVYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMDTS 240
QY 241 TAVFGTGTGTLTVL 253
Db 241 TAVFGTGTGTLTVL 253

RESULT 7

US-10-072-301-23
; Sequence 23, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-072-301-23

Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
QY 61 YSPSLKSRLLTIKDPKQNVVLAMSNMDDPADTATYSCALDMPHDSGPOSFDSADVWGPG 120

```
Db 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHQQYYDTSGQPY-YFDPMGG 119
Qy 121 TMTVYSSGGGGSGGGSGGGSGGSSSYELMQLP-SVSVSPQQTASITCSGDNLDKXA 179
Db 120 TLVTYSSGGGGSGGGSGGGSGGSSNIVTQSPSLASVDRTVMTCRASQDIRKUL 179
Qy 180 CMYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVCOAMD 239
Db 180 NMVQOKPKAPKVLIIYASDLDTGIPSRFSGSGSDTFLITISLPEDIAITYCCQSDY 239
Qy 240 STAVFGTGTULTV 252
Db 240 LPLTFGGGTIVDI 252
```

```
RESULT 8
US-10-072-301-31
; Sequence 31, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-31
```

```
Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Qy 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHQQYYDTSGQPY-YFDPMGG 119
Db 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHQQYYDTSGQPY-YFDPMGG 119
Qy 121 TMTVYSSGGGGSGGGSGGGSGGSSSYELMQLP-SVSVSPQQTASITCSGDNLDKXA 179
Db 120 TLVTYSSGGGGSGGGSGGGSGGSSNIVTQSPSLASVDRTVMTCRASQDIRKUL 179
Qy 180 CMYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVCOAMD 239
Db 180 NMVQOKPKAPKVLIIYASDLDTGIPSRFSGSGSDTFLITISLPEDIAITYCCQSDY 239
Qy 240 STAVFGTGTULTV 252
Db 240 LPLTFGGGTIVDI 252
```

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RESULT 9
US-10-071-866-23
; Sequence 23, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST H
```

```
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23
```

```
Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Qy 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHQQYYDTSGQPY-YFDPMGG 119
Db 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHQQYYDTSGQPY-YFDPMGG 119
Qy 121 TMTVYSSGGGGSGGGSGGGSGGSSSYELMQLP-SVSVSPQQTASITCSGDNLDKXA 179
Db 120 TLVTYSSGGGGSGGGSGGGSGGSSNIVTQSPSLASVDRTVMTCRASQDIRKUL 179
Qy 180 CMYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYVCOAMD 239
Db 180 NMVQOKPKAPKVLIIYASDLDTGIPSRFSGSGSDTFLITISLPEDIAITYCCQSDY 239
Qy 240 STAVFGTGTULTV 252
Db 240 LPLTFGGGTIVDI 252
```

```
RESULT 10
US-10-071-866-31
; Sequence 31, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-071-866-31
```

```
Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Db 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMDDKC 60
Qy 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHQQYYDTSGQPY-YFDPMGG 119
Db 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHQQYYDTSGQPY-YFDPMGG 119
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US-09-880-748-1548

Query Match

Best Local Similarity 58.0%; Score 783; DB 10; Length 250;
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

```
QY 1 QVTLKESGPTLVKPTQTLTTLTCTLSGFSSTGVSVMIRPPGKALEWLASINMNDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCAVSGYIS-SGYWGMIRPPGKALEWISYHSGSTY 59
QY 61 YSPSLKSRLLTITKDTPEKQVVLAMSNMPPADTATYSCALDMPHDSGPGSPASDVMGPG 120
DB 60 YNPSLSKSRVTISVDTSKQPSLKLSSVTADTAIVYCA--RVHYDILGTYLMAFDINGOG 117
QY 121 TMVTSSGGGSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCGDNLDGDIYAC 180
DB 118 TMVTSSGGGSGGGSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCGDNLDGDIYAC 180
QY 175 WYQOKRGPAPVLYIYGNKRRPSGIPERFSGNSGNTATLTISGTOAMDEADYCCAMDT 240
DB 175 WYQOKRGPAPVLYIYGNKRRPSGIPERFSGNSGNTATLTISGTOAMDEADYCCAMDT 234
QY 241 --TAVFGTGTCLTVL 253
DB 235 GNHVVFQGGTQTLTVL 249
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RESULT 14

US-10-293-418-1548
Sequence 1548; Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:

```
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P2
/ CURRENT APPLICATION NUMBER: US/10/293,418
/ PRIOR FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-16
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1548
/ LENGTH: 250
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-1548
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Query Match 58.0%; Score 783; DB 12; Length 250;
Best Local Similarity 63.5%; Pred. No. 2e-47;

Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

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QY 1 QVTLKESGPTLVKPTQTLTTLTCTLSGFSSTGVSVMIRPPGKALEWLASINMNDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCAVSGYIS-SGYWGMIRPPGKALEWISYHSGSTY 59
QY 61 YSPSLKSRLLTITKDTPEKQVVLAMSNMPPADTATYSCALDMPHDSGPGSPASDVMGPG 120
DB 60 YNPSLSKSRVTISVDTSKQPSLKLSSVTADTAIVYCA--RVHYDILGTYLMAFDINGOG 117
QY 121 TMVTSSGGGSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCGDNLDGDIYAC 180
```

DB 118 TMVTSSGGGSGGGSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCGDNLDGDIYAC 174

QY 181 WYQOKRGPAPVLYIYGNKRRPSGIPERFSGNSGNTATLTISGTOAMDEADYCCAMDT 240
DB 175 WYQOKRGPAPVLYIYGNKRRPSGIPERFSGNSGNTATLTISGTOAMDEADYCCAMDT 234QY 241 --TAVFGTGTCLTVL 253
DB 235 GNHVVFQGGTQTLTVL 249

RESULT 15

US-09-880-748-1651
Sequence 1651; Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:

```
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1651
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1651
```

Query Match 57.7%; Score 779.5; DB 10; Length 247;
Best Local Similarity 60.5%; Pred. No. 3.5e-47;

Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;

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QY 1 QVTLKESGPTLVKPTQTLTTLTCTLSGFSSTGVSVMIRPPGKALEWLASINMNDKC 60
DB 1 QVQLQESGPGLVKPSSETLSLTCAVSGYIS-SGYWGMIRPPGKALEWISYHSGSTY 59
QY 61 YSPSLKSRLLTITKDTPEKQVVLAMSNMPPADTATYSCA-----LDMPHDSGPG 109
DB 60 YNPSLSKSRVTISVDTSKQPSLKLSSVTADTAIVYCAFRYDILGTYDDM----- 111
QY 110 SPASDVMGPGMTVYSSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITC 169
DB 112 ----DVMKRGTLVTVSSGGGSGGGSGGGSGGGSS-----ELTQDPASVALGQVRLTIC 160
QY 170 SGDNLDGDIYACWYQOKRGPAPVLYIYGNKRRPSGIPERFSGNSGNTATLTISGTOAMDE 229
DB 161 QGDLSLSYASWYQOKRGPAPVLYIYGNKRRPSGIPERFSGNSGNTATLTITGAQARDE 220
QY 230 ADYCCAMDT--TAVFGTGTCLTVL 253
DB 221 ADYCCNSRDSGNHVVFQGGTQTLTVL 246
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Search completed: May 13, 2004, 15:43:33
Job time : 38.4587 secs

Matches 95; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
 QY 148 SYELMOLPSVSVSGQTASITSGSDNIGDYACMYQOKPGRSPVLVIYGNKRPSPGIPRS 207
 Db 1 SYELTOPSVSVSGQTASITSGSDNIGDYACMYQOKPGRSPVLVIYGNKRPSPGIPRS 60
 QY 208 FSGNSGNTATLTISGTQAMDADYYCOAMDST-AVFGTGLTTL 253
 Db 61 FSGNSGNTATLTISGTQAMDADYYCOAMDSTIYVFGGGLTTL 107

RESULT 3
 S41374
 single chain Fv antibody - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C/Accession: S41374
 R/Artemenko, O.; Weller, B.W.; Muentz, K.; Conrad, U.
 submitted to the EMBL Data Library, January 1994
 A/Description: Construction and functional characterization of a single chain Fv antibody
 A/Reference number: S41374
 A/Accession: S41374
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-249 <ART>
 A/Cross-references: EMBL:229480

Query Match
 Best Local Similarity 36.0%; Score 486.5; DB 2; Length 249;
 Matches 112; Conservative 34; Mismatches 90; Indels 21; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRPKALEWLASI-NMNDK 59
 Db 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRPKALEWLASI-NMNDK 59
 QY 60 CYSPLKRLITTKDTTPKQVVLAMSNMNDPADTATYSCALDMPHDSGQSPDASDVW 119
 Db 59 KVPFQDKATITADTSNTAVLLSLTSEDYVYCA-----RRDTLYTSLGYWQ 111
 QY 120 GTMTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 114
 Db 112 GSTVTVS-----SSGGSGGGSGGGSGGGSDIELTQSPSVVIVPGESVISCSSKSLAS 166
 QY 175 -GDRYACMYQOKPGRSPVLVIYGNKRPSPGIPRSFGNSGNTATLTISGTQAMDADYY 233
 Db 167 DGDYSLFWFLQRPQSPQLILYRMSNLASGVPRFSGSGSGTFTLRISRVAEDVGY 226
 QY 234 COAMDSTAVFGTGL 250
 Db 227 CMQHRYPVLTFGAGTKL 243

RESULT 4
 PC4283
 anti-Ss-A/Ro 60K peptide 118 chain E-60 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
 C/Accession: PC4283
 R/Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
 Biochem. Biophys. Res. Commun. 232, 101-106, 1997
 A/Title: Molecular cloning of anti-Ss-A/Ro 60-kDa peptide fab fragments from infiltrating
 A/Reference number: PC4279; PMID:97236289; PMID:9125110
 A/Accession: PC4283
 A/Molecule type: protein
 A/Residues: 1-107 <SDU>
 C/Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren's
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/13-87/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 35.9%; Score 485; DB 2; Length 107;
 Matches 93; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 150 ELMOLPSVSVSGQTASITSGSDNIGDYACMYQOKPGRSPVLVIYGNKRPSPGIPRS 209
 Db 1 ELMOLPSVSVSGQTASITSGSDNIGDYACMYQOKPGRSPVLVIYGNKRPSPGIPRS 60
 QY 210 GNSGNTATLTISGTQAMDADYYCOAMDST-STAVFGTGLTTL 253
 Db 61 GNSGNTATLTISGTQAMDADYYCOAMDSTIYVFGGGLTTL 106

RESULT 5
 A49002
 Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
 C/Accession: A49002
 R/Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, R.
 Arthritis Rheum. 35, 900-904, 1992
 A/Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II ger
 A/Reference number: A49002; PMID:92352481; PMID:1322670
 A/Accession: A49002
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-124 <STU>
 A/Cross-references: GB:M9808; NID:9185515; PID:AAA52989.1; PID:9567176
 A/Experimental source: EBV-transformed lymphoblastoid cell line SSH23
 A/Note: Sequence extracted from NCBI Backbone (NCBI:110261, NCBI:110262)
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/15-99/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 35.8%; Score 483.5; DB 2; Length 124;
 Matches 97; Conservative 7; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRPKALEWLASI-NMNDK 60
 Db 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRPKALEWLASI-NMNDK 60
 QY 61 YSPFLKRLITTKDTTPKQVVLAMSNMNDPADTATYSCALDMPHDSGQSPDASDVW 117
 Db 61 YSPFLKRLITTKDTTPKQVVLAMSNMNDPADTATYSCALDMPHDSGQSPDASDVW 114
 QY 118 GPGTMTVSS 127
 Db 115 GQGTLYTVSS 124

RESULT 6
 A56446
 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
 C/Species: Mus musculus (house mouse)
 C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
 C/Accession: A56446
 R/Tang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.
 J. Biol. Chem. 270, 7829-7835, 1995
 A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical
 A/Reference number: A56446; PMID:95229583; PMID:7713873
 A/Accession: A56446
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-268 <TAN>
 A/Cross-references: GB:U20617
 C/Keywords: heterotrimer; immunoglobulin

Query Match
 Best Local Similarity 35.8%; Score 483; DB 2; Length 268;
 Matches 108; Conservative 38; Mismatches 87; Indels 24; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRPKALEWLASI-NMNDK 59
 Db 3 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRPKALEWLASI-NMNDK 59
 QY 60 CYSPLKRLITTKDTTPKQVVLAMSNMNDPADTATYSCALDMPHDSGQSPDAS--DV 116

Db 61 KVDPKFGKATITADTSSNTAVYLQSLSTSEDTAVYYCA-----SYLTREYNY 109
QY 117 WGGGTMVTVSSGGGSGGGGSGGGGSGGGSSYLEMQLPSV-SVSPGQTASITCSGDNLG 175
Db 110 WGGITVTVS-----SGGGSGGGGSDIELTQSPAIMSASLGEKVTMSCRSS-S 163
QY 176 DKACVYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYCC 235
Db 164 VNFITYYQOKSDASPKLWMTYITSHLPFGVPARFSSGSGNSYSLTISMEGDAATYYCQ 223
QY 236 AMDSTAVFGTGTCLTV 252
Db 224 QFTSPFTFGSGTKLEI 240

RESULT 7
S25739
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25739
R/Combrlato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A>Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25739
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-151 <COM>
A/Cross-references: EMBL:X57803; NID:933703; PIDN:CAA40941.1; PID:933704
C/Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 479; DB 2; Length 151;
Best Local Similarity 84.5%; Pred. No. 2, 2e-25;
Matches 93; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 144 GGGSSYLEMQLPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYGDNRKPSG 203
Db 16 GSVAASYELTQPPSVSVSPGQTASITCSGDTLGDKYACWYQOKPGRSPVLVIYQDSKRPSSG 75

QY 204 IPERFSGNSGNTATLTISGTQAMDEADYCCQAMDSTAVFGTGTCLTVL 253
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYCCQALGGQHCVFGGGTCLTVL 125

RESULT 8
S25751
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25751
R/Combrlato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A>Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25751
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-231 <COM>
A/Cross-references: EMBL:X57816; NID:933731; PIDN:CAA40953.1; PID:933732
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Db 16 GSVAASYELTQPPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYHNSKRPSSG 75
QY 204 IPERFSGNSGNTATLTISGTQAMDEADYCCQAMDSTAVFGTGTCLTVL 253
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYCCQAMDSIYVFGGTCLTVL 125

RESULT 9
I4HUBU
Ig lambda chain V-IV region (Bau) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
C/Accession: A01981
R/Baczko, K.; Braun, D.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 355, 131-154, 1974
A>Title: Pattern of antibody structure. The primary structure of a monoclonal immunoglob
A/Reference number: A01981; MUID:75059189; PMID:4435717
A/Accession: A01981
A/Molecule type: protein
A/Residues: 1-106 <BAC>
C/Comment: This is a Bence Jones protein.
C/Genetics:
A/Gene: GDB:IGLV@
A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer
F/14-88/Domain: immunoglobulin homology <IMM>
F/21-66/Disulfide bonds: #status predicted

Query Match 35.1%; Score 474; DB 1; Length 106;
Best Local Similarity 83.8%; Pred. No. 3, 2e-25;
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 149 YELMQLPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYGDNRKPSGIPERF 208
Db 1 YGLTQPPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYHNSKRPSSGIPERF 60

QY 209 SGNNSGNTATLTISGTQAMDEADYCCQAMDSTAVFGTGTCLTVL 253
Db 61 SGNNSGNTATLTISGTQAMDEADYCCQAMDSYVIVGGGTCLTVL 105

RESULT 10
S16440
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S16440
R/Combrlato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A>Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin la
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S16440
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <COM>
A/Cross-references: EMBL:X57826
C/Genetics:
A/Intons: 16/1
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.4%; Score 478; DB 2; Length 231;
Best Local Similarity 83.6%; Pred. No. 3, 9e-25;
Matches 92; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 144 GGGSSYLEMQLPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYGDNRKPSG 203
Db 16 GSVAASYELTQPPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYQDSKRPSSG 75

QY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCOAMDSTGA 242
 Db 76 IPERFSGNSGNTATLTISGTQAMDEADYYCOAMDSSSTA 114

RESULT 11

257573
 Ig lambda chain - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S25753
 R/Contributor: G. Klobeck, H.G.
 A/Title: V(Lambda) 21, 1513-1522, 1991
 A/Reference number: S16439; PMID:91257162; PMID:1904362
 A/Accession: S25753
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-231 <COM>
 A/Cross-references: EMBL:X57818; NID:g33735; PIDN:CAA40955.1; PID:g33736
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/146-214/Domain: immunoglobulin homology <IMM>

Query Match 34.9%; Score 472; DB 2; Length 231;
 Best Local Similarity 80.9%; Pred. No. 9.8e-25;
 Matches 89; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 144 GGGSTYELMQLPSVSVSPQGTASITCSGDNIGDKYACWYQKRPSPVLYIGDKRPSGIPER 203
 Db 16 GSVASSTYELTQPPSVSVSPQGTASITCFDCKDKXSMYQKRPSPVLYIGDKRPSGIPER 75
 QY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCOAMDSTGAFTGKTLTVL 253
 Db 76 IPERFSGNSGNTATLTISGTQAMDEADYYCOAMDSTGAVFGGKTLTVL 125

RESULT 12

S36065
 Ig lambda chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
 C/Accession: S36065
 R/Williams, S.C.
 A/Submitted to the EMBL Data Library, April 1993
 A/Reference number: S36046
 A/Accession: S36065
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-95 <WILL>
 A/Cross-references: EMBL:Z22208; NID:g312871; PIDN:CAA80216.1; PID:g312872
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 470; DB 2; Length 95;
 Best Local Similarity 92.6%; Pred. No. 5.3e-25;
 Matches 88; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 148 STYELMQLPSVSVSPQGTASITCSGDNIGDKYACWYQKRPSPVLYIGDKRPSGIPER 207
 Db 1 STYELTQPPSVSVSPQGTASITCSGDKLDDKXACWYQKRPSPVLYIGDKRPSGIPER 60
 QY 208 FSGNSGNTATLTISGTQAMDEADYYCOAMDSTGA 242
 Db 61 FSGNSGNTATLTISGTQAMDEADYYCOAMDSSSTA 95

RESULT 13

LAHUX
 Ig lambda chain V-IV region (X) - human
 C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
 C/Accession: A01982
 R/Milstein, C.; Clegg, J.B.; Jarvis, J.M.
 Biochem. J. 110, 631-652, 1968
 A/Title: Immunoglobulin lambda-chain. The complete amino acid sequence of a Bence-Jon
 A/Reference number: A90243; PMID:69088380; PMID:4883841
 A/Accession: A01982
 A/Molecule type: protein
 A/Residues: 1-106 <MIL>
 C/Comment: This is a Bence Jones protein.
 C/Genetics:
 A/Gene: GDB:IGLV6
 A/Cross-references: GDB:119342; OMIM:147240
 A/Map position: 22q11.2-22q11.2
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k)
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer
 F/14-88/Domain: immunoglobulin homology <IMM>
 F/21-86/Disulfide bonds: #status predicted

Query Match 34.8%; Score 470; DB 1; Length 106;
 Best Local Similarity 83.8%; Pred. No. 5.9e-25;
 Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 149 YELMQLPSVSVSPQGTASITCSGDNIGDKYACWYQKRPSPVLYIGDKRPSGIPER 208
 Db 1 YDLTQPPSVSVSPQGTASITCSGDKLDDKXACWYQKRPSPVLYIGDKRPSGIPER 60
 QY 209 SGNNSGNTATLTISGTQAMDEADYYCOAMDSTGAFTGKTLTVL 253
 Db 61 SGNNSGNTATLTISGTQAMDEADYYCOAMDSTGAVFGGKTLTVL 105

RESULT 14

S31513
 Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C/Accession: S31513
 R/Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
 Submitted to the EMBL Data Library, December 1992
 A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut
 A/Reference number: S31509
 A/Accession: S31513
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-138 <CHA>
 A/Cross-references: EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PID:g33085
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/30-114/Domain: immunoglobulin homology <IMM>

Query Match 34.7%; Score 469; DB 2; Length 138;
 Best Local Similarity 74.0%; Pred. No. 9.1e-25;
 Matches 94; Conservative 7; Mismatches 20; Indels 6; Gaps 2;

QY 1 QVTLKESGPTLVKPGTTLTCTLSGFSISGVSVMINQPPKALSLTASINMDDKC 60
 Db 16 QTLKESGPTLVKPGTTLTCTLSGFSISGVSVMINQPPKALSLTASINMDDKC 75
 QY 61 YSPSLKSLTITTKTPKXQVVLANSNMDPADTATYSCALDMPHDSQPSFDAS-DVWGP 119
 Db 76 YSPSLKSLTITTKTQSONQVVLTWNTMDPVDATATYCA-----HRGIAVATGKNFDYMQQ 130
 QY 120 GTMVTVS 126
 Db 131 GTLVTVS 137

RESULT 15

SG9339
 Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #ext_change 01-Dec-2000
 C:Accession: S69339; S72664
 R:Khamlich, A.A.; Aucturiarier, P.; Preud'homme, J.L.; Cogne, M.
 Eur. J. Biochem. 229, 54-60, 1995
 A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
 A:Reference number: S69339; PMID:95262687; PMID:7744049
 A:Accession: S69339
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <KHA>
 A:Cross-references: EMBL:X81695
 R:Khamlich, A.A.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S72664
 A:Accession: S72664
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140, 'C', 142-374 <KH2>
 A:Cross-references: EMBL:X81695
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 34.5%; Score 466; DB 2; Length 374;
 Best local similarity 71.7%; Pred. No. 4.1e-24;
 Matches 91; Conservative 11; Mismatches 21; Indels 4; Gaps 1;

QY	1	QVTLKESGPTLVKPTOTLTTLCTLSGFSSTSGSVGVGWIROPFGKALEWLASINNDKC	60
DB	20	QITLKESGPTLVKPTOTLTTLCTFSGFSLSKSGVGWIRPGQALEWIALIFWDDDR	79
QY	61	YSPSLKSRLLTTRDPKNOVLAMSNMDPADTATYSCALDMPHDSGPOSFDASDVWGPG	120
DB	80	YSPSLRTRLLTTRDKSKNOVLMTINVPADTATYTCGYSGVGGRFHS---WGOG	135
QY	121	TWTVSS	127
DB	136	TLTVSS	142

Search completed: May 13, 2004, 15:08:43
 Job time : 11.4218 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.1233 Seconds

(without alignments)
1849.388 Million cell updates/sec

Title: US-10-072-301-25

Sequence: 1351
1 QVTLKESGPTLVKPTQTTL.....CQAMDSTAVFGNGTKLTVL 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	474	35.1	106	LV4A_HUMAN	P01715 homo sapien
2	470	34.8	106	LV4B_HUMAN	P01716 homo sapien
3	457	33.8	125	HV2D_HUMAN	P01817 homo sapien
4	441	32.6	106	LV4E_HUMAN	P06889 homo sapien
5	436	32.3	121	HV2E_HUMAN	P01818 homo sapien
6	423.5	31.3	120	HV2B_HUMAN	P01815 homo sapien
7	418	30.9	107	LV4C_HUMAN	P01717 homo sapien
8	403	29.8	106	LV4D_HUMAN	P01718 homo sapien
9	398.5	29.5	147	LV4H_HUMAN	P04438 homo sapien
10	393	29.1	108	LV5A_HUMAN	P01719 homo sapien
11	389	28.8	111	LV3B_HUMAN	P80748 homo sapien
12	384	28.4	119	HV2C_HUMAN	P01816 homo sapien
13	369.5	27.4	126	HV2A_HUMAN	P01817 homo sapien
14	351	26.0	108	LV3A_HUMAN	P01714 homo sapien
15	351	26.0	111	LV7D_HUMAN	P01720 homo sapien
16	337	24.9	111	LV7E_HUMAN	P01702 homo sapien
17	336	24.9	130	LV1G_HUMAN	P06316 homo sapien
18	325	24.1	109	LV1F_HUMAN	P04208 homo sapien
19	324	24.0	129	HV2F_HUMAN	P01824 homo sapien
20	324	24.0	144	HV4J_MOUSE	P01819 mus musculu
21	320	23.7	109	LV1I_HUMAN	P06888 homo sapien
22	319	23.6	111	LV2G_HUMAN	P01710 homo sapien
23	317	23.5	111	LV1C_HUMAN	P01701 homo sapien
24	313.5	23.2	112	LV1B_HUMAN	P01700 homo sapien
25	312	23.1	111	LV2E_HUMAN	P01709 homo sapien
26	310	22.9	109	LV2F_HUMAN	P01708 homo sapien
27	309.5	22.9	110	LV2J_HUMAN	P01713 homo sapien
28	309	22.9	111	LV2C_HUMAN	P01706 homo sapien
29	308.5	22.8	112	LV2K_HUMAN	P04209 homo sapien
30	303.5	22.5	112	LV1H_HUMAN	P06887 homo sapien
31	303.5	22.5	112	LV6A_HUMAN	P01721 homo sapien
32	302	22.4	111	LV6C_HUMAN	P06317 homo sapien
33	301	22.3	111	LV2I_HUMAN	P01712 homo sapien

34	296.5	21.9	131	1	LV6E_HUMAN	P06319 homo sapien
35	294	21.8	111	1	LV2B_HUMAN	P01705 homo sapien
36	292.5	21.7	135	1	HV02_XENLA	P20957 xenopus lae
37	290	21.5	137	1	HV46_MOUSE	P01822 mus musculu
38	289	21.4	111	1	LV2A_HUMAN	P01704 homo sapien
39	283	20.9	111	1	LV1A_HUMAN	P01699 homo sapien
40	283	20.9	111	1	LV6D_HUMAN	P06318 homo sapien
41	280.5	20.8	116	1	HV6I_MOUSE	P18532 mus musculu
42	279	20.7	115	1	HV44_MOUSE	P01820 mus musculu
43	277	20.5	111	1	LV2H_HUMAN	P01711 homo sapien
44	275.5	20.4	112	1	LV6B_HUMAN	P01722 homo sapien
45	274	20.3	111	1	LV2D_HUMAN	P01707 homo sapien

ALIGNMENTS

RESULT 1	LV4A_HUMAN	STANDARD;	PRT;	106 AA.
ID	P01715;			
AC	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Ig lambda chain V-IV region Bau.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=75059189; PubMed=4435717;			
RA	Baczko K., Braun D., Hilschmann N.;			
RT	Pattern of antibody structure, the primary structure of monoclonal			
RT	immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones			
RT	protein Bau.)			
RL	Hoppe-Sevler's Z. Physiol. Chem. 355:131-154(1974).			
CC	-1- MISCELLANEOUS: This is a Bence-Jones protein.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR; A01981; L4HDBU.			
DR	HSSP; P80748; 2LOI.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; P:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Bence-Jones protein.			
FT	DOMAIN 1 102			
FT	NON_TER 106			
SQ	SEQUENCE 106 AA; 11305 MW; 4B6A688E0EC46571 CRC64;			
Query Match	35.1%; Score 474; DB 1; Length 106;			
Best Local Similarity	83.8%; Pred. No. 7.4e-28;			
Matches	88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;			
QY	149 YELMLPSVSVSGQTASTTCGSDNIGDYACWYQOKPGRSPVLVYGDNKRPSGIPERF 208			
DB	1 YGLTGPSPSLSVSGQASTTTCGSDKLGEGYVCMYQOKPQSPVLVYHNSKRSGLPERF 60			
QY	209 SGSGNSGNTATLTITSGTQAMDEADYVQAMDSTAVFGTKLTVL 253			
DB	61 SGSGNSGNTATLTITSGTQAMDEADYVQAMDSTAVFGTKLTVL 105			
RESULT 2				
LV4B_HUMAN	STANDARD;	PRT;	106 AA.	
ID	P01716;			
AC	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			

DR 10-OCT-2003 (Rel. 42, Last annotation update)
DR IG lambda chain V-IV region X.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=6908380; PubMed=4883841;
RA Milstein C., Clegg J.B., Jarvie J.M.,
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RL Biochem. J. 110:631-652(1968).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01982; L4HUX.
DR HSSP; P80748; 2L0T.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 102 IG-LIKE.
FT NON TER 106 106
SQ SEQUENCE 106 AA; 11334 MW; 24D04344A812855 CRC64;

Query Match 34.8%; Score 470; DB 1; Length 106;
Best Local Similarity 83.8%; Pred. No. 1.4e-27;
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 149 YELMQLPSVSVSPQQTASITCSGDNLDGKYACWYQKRGSPVLYYGNKRSPTPERF 208
DB 1 YDLRQPSVSVSPQQTASITCSGDKLDKVCWYQKRGSPVLYYGNKRSPTPERF 60
QY 209 SGSNSGNTATLTISGTQAMDEADYVCOAMDSTAVFGTGTGTLTVL 253
DB 61 SGSNSGNTATLTISGTQAMDEADYVCOAMDSTAVFGTGTGTLTVL 105

RESULT 3
HV2D HUMAN STANDARD; PRT; 125 AA.
AC P01817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-II region MCB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=8118242; PubMed=6780622;
RA Gerber-Jensen B., Kazin A., Kenoe J.M., Erickson B.W.,
RT Litman G.W.,
RT "Molecular basis for the temperature-dependent insolubility of
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
RT region of MCB";
RL J. Immunol. 126:1212-1216(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
CC CRYOIMMUNOGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02092; MHMUC.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1-like.

DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT DOMAIN 1 113
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT NON TER 125 125
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF40F47B5 CRC64;

Query Match 33.8%; Score 457; DB 1; Length 125;
Best Local Similarity 70.9%; Pred. No. 1.5e-26;
Matches 90; Conservative 11; Mismatches 24; Indels 2; Gaps 1;
QY 1 QVTLKSGPTLVKPTQTLTLCTLTGFSISTSGVGMROPKALFIMLWINDKX 60
DB 1 QTLKSGPTLVKPTQTLTLCTLTGFSISTSGVGMROPKALFIMLWINDKX 60
QY 61 YSPSLKSLRTTKDTPKQVYVLAQNDPADTATYSCALDMPHDSQSFSDASDVGPG 120
DB 61 YSPSLKSLRTTKDTPKQVYVLAQNDPADTATYSCALDMPHDSQSFSDASDVGPG 118
QY 121 TWTVSS 127
DB 119 TLTVSS 125

RESULT 4
LV4E HUMAN STANDARD; PRT; 106 AA.
AC P06889;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-IV region MOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=87156515; PubMed=3103603;
RA Holm E., Sletten K., Huby G.,
RT "Structural studies of a carbohydrate-containing
RT immunoglobulin-lambda-light chain amyloid fibril protein (AL) of
RT variable subgroup IIT";
RL Biochem. J. 239:545-551(1986).
CC -1- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
CC HOMOLOGY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26019; L4HUX.
DR HSSP; P80748; 2L0T.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT DOMAIN 1 103
FT DISULFID 21 86 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (PROBABLE).
FT NON TER 106 106
SQ SEQUENCE 106 AA; 11272 MW; D9BB77D4797D2123 CRC64;

Query Match 32.6%; Score 441; DB 1; Length 106;
Best Local Similarity 77.1%; Pred. No. 1.7e-25;
Matches 81; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
QY 149 YELMQLPSVSVSPQQTASITCSGDNLDGKYACWYQKRGSPVLYYGNKRSPTPERF 208

DB 1 YELTOPSVSVSPGQTATISCSGDKLGESYDWWQSPGSPULVIYEGDKRPSGIPZRF 60
 QY 209 SGSNSGNTATLTISGTOAMDEADYCOAMDTSTAVAGTGKLTVL 253
 DB 61 SGSNSGNTATLTISGTSMDADYCOAMSSSVLFGGKLTVL 105

RESULT 5

HV2E_HUMAN STANDARD; PRT; 121 AA.

AC P01818;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region HE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;

SEQUENCE

RA MEDLINE=70114712; PubMed=5264153;
 RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
 RT "Subgroups of amino acid sequences in the variable regions of
 immunoglobulin heavy chains";
 RL Proc. Natl. Acad. Sci. U.S.A. 64:1997-1003(1969).
 CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
 CELL LINE.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02093; GIHUE.

DR HSSP; P01825; 7FAB.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding; NAS.

DR GO; GO:0005953; P:immune response; NAS.

DR InterPro; IPR007110; Ig_Like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Pyroliidone carboxylic acid.

FT DOMAIN 1 120 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 1 120

FT NON_TER 121 121

FT SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 32.3%; Score 436; DB 1; Length 121;
 Best Local Similarity 68.8%; Pred. No. 4.6e-25;

Matches 88; Conservative 13; Mismatches 19; Indels 8; Gaps 3;

QY 1 QVTLKSGPTLVKPTOTLTCTLSGFSSTSGSVSGMIRPGKALEWLA-SINMNDK 59
 DB 1 QVTLKSGPTLVKPTOTLTCTLSGFSSTSGSVSGMIRPGKALEWLA-SINMNDK 60
 QY 60 CSPSLKSLRTITKDPKQOVVLAMSNMPPADPATYSCALDMPHSGPSPADSWGP 119
 DB 61 RSPSLKSLRTITKDPKQOVVLAMSNMPPADPATYSCALDMPHSGPSPADSWGP 113
 QY 120 GTWVTYSS 127
 DB 114 GTFKAVSS 121

RESULT 6

HV2B_HUMAN STANDARD; PRT; 120 AA.

AC P01815;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region COR.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_Taxid=9606;

SEQUENCE

RA MEDLINE=70258837; PubMed=5449120;

RA Press E.M., Hogg N.M.;

RT "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains";
 RL Biochem. J. 117:641-660(1970).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CELL LINE.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02089; GIHUCO.

DR HSSP; P01825; 7FAB.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding; NAS.

DR GO; GO:0005953; P:immune response; NAS.

DR InterPro; IPR007110; Ig_Like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Glycoprotein; Pyroliidone carboxylic acid.

FT DOMAIN 1 110 IG-LIKE.

FT MOD RES 1 110 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 22 94

FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).

FT NON_TER 120 120

FT SEQUENCE 120 AA; 13226 MW; 158A8B29AE7BB98 CRC64;

Query Match 31.3%; Score 423.5; DB 1; Length 120;
 Best Local Similarity 67.2%; Pred. No. 3.6e-24;

Matches 86; Conservative 14; Mismatches 19; Indels 9; Gaps 3;

QY 1 QVTLKSGPTLVKPTOTLTCTLSGFSSTSGSVSGMIRPGKALEWLA-SINMNDK 60
 DB 1 QVTLKSGPTLVKPTOTLTCTLSGFSSTSGSVSGMIRPGKALEWLA-SINMNDK 60
 QY 61 YPSLSKSLRTITKDPKQOVVLAMSNMPPADPATYSCA-LDMPHSGPSPADSWGP 119
 DB 61 YPSLSKSLRTITKDPKQOVVLAMSNMPPADPATYSCA-LDMPHSGPSPADSWGP 112
 QY 120 GTWVTYSS 127
 DB 113 GTFKAVSS 120

RESULT 7

LIV4C_HUMAN STANDARD; PRT; 107 AA.

AC P01717;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-IV region H11.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_Taxid=9606;

SEQUENCE.

RA MEDLINE=78187276; PubMed=418804;

RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;

RT "Amino acid sequence of the variable region of the light (lambda)
 chain from human myeloma cryoimmunoglobulin IgG H11.";
 RL Biochemistry 17:1718-1723(1978).

CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
 IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
 155-118 (H1L NUMBERING) INSTEAD OF V1L.

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR; A01983; L4HDL.

DR HSSP; P80748; 21OI.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO:0003823; F:antigen binding; NAS.
 DR GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 97
 FT NON TER 107 107 IG-LIKE.
 SQ SEQUENCE 107 AA; 11517 MW; A5C9AFBE0CC590A CRC64;

Query Match 30.9%; Score 418; DB 1; Length 107;
 Best Local Similarity 74.5%; Pred. No. 7.9e-24;
 Matches 79; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 148 SYELMLPSVSPGQTASTTCGGDNLGKVCYQKRGSPVLVIYGDNRKPSGIPER 207
 DB 1 SYELTPPSVSPGQTASTTCGGDNLGKVCYQKRGSPVLVIYKDTPRSGIPOR 60
 QY 208 FSGNSGNTATLTISGTCQAMDEADYVCOAMDSTVFGTKLTVL 253
 DB 61 FSSSTGTTVTLTISGVQMEDADYVCOAMDNSASIFGGTKLTVL 106

RESULT 8
 ID LV4D_HUMAN STANDARD; PRT; 106 AA.
 AC P01718;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-IV region Kern.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71150336; PubMed=5549568;
 RA Ponstingl H., Hees M., Hilschmann N.;
 RT "Structural rule of antibodies. Primary structure of a monoclonal
 RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
 RT protein Kern). V. The complete amino acid sequence and its genetic
 RT interpretation.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ MARKER.
 CC -1- SMITILARITY: This is a Bence-Jones protein.
 DR PIR; A01984; L4HUKN.
 DR HSSP; P80748; 2LOI.
 DR GO:0005576; C:extracellular; NAS.
 DR GO:0003823; F:antigen binding; NAS.
 DR GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 102
 FT DISULFID 21 86 BY SIMILARITY.
 FT NON TER 106 106
 SQ SEQUENCE 106 AA; 11277 MW; C8B4A05B9CB43CBE CRC64;

Query Match 29.8%; Score 403; DB 1; Length 106;
 Best Local Similarity 72.4%; Pred. No. 9.4e-23;
 Matches 76; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 149 YELMLPSVSPGQTASTTCGGDNLGKVCYQKRGSPVLVIYGDNRKPSGIPER 208
 DB 1 YALTPPSVSPGQTASTTCGGDNLGKVCYQKRGSPVLVIYHTSRSPSEIPER 60

QY 209 SGNSGNTATLTISGTCQAMDEADYVCOAMDSTVFGTKLTVL 253
 DB 61 SGSSGNTATLTISGASVDEADYFCQMTDITRAIFGGTKLTVL 105

RESULT 9
 ID HVZH_HUMAN STANDARD; PRT; 147 AA.
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region SESS precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84298107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RT "Rearranged immunoglobulin heavy chain variable region (VR)
 RT pseudogene that deletes the second complementarity-determining
 RT region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 DR PIR; A02090; G2HUCS.
 DR HSSP; P01825; 7FAB.
 DR GO:0005576; C:extracellular; NAS.
 DR GO:0003823; F:antigen binding; NAS.
 DR GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SESS.
 FT DOMAIN 20 118 V SEGMENT.
 FT DOMAIN 119 132 D SEGMENT.
 FT DOMAIN 133 147 J SEGMENT.
 FT NON TER 147 147
 SQ SEQUENCE 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;

Query Match 29.5%; Score 398.5; DB 1; Length 147;
 Best Local Similarity 63.9%; Pred. No. 2.8e-22;
 Matches 78; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLTCTLSGFSSTSGSVGWRORPKRLKLEWLASINNDKX 60
 DB 20 QVNLRESGPAVLVKAHTLTITCTFSGLSVNTKMSVSWTRORPGALEWLAIDWDKX 79
 QY 61 YSSSLKSLRLTITCTPKNOVVLAMSNMDPADATATYSCA-LDMPPHDSGQSFDAEDVNGP 119
 DB 80 YGTSLETRLTISKDTSKNQVVLKVTMDPADATATYCARMQVTWREWITSNARDINGQ 139

QY 120 GT 121
 DB 140 GT 141

RESULT 10
 ID LV5A_HUMAN STANDARD; PRT; 108 AA.
 AC P01719;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-V region DEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;

[1]
 RN SEQUENCE.
 RX MEDLINE=75112179; PubMed=4452363;
 RA Eulitz M.;
 RT "A new subgroup of human L-chains of the lambda-type. Primary
 structure of Bence-Jones protein DEL.",
 RL Eur. J. Biochem. 50:49-69(1974).
 CC -1- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
 CHAIN SUBGROUP V.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A01985; LSHUDL.
 DR HSSP; P80748; 2LOI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 97
 FT NON_TER 108 108
 FT SEQUENCE 108 AA; 11342 MW; B8E8BD9C09CE451 CRC64;
 SQ
 Query Match 29.1%; Score 393; DB 1; Length 108;
 Best Local Similarity 71.0%; Pred. No. 5e-22;
 Matches 76; Conservative 9; Mismatches 20; Indels 2; Gaps 1;
 QY 149 YEIMQLPSVSVSPGQTASITCGSDNIGDKYACMYOQKPSRPLYVYGNKRPSPGIPERF 208
 DB 1 YVLTQPPSVSVAPGQTARITCGSDIGSGSVHMYQKPGQAPLVYVHEDNRAGIPERF 60
 QY 209 SGNNGNTATLTITSGTQAMDEADYVCOAMDST--VFSTGTGLTVL 253
 DB 61 SGNNGNTATLTISRVEAGDEADYVCEVDDRTAHVVFSGTGLTVL 107
 RESULT 11
 LV3B HUMAN STANDARD; PRT; 111 AA.
 AC P80748;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-II region LOI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
 RC TISSUE=Trine;
 RX MEDLINE=99441384; PubMed=10510403;
 RA Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
 RT "Nephrilysin, lambda light chain dimer: a unique human
 minautoantibody against complement factor H.",
 RL J. Immunol. 163:4590-4596(1999).
 CC -1- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
 TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
 CC -1- SUBUNIT: Homodimer.
 CC -1- DISEASE: The blocking of factor H by LOI protein leads to the
 development of membranoproliferative glomerulonephritis (MPGN).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PDB; 2LOI; 29-DEC-99.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_V.
 DR InterPro; IPR003596; IGV.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT DOMAIN 1 97
 FT BINDING 15 15 SCR3.
 FT BINDING 25 25 SCR3.
 FT BINDING 29 29 SCR3.
 FT BINDING 48 51 SCR3.
 FT BINDING 94 94 SCR3.
 FT DISULFID 21 86 BY SIMILARITY.
 FT STRAND 4 4
 FT STRAND 8 8
 FT TURN 13 14
 FT TURN 16 22
 FT STRAND 32 37
 FT TURN 38 40
 FT STRAND 41 46
 FT TURN 49 50
 FT STRAND 54 54
 FT TURN 55 55
 FT TURN 58 59
 FT STRAND 60 61
 FT STRAND 64 65
 FT TURN 66 67
 FT STRAND 68 74
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 91 93
 FT STRAND 97 98
 FT STRAND 102 104
 FT TURN 107 108
 FT NON_TER 111 111
 FT SEQUENCE 111 AA; 11935 MW; 69498BEBFDE82053 CRC64;
 SQ
 Query Match 28.8%; Score 389; DB 1; Length 111;
 Best Local Similarity 70.1%; Pred. No. 1e-21;
 Matches 75; Conservative 12; Mismatches 18; Indels 2; Gaps 1;
 QY 149 YEIMQLPSVSVSPGQTASITCGSDNIGDKYACMYOQKPSRPLYVYGNKRPSPGIPERF 208
 DB 1 YVLTQPPSVSVAPGQTARITCGSDIGSGSVHMYQKPGQAPLVYVHEDNRAGIPERF 60
 QY 209 SGNNGNTATLTITSGTQAMDEADYVCOAMDST--VFSTGTGLTVL 253
 DB 61 SGNNGNTATLTISRVEAGDEADYVCEVDDRTAHVVFSGTGLTVL 107
 RESULT 12
 HV2C HUMAN STANDARD; PRT; 119 AA.
 AC P01816;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region DAW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains.",
 RL Biochem. J. 117:641-660(1970).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
 SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02091; G1HDM.
 DR HSSP; P01789; IMCP.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; IgV_1.
 DR SMART: SM00406; IGv_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Pyroliadone carboxylic acid.
 FT DOMAIN 1 113
 FT MOD RES 1 113
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 13045 MW; 4813800214BAD789 CRC64;

Query Match
 Best Local Similarity 28.4%; Score 384; DB 1; Length 119;
 Matches 79; Conservative 12; Mismatches 28; Indels 8; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTCTLSGFSLSGVSVMIRPPGKALEWLASINNDKX 60
 DB 1 QVTLKESGPTLVKPTQTLTCTLSGFSLSGVSVMIRPPGKALEWLASINNDKX 60
 QY 61 YSPSLKRLTITKDTKPNQVVLAMSNMADPATATYSCALDMPHDSGQSPDASDVPWGP 120
 DB 61 YASLSLRLAVSKDTSKNQVVLAMNTVGRDITATYCA-----RSCGSGYF---DYWGQG 112
 QY 121 TMTVSS 127
 DB 113 ILVTSS 119

RESULT 13

ID HV2A_HUMAN STANDARD; PRT; 126 AA.
 AC P01814;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-IT region OU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74005511; PubMed=4742735;
 RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;
 RT "Complete amino acid sequence of the mu heavy chain of a human IgM
 immunoglobulin."
 RL Science 182:287-291(1973).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02088; MHUOU.
 DR HSSP: P01825; 7PAB.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG_LIKE.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IgV_1.
 DR SMART: SM00406; IGv_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Pyroliadone carboxylic acid.
 FT DOMAIN 1 113
 FT MOD RES 1 113
 FT NON TER 126 126
 FT DISULFID 126 97
 FT DISULFID 126 126
 SQ SEQUENCE 126 AA; 14276 MW; A85C0B80DAB2C96F CRC64;

Query Match

Best Local Similarity 27.4%; Score 369.5; DB 1; Length 126;
 Matches 80; Conservative 15; Mismatches 30; Indels 3; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLTCTLSGFSLSGVSVMIRPPGKALEWLASINNDKX 60
 DB 1 QVTLKESGPTLVKPTQTLTCTLSGFSLSGVSVMIRPPGKALEWLASINNDKX 60

DB 1 QVTLKESGPTLVKPTQTLTCTLSGFSLSGVSVMIRPPGKALEWLASINNDKX 60
 QY 61 YSPSLKRLTITKDTKPNQVVLAMSNMADPATATYSCALDMPHDSGQSPDASDVPWGP 119
 DB 60 YMSLSLRLAVSKDTSKNQVVLAMNTVGRDITATYCA-----RSCGSGYF---DYWGQG 118
 QY 120 GTMTVSS 127
 DB 119 GTTVVSS 126

RESULT 14

ID LV3A_HUMAN STANDARD; PRT; 108 AA.
 AC P01720;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-VII region SH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=7016723; PubMed=4909564;
 RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
 complete amino acid sequence and the location of the disulfide
 bridges."
 RL J. Biol. Chem. 245:2171-2176(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A01980; L3HUSH.
 DR HSSP: P80749; 2LOI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG_LIKE.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IgV_1.
 DR SMART: SM00406; IGv_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 97
 FT DISULFID 21 97
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match
 Best Local Similarity 26.0%; Score 351; DB 1; Length 108;
 Matches 70; Conservative 14; Mismatches 20; Indels 2; Gaps 1;

QY 150 ELMOLPVSVSFGQPTATITGSGDNLGDKYACMYOQKQSPVLVYGDNKRPSGIPRFS 209
 DB 2 ELTQDPVAVSVAGQTVRITTCGDSLRGYDAWYQKQKGAFLVITYRANRPSGIPRFS 61

QY 210 GSNAGTATLTISGQANDADYYCOAMDTS--TAVGTGTLTVL 253
 DB 62 GSSGHTASLTITGAQADEADYYCNSRDSGKRVLFGGQTKLTVL 107

RESULT 15

ID LV7A_HUMAN STANDARD; PRT; 111 AA.
 AC P01720;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-VII region MOT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81122740; Pubmed=6780787;
 RA Kojima M., Odani S., Ikenaka T.;
 RT "Amino acid sequence of the lambda type light chain of a human IgG1
 myeloma protein (MOT) with unusual antigenicity: a possible new
 subgroup of lambda chain having a unique N-terminal sequence.";
 RL Mol. Immunol. 17:1407-1414(1980).
 CC -1- MISCELLANEOUS: THIS SEQUENCE REPRESENTS A NEW LAMBDA CHAIN
 SUBGROUP. IT HAS AN AMINO-TERMINAL EXTENSION OF THREE RESIDUES
 COMPARED WITH OTHER HUMAN LAMBDA CHAINS.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
 MARKERS.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A01986; L7H0MT.
 DR HSSP; P80748; ZLOT.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 105 IG-LIKE.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11942 MW; 140A28A2F86A6911 CRC64;

Query Match 26.0%; Score 351; DB 1; Length 111;
 Best Local Similarity 61.7%; Pred. No. 5.4e-19;
 Matches 66; Conservative 17; Mismatches 22; Indels 2; Gaps 1;
 QY 149 YEIMQLPSVSVSGQTASITCSGDNLGDKYACWYQOKPGSPVLYIGDNKRPSGIPERF 208
 DB 4 YELTOPPSVSLAAGQTAMITCEGNDIGERSVHWYQOKPGQAPVPVYDDADRRSGVPAHF 63
 QY 209 SGSNSGNTATLTITSGTQAMDEADYCOANDTST--AVFGTGKLTVL 253
 DB 64 SGYNSGNSAILTITNVEAGDEADYFCQSWDNGSYEVVFGTGMVTVL 110

Search completed: May 13, 2004, 15:02:05
 Job time : 7.1233 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 34.0199 Seconds

(without alignments)
2346.453 Million cell updates/sec

Title: US-10-072-301-25

Perfect score: 1351
Sequence: 1 QVTLKESGPTLVKPTQTLTL.....CQAMDSTAVFGTGTQTLTL 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528.5	39.1	298	11	Q9QYF0
2	472.2	34.9	241	11	Q921A6
3	460	33.6	121	4	Q9UL96
4	454	33.6	243	11	Q7TQW2
5	419.5	31.1	218	11	Q925S1
6	417	30.9	233	4	Q8TBC9
7	410.5	30.4	234	4	Q8N355
8	390.5	28.9	118	11	Q8N1U5
9	389	28.8	233	4	Q8NSF4
10	382.5	28.3	107	4	Q9UL82
11	376	27.8	97	4	Q43334
12	374	27.7	107	4	Q9NSD6
13	368.5	27.3	234	4	Q7Z2U7
14	353	26.1	233	4	Q96169
15	346	25.6	492	4	Q7Z374
16	335	24.8	110	4	Q8TE63

17	328.5	24.3	150	4	Q95973	Q95973 homo sapien
18	327.5	24.2	236	4	Q8NEJ1	Q8NEJ1 homo sapien
19	324.5	24.0	496	4	Q96KX8	Q96KX8 homo sapien
20	320	23.7	613	4	Q96EY0	Q96EY0 homo sapien
21	319.5	23.6	588	4	Q8WUX4	Q8WUX4 homo sapien
22	319.5	23.6	597	4	Q9BU10	Q9BU10 homo sapien
23	319.5	23.6	618	4	Q96AA6	Q96AA6 homo sapien
24	318.5	23.6	236	4	Q96E61	Q96E61 homo sapien
25	317	23.5	237	4	Q8WTK4	Q8WTK4 homo sapien
26	316.5	23.4	597	4	Q9BQB8	Q9BQB8 homo sapien
27	315.5	23.4	478	4	Q7Z379	Q7Z379 homo sapien
28	315	23.3	237	4	Q8WTK6	Q8WTK6 homo sapien
29	314.5	23.3	130	4	Q81ZD7	Q81ZD7 homo sapien
30	312	23.1	101	4	Q81ZD8	Q81ZD8 homo sapien
31	310.5	23.0	121	11	Q99NG4	Q99NG4 mus musculu
32	310.5	23.0	479	11	Q99M22	Q99M22 mus musculu
33	310.5	23.0	482	11	Q91X92	Q91X92 mus musculu
34	307	22.7	116	4	Q96UD0	Q96UD0 homo sapien
35	305.5	22.6	112	4	Q96UD1	Q96UD1 homo sapien
36	305	22.6	119	4	Q9UL73	Q9UL73 homo sapien
37	301	22.3	613	4	Q8WTK1	Q8WTK1 homo sapien
38	295.5	21.9	122	4	Q9UL75	Q9UL75 homo sapien
39	295	21.8	112	4	Q96UD2	Q96UD2 homo sapien
40	294	21.8	235	11	Q99M11	Q99M11 mus musculu
41	293	21.7	81	4	Q7Z2E8	Q7Z2E8 homo sapien
42	291.5	21.6	473	4	Q8TC63	Q8TC63 homo sapien
43	291	21.5	108	4	Q96S80	Q96S80 homo sapien
44	290	21.5	499	4	Q8NSK4	Q8NSK4 homo sapien
45	282	20.9	139	4	Q86SX2	Q86SX2 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9QYF0	PRELIMINARY;	PRT;	298 AA.
AC	Q9QYF0;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	CN 8 scFv.			
GN	CN 8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Balb/C; TISSUE=Spleen;			
RX	MEDLINE=20183931; PubMed=10706631;			
RA	Shinohara N., Demura T., Fukuda H.;			
RT	"Isolation of a vascular cell wall-specific monoclonal antibody			
RT	recognizing a cell polarity by using a phase display subtraction			
RT	method."			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).			
DR	EMBL; AB036341; BAA8633.1; -.			
DR	PIR; A39333; A39333.			
DR	PIR; S19112; S19112.			
DR	HSSP; P01607; IRII.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_2.			
DR	SMART; SM00406; IGV; 2.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
SQ	SEQUENCE 298 AA; 31867 MW; E0P96B8A17004317 CRC64;			

Query Match 39.1%; Score 528.5; DB 11; Length 298;
Best Local Similarity 46.1%; Pred. No. 7.9e-35;
Matches 117; Conservative 27; Mismatches 93; Indels 17; Gaps 5;
1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSSTGVSQWIRDPGKALEWLASINWDDKC 60

SEQUENCE 243 AA; 25976 MW; BEP64D2DCFA76 CRC64;
Query Match 33.6%; Score 454; DB 11; Length 243;
Best Local Similarity 40.5%; Pred. No. 6.5e-29;
Matches 106; Conservative 42; Mismatches 78; Indels 36; Gaps 10;
QY 1 QVTLKSGPLVPTOTLTITCTSGFSLSTSGVSGWIRPPKALTEMLASI-----53
DB 1 QVQLOQSGSELVPRGASVSLSCASGVTPTTMMH--WKORRGGGLEMIIGIYPPSGIT 58
QY 54 MNMDDKCYSPSLKSLRLITKDPKNOVLAMSNMDDADATATYSCALDMPHDSGPOSFPA 113
DB 59 N-----YDEKFKNGKILFTVDTSSSTAYMHLSSLASDESAVYYCA-----RGGRG 102
QY 114 SDVWGEGTAVTVSSGGGGSGGGGGSGGGSSSTELMQ-LPSVSVSPQQTASITC-SG 171
DB 103 LDVWAGTTLTVS-----SGGGSGGGGGSGGGSGDQOMQSSSFSVSLGDRITITCKAS 157
QY 172 DNLGDTYACVQOKPGRSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEAD 231
DB 158 EDIYNRLA-WYQKPGNAPRLISGATSLFTGVSPFSGSGSKDYTLTSLQTEDEVAT 216
QY 232 YYCOA-WDTSTAVFGTGTCLTV 252
DB 217 YYCOQYWSTRT--FGGTTLEI 236

RESULT 5

Q92551 PRELIMINARY; PRT; 218 AA.
AC 092561 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X., Su C.;
RA "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PR00047; IG_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 31.1%; Score 419.5; DB 11; Length 218;
Best Local Similarity 41.9%; Pred. No. 3.5e-26;
Matches 95; Conservative 37; Mismatches 74; Indels 21; Gaps 7;
QY 1 QVTLKSGPLVPTOTLTITCTSGFSLSTSGVSGWIRPPKALTEMLASINMND-K 59
DB 3 QVTLQSGSELKPKRGSTVRISCRASGVTFTTAMQ--WYQKPGKGLKMIWINTHSVVP 60

QY 60 CYSPLKSLRLITKDPKNOVLAMSNMDDADATATYSCALDMPHDSGPOSFADSPWGP 119
DB 61 KLAEEKRGAPASLETASTATLOISNLKNEBTATITFCM--RWDVDCG-----PAYWQ 112
QY 120 GTMTVTVSSGGGGSGGGGGSGGGGGSGGSSYELMQLP-SVSVSPQQTASITC---SGDNL 174
DB 113 GTTIVTVS-----SGGGSGGGGGSGGGSDIVLTQSPASIALVSLGQATISCRASISVDNI 167
QY 175 GPKVACWYQKRGKRPSPVLVIYGNKRPSPGIPERFSGNSGNTATLTIT 221
DB 168 GISFNMWFOQKPGQPPKLLIYAASKGSGVPAGLLASGSDTFSINI 214

RESULT 6

Q8TBG9 PRELIMINARY; PRT; 233 AA.
AC Q8TBG9;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH2823.1; -.
DR PIR; S12442; S12442.
DR PIR; S30526; S30526.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PR00047; IG_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD64DF92 CRC64;

Query Match 30.9%; Score 417; DB 4; Length 233;
Best Local Similarity 75.0%; Pred. No. 6e-26;
Matches 84; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 144 GGGSSYELMQLPSPVSPQQTASITCSGDNLDKTYACWYQKRGKRPSPVLVIYGNKRPSPG 203
DB 16 GSEASYELTQPPSVSPVSPQQTARITCSGDALFKQIAYWYQKRGQAPVLVIYKDNRPSPG 75
QY 204 IPERFSGNSGNTATLTISGTQAMDEADYVCGAMDSTA--VFGTGTCLTVL 253
DB 76 IPERFSGSSGTTVTLTISGVQADEADYVCGSADSSGTYVWFGGTTCLTVL 127

RESULT 7

Q8N355 PRELIMINARY; PRT; 234 AA.
AC Q8N355;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028090; AAR28090.1; -
 DR PIR; S12441; -
 DR InterPro; IPR003599; IG
 DR InterPro; IPR007110; IG_1like
 DR InterPro; IPR003597; IG_CL
 DR InterPro; IPR003006; IG_MHC
 DR InterPro; IPR003596; IG_V
 DR Pfam; PF00047; IG; 2
 DR SMART; SM00409; IG; 1
 DR SMART; SM00406; IG; 1
 DR SMART; SM00407; IG; 1
 DR PROSITE; PS50835; IG_LIKE; 2
 DR PROSITE; PS00290; IG_MHC; 1
 DR Hypothetical protein.
 SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match 30.4%; Score 410.5; DB 4; Length 234;
 Best Local Similarity 70.8%; Pred. No. 26-25;
 Matches 80; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 144 GGGSSYELMQLPSVSPGQTASITCSGDNLDKXACWYQOKRPSPLVLYGDKRPSG 203
 DB 16 GAVTSVLTQPPSVSVAPOQTARITCGNNITGSKVHWYQOKRQAPLVLYDDSDRPSG 75
 QY 204 IERFSGNSGNTATLTISGTQAMDEADYCCQAMDST--AVFGTGTLTVL 253
 DB 76 IERFSGNSGNTATLTISRVDAGDEADYCCQMDSSDHPVFGGTTLTVL 128

RESULT 8
 ID 0811US PRELIMINARY; PRT; 118 AA.
 AC 0811US
 DT 01-JUN-2003 (TRENBLrel. 24; Created)
 DT 01-JUN-2003 (TRENBLrel. 24; Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25; Last annotation update)
 DE Anti-human Fc gamma receptor III 368 gamma heavy chain variable region (Fragment).
 DE Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/c;
 RA Bruenke J., Valerius T., Repp R., Fey G.H.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY173025; AA018227.1; -
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; IG
 DR InterPro; IPR007110; IG_1like
 DR InterPro; IPR003596; IG_V
 DR Pfam; PF00047; IG; 1
 DR SMART; SM00409; IG; 1
 DR SMART; SM00406; IG; 1
 DR PROSITE; PS50835; IG_LIKE; 1
 DR PROSITE; PS00290; IG_MHC; 1
 DR Receptor.
 KW NON_TER
 FT 118 118
 SQ SEQUENCE 118 AA; 12979 MW; F57BB07033742B99 CRC64;

Query Match 28.9%; Score 390.5; DB 11; Length 118;
 Best Local Similarity 61.4%; Pred. No. 3.7e-24;
 Matches 78; Conservative 17; Mismatches 23; Indels 9; Gaps 2;

QY 1 QVTLKSGPFLVPTLTCTLSGFSLSGVSVMIRPPGALFLWLASIMWDDKC 60
 DB 1 QVTLKSGPFLVPTLTCTLSGFSLSGVSVMIRPPGALFLWLASIMWDDKC 60
 QY 61 YSPSLKSRITITKTPKQNVLIAMSNMPPADTATYSCALDMPPHDSGQSFDAADVGP 120
 DB 61 YNPALKSRITITKTDYSSNOVFLKIASVDTADTATYCA-----QINPAHF--ATWGQG 111

QY 121 TMTVSS 127
 DB 112 TLTVSA 118

RESULT 9
 ID 08NSF4 PRELIMINARY; PRT; 233 AA.
 AC 08NSF4
 DT 01-OCT-2002 (TRENBLrel. 22; Created)
 DT 01-OCT-2002 (TRENBLrel. 22; Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25; Last annotation update)
 DE Hypothetical protein.
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032452; AAR32452.1; -
 DR PIR; S12441; S12441.
 DR InterPro; IPR003599; IG
 DR InterPro; IPR007110; IG_1like
 DR InterPro; IPR003597; IG_CL
 DR InterPro; IPR003006; IG_MHC
 DR InterPro; IPR003596; IG_V
 DR Pfam; PF00047; IG; 2
 DR SMART; SM00409; IG; 1
 DR SMART; SM00407; IG; 1
 DR SMART; SM00406; IG; 1
 DR PROSITE; PS50835; IG_LIKE; 2
 DR PROSITE; PS00290; IG_MHC; 1
 DR Hypothetical protein.
 SQ SEQUENCE 233 AA; 24961 MW; F092CFB6A6E3A9A CRC64;

Query Match 28.8%; Score 389; DB 4; Length 233;
 Best Local Similarity 72.5%; Pred. No. 1.1e-23;
 Matches 79; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 147 SSYELMQLPSVSPGQTASITCSGDNLDKXACWYQOKRPSPLVLYGDKRPSG 206
 DB 19 ASYELTQPPSVSVAPOQTARITCGNLTGSKVHWYQOKRQAPLVLYDDSDRPSG 78
 QY 207 RFGSGNSGNTATLTISGTQAMDEADYCCQAMDST--VFGTGTTLTVL 253
 DB 79 RFGSGNSGNTATLTISGAGVEADYCCSDSSGNHWFGGTTLTVL 127

RESULT 10
 ID 09UL82 PRELIMINARY; PRT; 107 AA.
 AC 09UL82
 DT 01-MAY-2000 (TRENBLrel. 13; Created)
 DT 01-MAY-2000 (TRENBLrel. 13; Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25; Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Werf P.L., Kalle N.N., Berny S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035032; AAD56268.1; -

DR HSSP; P01703; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11445 MW; 52FOCC1AB26821DC CRC64;

Query Match
Best Local Similarity 72.0%; Pred. No. 1.4e-23;
Matches 77; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 148 STEMLPVSVSPPGQTASITGSGDNLGDKYACVQKGRSPVLYTGDNKRPSPGIPR 207
DB 1 SYELTPSSVSVPGGTARITCSGDLAKKYAWFOOKGQAPILVIFDTERPSGIPR 60
QY 208 FSGNSGNTATLTISGTQAMDEADYYC-QAMDTSTVFSGTGLTVL 253
DB 61 FSGSSGTTVTLTISGAQVEADYYCYSHSDNNGVFGGTLTVL 107

RESULT 11
043234 PRELIMINARY; PRT; 97 AA.
AC 043234;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Rheumatoid factor RF-ET13 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Borretzen M., Natvig J.B., Thompson K.M.;
RT "Heterogenous RF structures between and within healthy individuals are
RT not related to HLA DRB1*0401.";
RL Mol. Immunol. 0:0-0(1997).
DR EMBL; AF035802; AAB8534.1; -
DR HSSP; P01789; 1MCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 97
SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;

Query Match
Best Local Similarity 76.0%; Score 376; DB 4; Length 97;
Matches 73; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 3 TLKESPTLVKPTQTLTCTGSLSTSVGVNIROPCKALEWASINMNDKYS 62
DB 1 TLKESPALVKEPTLTCTGSGFSLNRMRGWSVIRQPKAVEMLAHIFANDEKYS 60
QY 63 PSLKSLRTTKDTPKQNVLAAMNMPADATATYCA 98
DB 61 TSLKSLRTTKDTPKQNVLAAMNMPADATATYCA 96

RESULT 12
09NSD6 PRELIMINARY; PRT; 107 AA.
AC 09NSD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Lymphocytes;
RA Hermann A.;
RT "Autoimmunity";
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; I43092; AAA69746.2; -
DR HSSP; P01709; 2MCG.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match
Best Local Similarity 70.8%; Pred. No. 7e-23;
Matches 75; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 150 ELMOLPVSVSPPGQTASITGSGDNLGDKYACVQKGRSPVLYTGDNKRPSPGIPR 209
DB 1 ELTOPVVSVALGQTVRITCGDLSRYASVYQKPGQAPVLYGKNRRSPGLPDRS 60
QY 210 GNSGNTATLTISGTQAMDEADYYCQAMDTSTVFSGTGLTVL 253
DB 61 GSSGNTATLTITGAQVEADYYCNSRDSGNHVPFGGTLTVL 106

RESULT 13
072207 PRELIMINARY; PRT; 234 AA.
AC 072207;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martusella K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Yoshitake S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC054883; AAHS4883.1; -
 KM Hypothetical protein.
 SQ SEQUENCE 234 AA; 25015 MW; 9A5723ABC93A06F CRC64;

Query Match 27.3%; Score 368.5; DB 4; Length 234;
 Best Local Similarity 65.5%; Pred. No. 5e-22;
 Matches 72; Conservative 12; Mismatches 23; Indels 3; Gaps 1;

QY 147 SSYELMQLPSVSPQQTASITGSGNLDKXACWQOKRSPVLVYIGDKRPSGIP 206
 DB 19 ASVVLQPPSVSAFPAKTAITTCGADNIGAKSVHWYQOKTQDAPVLVYHDNDPSGIP 78
 QY 207 RFGSGNSGNTATLTISGTQAMDEADYCCQAMDSTA--VFSTGFKLTVL 253
 DB 79 RFGSGNSGNTATLTISRVPDDEADYFCQVWDSGGQJMMRGCTKLTVL 128

RESULT 14

Q96169 PRELIMINARY; PRT; 233 AA.

AC Q96169 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=8-cell;
 RA Strausberg R.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007782; AAH07782.1; -
 DR PIR; S12440; S12440.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004812; F:RNA ligase activity; IEA.
 DR GO; GO:0006418; P:amino acid activation; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00178; AA tRNA LIGASE_1; 1.
 DR PROSITE; PS00835; IG LIKE_2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 233 AA; 24802 MW; C694F8397827650B CRC64;

Query Match 26.1%; Score 353; DB 4; Length 233;
 Best Local Similarity 60.7%; Pred. No. 8.9e-21;
 Matches 68; Conservative 15; Mismatches 27; Indels 2; Gaps 1;

QY 144 GGGSSYELMQLPSVSPQQTASITGSGNLDKXACWYQOKRSPVLVYIGDKRPSG 203
 DB 16 GSSTSYVLQPPASVSAFPAKTAITTCGSGNIGAKSVHWYQARPGAPLIVYENKERPA 75
 QY 204 IPRFSGNSGNTATLTISGTQAMDEADYCCQAMDSTA--VFSTGFKLTVL 253
 DB 76 IPRFSGNSGNTATLTISRVPDDEADYFCQVWDSGGQJMMRGCTKLTVL 127

RESULT 15

Q72374 PRELIMINARY; PRT; 492 AA.

AC Q72374 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein DKFP686C02218 (Fragment).
 GN DKFP686C02218.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Bioecker H., Bioecker M., Mewes H.W., Weil B., Amid C., Oanger A.,
 RA Fobo G., Han M., Mermann S.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX38877; CAD98001.1; -
 KM Hypothetical protein.
 FT NON-TER
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 25.6%; Score 346; DB 4; Length 492;
 Best Local Similarity 38.1%; Pred. No. 8.1e-20;
 Matches 91; Conservative 26; Mismatches 84; Indels 38; Gaps 6;

QY 1 QVTLKSGFTLVKPTQTLTCTLSGFLSTSGVSVGMIRQPGKALEWLASTIMNDKC 60
 DB 32 QLOLQSGPGLVKPSSETLSLCTVSGSVSNRNTYMGIRQPGKLEWISITYNNTY 91
 QY 61 YSPSLKSLTITKTTPKQVVLAMSNMDPADTATYSCALDMPPHDSGPGFSDVVGPG 120
 DB 92 YSPSLKSLTITFVDTSKNHFSLRLTSVYADTAVYCV---RIVEGPGM--FDPWCGG 145
 QY 121 TMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSPQQTASITGSGNLDKXAC 180
 DB 146 TLVTVSSASP-----TSKVPFLSLDSTPDGNNV--VAC 178
 QY 181 WYQKPRGSPVLVY---GDKRPSGIP--ERFSGNSGNTATLTISGTQAMDEADYCC 234
 DB 179 LVQGFPPQEPPLSVTSSSGQNVTAARNFPPSQDASGDLTYTSQTLTPATCCPDGKSVTC 237

Search completed: May 13, 2004, 15:06:59
 Job time : 35.0199 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 53.1029 Seconds

(without alignments)
1372.754 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371

Sequence: 1 QVQLDSGSGVLVPSSETLSL.....AMDESINGVVFSGGTQVTVL 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_290u04:*

1: geneseq219808:*\n2: geneseq219908:*\n3: geneseq220008:*\n4: geneseq220018:*\n5: geneseq220028:*\n6: geneseq220038:*\n7: geneseq220048:*\n8: geneseq220058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1031.5	75.2	252	5	ABP45212 Human Bly
2	1020.5	74.4	246	3	AAV15126 Anti-murI
3	1008.5	73.6	240	4	AAAB46058 Human TF
4	1003.5	73.2	244	6	AAE36248 TRAIL rec
5	1002	73.1	241	4	AAAB46061 Human TF
6	1002	73.1	255	5	ABP45631 Human Bly
7	1001.5	73.0	244	4	AAAB46060 Human TF
8	997.5	72.8	244	2	AAV21883 Anti-murI
9	994.5	72.5	252	5	ABP45983 Human Bly
10	987	72.0	251	5	ABP45499 Human Bly
11	987	72.0	255	5	ABP45586 Human Bly
12	985.5	71.9	250	6	AAE36254 TRAIL rec
13	984	71.8	239	4	AAAB46059 Human TF
14	982	71.6	251	5	ABP45535 Human Bly
15	966	70.5	247	5	ABP45970 Human Bly
16	963	70.2	243	4	AAAB46056 Human TF
17	947	69.1	242	4	AAAB46057 Human TF
18	945	68.9	247	5	ABP45982 Human Bly
19	939.5	68.5	254	5	ABP45648 Human Bly
20	935	68.2	251	5	ABP45951 Human Bly
21	929	67.8	251	6	ABU19829 Human Bly
22	927	67.6	247	5	ABP45987 Human Bly
23	925.5	67.5	256	5	ABP45596 Human Bly
24	921	67.2	251	5	ABP45527 Human Bly
25	915.5	66.8	244	2	AAV06718 Antibody

ALIGNMENTS

26	915.5	66.8	258	5	ABP46072 Human Bly
27	915.5	66.8	266	5	ABG97835 Single ch
28	915.5	66.8	266	5	ABG35316 Thrombopo
29	905	66.0	251	5	ABP44979 Human Bly
30	898	65.5	245	5	ABP45853 Human Bly
31	896	65.4	253	5	ABP45608 Human Bly
32	890.5	65.0	254	5	ABP45947 Human Bly
33	888.5	64.8	254	5	ABP45567 Human Bly
34	886	64.6	247	5	ABP45182 Human Bly
35	883	64.4	247	5	ABP45755 Human Bly
36	881.5	64.3	256	5	ABP45734 Human Bly
37	881	64.2	251	5	ABP45531 Human Bly
38	880.5	64.2	252	5	ABP45318 Human Bly
39	879.5	64.2	250	5	ABP45402 Human Bly
40	877	64.0	253	6	ABU19830 Human Bly
41	876.5	63.9	248	5	ABP45879 Human Bly
42	874	63.7	253	5	ABP45338 Human Bly
43	874	63.7	253	5	ABP44943 Human Bly
44	872	63.6	255	5	ABP44830 Human Bly
45	871	63.5	247	5	ABP45389 Human Bly

RESULT 1
ID ABP45212 standard; protein; 252 AA.

AC ABP45212;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1223.

XX Blye; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX Tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiHIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2001; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the

XX diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 1861-1862; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to

XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the

XX tumour necrosis factor (TNF) super family and induces B cell

XX proliferation and differentiation. The antibodies of the invention have

XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX Sequence 252 AA;

Query Match 75.2%; Score 1031.5; DB 5; Length 252;
 Best Local Similarity 78.1%; Pred. No. 1.1e-56;
 Matches 203; Conservative 15; Mismatches 31; Indels 11; Gaps 3;

QY 1 QVQLQSGPGVLPVPSSTLSLTCTVSGSGIGH--DYWWSWIRPPGGLMIGIFPDGSTN 58
 Db 1 QVQLQSGPGVLPVPSSTLSLTCTVSGSGFISRTSYWGMIRPPGGLMIGIYITGITY 60
 QY 59 YNPSLNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKAWLSEPPYFSSDGMVW 118
 Db 61 YNPSLKSRTTISADTSKQLSLKLSVTNADTAAYVCARAGYDLTGYPFF-----DSW 115
 QY 119 GGGTYTVTSGGGGSGGGSGGGSGGSGSNFMTLTPPPASGTPGQRVISICSGSSSDIG 178
 Db 116 GGGTYTVTSGGGGSGGGSGGGSGGSGSNFMTLTPPPASGTPGQRVITICSGSSSNIG 171
 QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPBGVDRFSGFSGTSASIVISGLQSEDEADYCA 238
 Db 172 SNTVNMVYQQLPGTAPKLLIYSNNQRPBGVDRFSGFSGTSASIVISGLQSEDEADYCA 231
 QY 239 AMDSLNGVVFQGGTKYTVL 258
 Db 232 TWDDSLNGVVFQGGTKYTVL 251

RESULT 2
 ID AAY15126 standard; protein, 246 AA.
 XX AAY15126;
 AC AAY15126;
 XX 07-FEB-2000 (first entry)
 DT 07-FEB-2000 (first entry)
 XX Anti-murine CTLA-4 M3 sFv.
 DE Anti-murine CTLA-4 M3 sFv.
 XX Anti-murine CTLA-4 sFv; M3 sFv; single chain antibody; murine CTLA4;
 KW membrane-associated protein; chimeric construct; extracellular domain;
 KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B;
 KW xenograft-specific immunosuppression.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 PN WO9957266-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-GB001350.
 XX
 PR 30-APR-1998; 98GB-00009280.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Lechler IR, Dorling A;
 XX
 DR WPI: 2000-038815/03.
 DR N-PSDB; AA28998.
 XX

XX
 PR Inhibiting T-cell mediated rejection of xenotransplanted organs.
 XX
 XX Claim 9, Fig 11, 43pp; English.
 PS

CC The present sequence is the anti-murine CTLA-4 sFv (M3 sFv). This is a
 CC membrane-associated protein which binds to CTLA-4. Chimeric constructs
 CC comprising DNA sequences encoding the extracellular domain of murine
 CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.
 CC The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated
 CC T-cells and antagonises the co-stimulatory signal provided by the
 CC interaction between donor B7 and recipient CD28. Cells expressing the
 CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in
 CC xenograft-specific immunosuppression
 XX

Sequence 246 AA;

Query Match 74.4%; Score 1020.5; DB 3; Length 246;
 Best Local Similarity 76.9%; Pred. No. 5.3e-56;
 Matches 200; Conservative 17; Mismatches 22; Indels 21; Gaps 4;

QY 1 QVQLQSGPGVLPVPSSTLSLTCTVSGSGSI--GHYWSWIRPPGGLMIGIFPDGSTN 58
 Db 3 QVQLQSGPGVLPVPSSTLSLTCTVSGSGSYWWSWIRPPGGLMIGIYISGISTN 62
 QY 59 YNPSLNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKAWLSEPPYFSSDGMVW 118
 Db 63 YNPSLKSRTTISADTSKQLSLKLSVTNADTAAYVCARAR-----KDKFDYW 110
 QY 119 GGGTYTVTSGGGGSGGGSGGGSGGSGSNFMTLTPPPASGTPGQRVISICSGSSSDIG 178
 Db 111 GGGTYTVTS-----SGGGSGGGSGGSGGSGSNFMTLTPPPASGTPGQRVITICSGSSSNIG 165
 QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPBGVDRFSGFSGTSASIVISGLQSEDEADYCA 238
 Db 172 SNTVNMVYQQLPGTAPKLLIYSNNQRPBGVDRFSGFSGTSASIVISGLQSEDEADYCA 225
 QY 239 AMDSLNGVVFQGGTKYTVL 258
 Db 226 AMDSL--FVFGGTKYTVL 243

RESULT 3
 ID AAB46058 standard; peptide, 240 AA.
 XX AAB46058;
 AC AAB46058;
 XX 23-MAR-2001 (first entry)
 DT 23-MAR-2001 (first entry)
 XX Human TF anti-idiotype antibody fragment ZA4.
 DE Human TF anti-idiotype antibody fragment ZA4.
 KW MOC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
 KW antidiocytic antibody; cytostatic; virucidal; antibacterial; TF antigen;
 KW antiparasitic; infectious disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200073430-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 29-MAY-2000; 2000MO-DE001809.
 XX
 PR 27-MAY-1999; 99DE-01024405.
 PR 09-SEP-1999; 99DE-01043016.
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Goletz S, Karsten U;
 XX
 DR WPI: 2001-049937/06.
 DR
 XX

PD 07-DEC-2000.
XX
PF 29-MAY-2000, 2000MO-DE001809.
XX
XX 27-MAY-1999, 99DE-01024405.
PR 09-SEP-1999, 99DE-01043016.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI
P1 Goletz S, Karsten U;
XX
XX WPI, 2001-049937/06.
DR
PT Vaccines against conformation-dependent or non-peptide antigens, based on
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
PS vaccines.
XX
PS Disclosure; Page 14, 36pp; German.

CC cytotatic, virucidal, antibacterial and antiparasitic. The invention
CC also describes (1) a corresponding vaccine (V2) against antigens which
CC are not proteins or peptides, as defined above but which have

Query Match 73.1%; Score 1002; DB 4; Length 241;
Best Local Similarity 77.5%; Pred. No. 7.3e-55;
Matches 200 / Conservative 13; Mismatch 27.

Sequence 241 AA:
SQ
which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
human antidiabetic antibody fragments against the MDCI-conformation
epitope having one of 31 approximately 60 residue amino acids sequences,
all fully defined in the specification; (4) MDCI-conformation epitope
mimics having one of 16-9-17 residue amino acid sequences, all fully in
the specification; (5) antidiabetic antibody fragments against the TF
fully defined in the specification; (6) TF carbohydrate epitope mimics,
having one of 25 7-13 residue amino acid sequences, all fully defined in
the specification; and (7) DNA sequences encoding the fragments and
derivatives defined in (3, 4, 5, or 6). (VI) and (VII) are used to treat
cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
and parasites. The vaccines are effective in cases where vaccination has
previously not been possible

Db 1 QVQLQESGGAGLLKPSRTLSLTCAVYGGSFSGYYMSWIRQPPKGLKLENIIGEINHSGSTINYN 60

[illegible]

241	DESINGWFEGGTRTVL	258
223	DDSLRSYVEGGGTRT	240
241	DESINGWFEGGTRTVL	258
223	DDSLRSYVEGGGTRT	240

RESULT 6
 ABP45631
 ID ABP45631 standard; protein, 255 AA.
 XX
 AC ABP45631;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Bly5 binding scFv SEQ ID 1642.
 XX
 KW Bly5; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KW tumor necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 15-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 WP1, 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 2362-2363; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Bly5) polypeptides. Bly5 is a member of the
 CC tumor necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Bly5. The antibodies bind to Bly5
 CC and so may be used to detect and quantitate the presence of Bly5 in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Bly5. They may also be
 CC administered to treat diseases associated with aberrant Bly5 expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 CC
 SQ Sequence 255 AA;
 Query Match 73.1%; Score 1002; DB 5; Length 255;
 Best Local Similarity 75.7%; Pzed. No. 7, 7e-55;
 Matches 196; Conservative 23; Mismatches 34; Indels 6; Gaps 2
 1 OVQLDSGGLVKKPSFTSLTCTVSGSGSGLDHWISIRPPGKGLMIGIPFDGSTNN 60
 1 QVQLDQWGGKLPKSTTSLTCAVVGSGSGYWSIRPSGKGLMIGIEINHGSTNN 60
 61 PSINLRVTISLDTSKNQLSLRTSVPAADTAVYFCARLGAW-LISEPPYFSGDGDWVG 119

Db	61	PSLSKRVITSDVASKNQPSLKLSSTVADTAAYTCARESSYDILTGYSPPRSRYGMDVWG	120
Qy	120	QGTVTYVSSGGGSGGGSGGGSGGGSNFM/LTQPPSASGTPGQRVISLSCGSSSDIGS	179
Db	121	RGLTVLVS-----SGGGSGGGSGGGSGGSGVLTQPPASASGTPGQRVITSLSCGSSSNIGS	175
Qy	180	NTVMVYQQLPGTAPKLLIYNNQRPSSGVDPDRFSPGSGTSAVLVTSGLQSEDEADYCYCA	239
Db	176	NTVMVYQRLPGAAQLLIYNNQRPSSGIPDRFSPGSGSGTSLVTSGLQSEDEADYCYCAS	235
Qy	240	WDESLNGVTFGGGTQVTVL 258	
Db	236	WDDSLNGRVTFGGGTQVTVL 254	
RESULT 7			
AAAB46060			
ID	AAAB46060	standard; peptide; 244 AA.	
AC	AAAB46060;		
XX			
DT	23-MAR-2001	(first entry)	
XX			
DE	Human TF anti-idiotypic antibody fragment ZA14.		
XX			
KW	MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;		
KM	antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;		
XX	antiparasitic; infectious disease.		
OS	Homo sapiens.		
XX			
PN	WO200073430-A2.		
XX			
PD	07-DEC-2000.		
XX			
PF	29-MAY-2000; 2000WO-DE001809.		
XX			
PR	27-MAY-1999; 99DE-01024405.		
PR	09-SEP-1999; 99DE-01043016.		
XX			
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		
XX			
PI	Goletz S, Karsten U;		
XX			
PS	WPI, 2001-049937/06.		
XX			
CC	This invention describes a novel vaccine (V1) against conformation-		
CC	dependent antigens (CDA) comprising DNA (I) and/or an antibody, or		
CC	peptide which immunologically imitates CDA, is new. (I) encodes a region		
CC	of an antidiotypic antibody (Ab2) or another peptide which: (a)		
CC	specifically binds to the binding site of an antibody (Ab1) or an antigen		
CC	binding molecule; and (b) immunologically mimics the initial antigen. The		
CC	epitope is partially or completely conformation-dependent, and has an		
CC	immunogenic structure defined by a specific spatial conformation of amino		
CC	acids. (I) is used in the form of linear or circular naked DNA and/or		
CC	with a viral vector and/or adjuvants. The products of the invention have		
CC	cytostatic, virucidal, antibacterial and antiparasitic. The invention		
CC	also describes (1) a corresponding vaccine (V2) against antigens which		
CC	are not proteins or peptides, as defined above but which have epitopes		
CC	which show an immunogenic structure; (2) preparing (V1) and (V2); (3)		
CC	human antidiotypic antibody fragments against the MUC1-conformation		
CC	epitope having one of 31 approximately 60 residue amino acids sequence,		
CC	all fully defined in the specification; (4) MUC1-conformation epitope		
CC	mimics having one of 16 9-17 residue amino acid sequences, all fully in		
CC	the specification; (5) antidiotypic antibody fragments against the TF		
CC	antigen having one of 24 approximately 200 residue amino acid sequences,		

CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25-7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3, 4, 5, or 6). (VI) and (VII) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible

XX Sequence 244 AA;

Query Match 73.0%; Score 1001.5; DB 4; Length 244;
 Best Local Similarity 76.1%; Pred. No. 7, 9e-55;
 Matches 197; Conservative 17; Mismatches 28; Indels 17; Gaps 4;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI-GHDYMSWIRPPGSGLEWIGTFIFDGSTNY 59
 DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI-GHDYMSWIRPPGSGLEWIGTFIFDGSTNY 59
 QY 60 NPSLNGRVITSLDTSKNQSLRTSVTAADTAVFYFCARLKGMALLSEPPYSSDQMDVWG 119
 DB 61 NPSLNGRVITSLDTSKNQSLRTSVTAADTAVFYFCARLKGMALLSEPPYSSDQMDVWG 119
 QY 120 QGTTVTSSGGSGSGSGSGSGSGSNFMLTQPPSASGTPGQRVISICSGSSSDIGS 179
 DB 110 QGTLVTVS-----SGSGSGSGSGSGSGSALQSVLTQPPSASGTPGQRVITISCGSSSNIGS 164
 QY 180 NTVMYQQLPGTAPKLLIYSNNQRPSPGVDRPFGSGKTSASLVISGLQSEDEADYCA 239
 DB 165 NTVMYQQLPGTAPKLLIYSNNQRPSPGVDRPFGSGKTSASLVISGLQSEDEADYCA 239
 QY 240 WDESLNGVFGGSGKTVTVL 258
 DB 225 WDSLRLALVFGGSGKTLTVL 243

RESULT 8

AAV21883
 ID AAV21883 standard; protein; 244 AA.

XX AAV21883;

DT 24-SEP-1999 (first entry)

DE Amino acid sequence of antibody B10A8.

KM Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;
 KW diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy; B10A8.

OS Homo sapiens.

XX Key Location/Qualifiers

FT MISC-difference 201

FT /label= unknown
 /note= "encoded by TST"

PN EP934953-A2.

PD 11-AUG-1999.

PF 01-DEC-1998; 98BP-00122546.

PR 03-DEC-1997; 97US-0067428P.

PA (BOE) BOEHRINGER MANNHEIM CORP.

PI Winter GP, Mahoney W, Sawyer JR;

DR WPI; 1999-432068/37.

DR N-PSDB; AAX86940.

PT New anti-complex antibody useful for diagnosing prostate cancer.

PS Claim 28; Page 25-27; 42pp; English.

XX The invention relates to an antibody that binds a complex between
 CC prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an
 CC affinity for the complex which is at least 10 fold higher than the
 CC affinity for either PSA or ACT alone. The antibody is used in diagnostic
 CC assays to detect PSA-ACT in serum samples from patients. The levels of
 CC PSA-ACT complex increase in patients suffering from prostate cancer
 CC compared to the levels in patients with benign or no growths in the
 CC prostate. Therefore detection of PSA in complex with ACT is useful for
 CC the early detection of prostate tumours, by distinguishing between benign
 CC and malignant conditions of the prostate as well as for the management of
 CC patients with prostate cancer, such as the disclosure of metastasis and
 CC the monitoring of the PSA levels after treatment. The antibodies may also
 CC be used in immunotherapy, affinity chromatography and isolation or
 CC purification of PSA-ACT, unlike prior art antibodies which bind to PSA-
 CC specific for PSA-ACT alone. Diagnostic assays using the antibodies are
 CC more accurate in diagnosing prostate cancer as they only detect the
 CC intact complex of PSA-ACT. Sequences AAV21880-884 represent specific
 CC examples of antibodies directed against PSA-ACT. The present sequence
 CC represents the amino acid sequence of antibody B10A8

XX Sequence 244 AA;

Query Match 72.8%; Score 997.5; DB 2; Length 244;
 Best Local Similarity 76.0%; Pred. No. 1, 4e-54;
 Matches 196; Conservative 14; Mismatches 31; Indels 17; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI-GHDYMSWIRPPGSGLEWIGTFIFDGSTNY 60
 DB 3 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI-GHDYMSWIRPPGSGLEWIGTFIFDGSTNY 62
 QY 61 PSLKSRVITISVDTSKNQSLRTSVTAADTAVFYFCARLKGMALLSEPPYSSDQMDVWG 120
 DB 63 PSLKSRVITISVDTSKNQSLRTSVTAADTAVFYFCARLKGMALLSEPPYSSDQMDVWG 110
 QY 121 GTVTVTSSGGSGSGSGSGSGSNFMLTQPPSASGTPGQRVISICSGSSSDIGS 180
 DB 111 GTTLVTVS-----SGSGSGSGSGSGSALQSVLTQPPSASGTPGQRVITISCGSSSNIGS 165
 QY 181 TVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRPFGSGKTSASLVISGLQSEDEADYCA 240
 DB 166 TVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRPFGSGKTSASLVISGLQSEDEADYCA 225
 QY 241 WDESLNGVFGGSGKTVTVL 258
 DB 226 WDSLRLALVFGGSGKTLTVL 243

RESULT 9

ABP45983
 ID ABP45983 standard; protein; 252 AA.

XX ABP45983;

DT 19-AUG-2002 (first entry)

DE Human Bly's binding scFv SEQ ID 1994.

KM Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; HIV; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2779-2780; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 252 AA;
XX
Query Match 72.5%; Score 994.5; DB 5; Length 252;
Best Local Similarity 74.6%; Pred. No. 2.2e-54;
Matches 194; Conservative 21; Mismatches 34; Indels 11; Gaps 3;
XX
QY 1 QVQLQESGGPGVLPSESTLSLTCTVSGSGSI--GHDYMSWIRORPGEGLIEWIGFIFFPGSTN 58
DB 1 QVQLQESGGPGVLPSESTLSLTCTVSGSGSISSGDIYMSWIRORPGEGLIEWIGFIYHSGSY 60
XX
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVFCAFLKGMALSEPPYFSSDDMDVY 118
DB 61 YNPSLKSRVTSMSVDTSKNQLSLRLTSVTAADTAVFCAFLKGMALSEPPYFSSDDMDVY 114
XX
QY 119 GGGTIVTVSSGGGSGGGSGGGSGGGSNFMFLTOPPSASGTPGQGVSTISGSSSDIG 178
DB 115 GGGTIVTVSSGGGSGGGSGGGSGGGS---ALSYVLTPPSASATPPGQGVSTISGSSRSNIG 171
XX
QY 179 SNTVMVYQQLPGTAPRLILYSNNORPSGVDRFSGKSTSAVLISGLQSEDEADYCA 238
DB 172 SNTVMVYQQLPGTAPRLILYSNNORPSGVDRFSGKSTSAVLISGLQSEDEADYCA 231
XX
QY 239 AMDESLGVVFGGKTATVTL 258
DB 232 TWDDRLRGVLFGGKTATVTL 251
XX
RESULT 10
ABP45499
ID ABP45499 standard; protein; 251 AA.
XX
XX ABP45499;
AC
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding seqv seq ID 1510.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2205-2206; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 251 AA;
XX
Query Match 72.0%; Score 987; DB 5; Length 251;
Best Local Similarity 75.8%; Pred. No. 6.5e-54;
Matches 197; Conservative 20; Mismatches 31; Indels 12; Gaps 4;
XX
QY 1 QVQLQESGGPGVLPSESTLSLTCTVSGSGSI--GHDYMSWIRORPGEGLIEWIGFIFFPGSTN 58
DB 1 QVQLQESGGPGVLPSESTLSLTCTVSGSGSISSTRTSWGIRORPGEGLIEWIGFIYHSGSY 60
XX
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVFCAFLKGMALSEPPYFSSDDMDVY 118
DB 61 YNPSLKSRVTSMSVDTSKNQLSLRLTSVTAADTAVFCAFLKGMALSEPPYFSSDDMDVY 115
XX
QY 119 GGGTIVTVSSGGGSGGGSGGGSGGGSNFMFLTOPPSASGTPGQGVSTISGSSSDIG 178
DB 116 GGGTIVTVSSGGGSGGGSGGGSGGGS---AQAVLTPPSASATPPGQGVSTISGSSSNIG 171
XX
QY 179 SNTVMVYQQLPGTAPRLILYSNNORPSGVDRFSGKSTSAVLISGLQSEDEADYCA 238
DB 172 SNTVMVYQQLPGTAPRLILYSNNORPSGVDRFSGKSTSAVLISGLQSEDEADYCA 231

(CDR3) "

FT XX MO200297033-A2.

XX XX

PD 05-DEC-2002.

XX PF 07-MAY-2002; 2002MO-US014268.

XX 25-MAY-2001; 2001US-0293473P.

PR 04-JUN-2001; 2001US-0294981P.

PR 02-AUG-2001; 2001US-0309176P.

PR 21-SEP-2001; 2001US-0323807P.

PR 09-OCT-2001; 2001US-0327364P.

PR 07-NOV-2001; 2001US-0331044P.

PR 14-NOV-2001; 2001US-0331310P.

PR 20-DEC-2001; 2001US-0341237P.

PR 05-APR-2002; 2002US-0369860P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PA

XX PI Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;

XX DR WPI, 2003-140454/13.

XX DR N-PSDB; AAD54855.

XX PT Novel antibody useful for treating cancers and other hyperproliferative

PT disorders, immunospecifically binds to TRAIL receptor and comprises

PT variable heavy or light chain complementarity determining regions.

XX Claim 1; Page 291-292; 301pp; English.

XX The present invention relates to novel antibodies that immunospecifically

CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for

CC creating, preventing or ameliorating cancer (e.g. colon, breast, uterine,

CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.

CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in

CC human. They are useful for detecting expression of TR4 polypeptide and

CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-

CC proliferative disorders. Antibodies of the invention are useful for

CC treating, preventing or ameliorating neurodegenerative disorders (e.g.

CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,

CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),

CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,

CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,

CC polypositis, immune-related glomerulonephritis, myasthenia gravis,

CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory

CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),

CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),

CC herpes viral infections and other viral infections) and proliferative

CC disorders. They are also useful for treating myelodysplastic syndromes

CC (e.g. aplastic anemia), ischaemic injury (such as that caused by stroke,

CC myocardial infarction and reperfusion injury), septic shock, cachexia,

CC anorexia and toxin-induced liver diseases (such as alcohol). They are

CC also useful for treating cardiovascular disorders including peripheral

CC artery diseases such as limb ischaemia, arrhythmia, congestive heart

CC failure and cardiovascular tuberculosis, diseases or disorders associated

CC with neovascularization and ocular disorders, for wound healing, for

CC promoting angiogenesis and as adjuvants to enhance immune responsiveness

CC to specific antigen e.g. viral antigen. They are also useful in the

CC preparation or recovery from surgery, trauma, radiation therapy and

CC transplantation. The present sequence is T1015A02 single chain Fv (scFv)

CC antibody that immunospecifically bind to TR4 protein. This sequence is

CC used in the invention

XX

XX Sequence 250 AA;

XX

Query Match 71.9%; Score 985.5; DB 6; Length 250;

Best Local Similarity 74.2%; Pred. No. 8e-54;

Matches 133; Conservative 24; Mismatches 30; Indels 13; Gaps 5;

QY 1 QVQLQSGGPGLVKPSSETLSITCTVSGSGSIQHD--YMSWIRQPPGEGLEWIGFIFPDGSGTN 58

DB 1 QVQLQSGGPGLVKPSSETLSITCTVSGSGSIQHD--YMSWIRQPPGEGLEWIGFIFPDGSGTN 60

QY 59 YNPSLNGRVTLISDTSKNQLSLRLTSVTAADPAVYFCARLKGAWLSEPPYFSDGDWV 118

DB 61 YKPSLRSRLTVSMDSIRNPSLKLTSVTAADPAVYFCARLKGAWLSEPPYFSDGDWV 113

QY 119 GQGTIVTVSSGGGGSGGGSGGGSGGGSGNFMFLTQPPASGTPGGRVSIISGSSSDIG 178

DB 114 GQGTIVTVSSGGGGSGGGSGGGSGGGSGNFMFLTQPPASGTPGGRVSIISGSSSDIG 169

QY 179 SNTVMNYQQLPGTAPRLTLISNNQRPSPGPRPSGKSGTSASLVISGLQSEDEAAYYCA 228

DB 170 GNTVMNYQQLPGTAPRLTLISNNQRPSPGPRPSGKSGTSASLVISGLQSEDEAAYYCA 229

QY 239 AMDESINGVYFGGSGTKVTVL 258

DB 230 AMDSLLIGYVFGTGTQIVL 249

RESULT 13

AB46059

ID AAB46059 standard; peptide; 239 AA.

XX AAB46059;

XX 23-MAR-2001 (first entry)

XX Human TF anti-Idiotypic antibody fragment ZA36.

XX MUCl, human; vaccine; conformation-dependent antigen; antibody; cancer;

XX antidiabetic; cytostatic; virucidal; antibacterial; TF antigen;

XX antiparasitic; infectious disease.

XX Homo sapiens.

XX WO200073430-A2.

XX 07-DEC-2000.

XX 29-MAY-2000; 2000MO-DE001809.

XX 27-MAY-1999; 99DE-01024405.

XX 09-SEP-1999; 99DE-01043016.

XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Goletz S, Karsten U;

XX WPI, 2001-049937/06.

XX Vaccine against conformation-dependent or non-peptide antigens, based on

PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor

PT vaccine.

XX Disclosure; Page 14; 36pp; German.

XX This invention describes a novel vaccine (V1) against conformation-

CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or

CC peptide which immunologically imitates CDA, is new. (I) encodes a region

CC of an antidiabetic antibody (Ab2) or another peptide which: (a)

CC specifically binds to the binding site of an antibody (Ab1) or an antigen

CC binding molecule; and (b) immunologically mimics the initial antigen. The

CC epitope is partially or completely conformation-dependent, and has an

CC immunogenic structure defined by a specific spatial conformation of amino

CC acids. (I) is used in the form of linear or circular naked DNA and/or

CC with a viral vector and/or adjuvants. The products of the invention have

CC cytostatic, virucidal, antibacterial and antiparasitic. The invention

CC also describes (1) a corresponding vaccine (V2) against antigens which

CC are not proteins or peptides, as defined above but which have epitopes

CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)

CC human antidiabetic antibody fragments against the MUCl-conformation

CC epitope having one of 31 approximately 60 residue amino acid sequences,

CC all fully defined in the specification; (4) MUCl-conformation epitope

CC mimics having one of 16 9-17 residue amino acid sequences, all fully in

CC the specification; (5) antiidiotypic antibody fragments against the TF
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25 7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3), 4, 5, or 6). (VI) and (VII) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible

Sequence 239 AA;

Query Match 71.8%; Score 984; DB 4; Length 239;
 Best Local Similarity 74.5%; Pred. No. 9.5e-54;

Matches 193; Conservative 17; Mismatches 27; Indels 22; Gaps 3;

QY 1 QVQLQESGGPGLVKPSETISLTCTVSGSI-GHDYMSWIRPPGEGLEWIGIFPDGSTNY 59
 DB 1 QVQLQESGGPGLVKPSETISLTCTVSGSISNNMWSVRQPPKGLIEWIGIYHSGSTNY 60
 QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAAYVFCALKXAMLSPEPPYSSDGMVWG 119
 DB 61 NPSLSKRVTLISVDKSKNPSLKSISVTAADTAAYVFCAR-----PSSING 104
 QY 120 QGTTVTVSSGGGSGSGSGSGSGSGSNFMTLTPPSASGTPQQRVVISCSGSSPDIGS 179
 DB 105 QGTLVTVS-----SGGSGSGSGSGSGSALQSVLTPPSASGTPQQRVVISCSGSSNIGS 159
 QY 180 NTVMVYQQLPGTAPRLILYSNNORPSGVPPDRFSGKSGTASLVISGLQSEDEADYYCAA 239
 DB 160 NYVMVYQQLPGTAPRLILYRNORPSGVPPDRFSGSKSGTASLVISGLRSEDEADYYCAA 219
 QY 240 WDSLNGVVFSGGKRVTVL 258
 DB 220 WDSLSRLVFGGKTVL 238

RESULT 14

ABP45535 ID ABP45535 standard; protein; 251 AA.

AC ABP45535;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1546.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostratic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2247-2249; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostratic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

Sequence 251 AA;

Query Match 71.6%; Score 982; DB 5; Length 251;
 Best Local Similarity 74.2%; Pred. No. 1.3e-53;

Matches 196; Conservative 18; Mismatches 30; Indels 20; Gaps 5;

QY 1 QVQLQESGGPGLVKPSETISLTCTVSGSI-GHDYMSWIRPPGEGLEWIGIFPDGSTNY 59
 DB 1 QVQLQESGGPGLVKPSETISLTCTVSGSIRGHHMNVVRQPPKGLIEWIGIYHSGSTNS 60
 QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAAYVFCAR-----LXAMLSPEPPYSSDG 114
 DB 61 NPSLSKRVTLISADSKNPSLKSISVTAADTAAYVFCARGYDVLG-----YLRK-- 110
 QY 115 MDVWGQTTVTVSSGGGSGSGSGSGSGSNFMTLTPPSASGTPQQRVVISCSGSS 174
 DB 111 LDYWGKGLTVTVSSGGGSGSGSGSGSGS-----AQPLVTPPSASGTPQQRVVISCSGSS 166
 QY 175 SDIGSNVVMYQQLPGTAPRLILYSNNORPSGVPPDRFSGKSGTASLVISGLQSEDEAD 234
 DB 167 SNIGSRVVMYQQLPGTAPRLILYSTRLPSPGVPPDRFSGSKSGTASLVISGLQSEDEAD 226
 QY 235 YYCAAMDSESLNGVVFSGGKRVTVL 258
 DB 227 YYCSAMDSESLNGVVFSGGKRVTVL 250

RESULT 15

ABP45970 ID ABP45970 standard; protein; 247 AA.

AC ABP45970;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1981.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostratic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001MO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
PT
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2764-2765; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 247 AA;

Query Match 70.5%; Score 966; DB 5; Length 247;
Best Local Similarity 72.7%; Pred. No.1.3e-52;
Matches 189; Conservative 22; Mismatches 33; Indels 16; Gaps 4;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSIG--HDYWSWIRQPPGEGLEWIGFIYPDGSTN 58
DB 1 QLQLQESGPGLVLPETLSLTCTVSGSGSVGRTHYWGWRIRLPKGMENIASISFDGTPF 60
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAIVYFCARLKGMWLSEPPYFSSDGMVW 118
DB 61 YNPSLKSRYSVSRDTSKNQFSLKTSVTADTAIVYCAR-----HDVY--GDLFDYW 110
QY 119 GGGTTVTVSAGGGSGGGSGGGSGGSGNFMLTQPPSASGTRPGORVSTSCGSSSDTG 178
DB 111 GGGTMTVTVSAGGGSGGGSGGGSGS---AQSVLTQPPSASGTRPGRVPTSCGSGSGNIG 166
QY 179 SNTVMVYQQLPGTAPRLILYSNNQRPSPGVDRPFGKSGTSASLIVISGLQSEDEADYCA 238
DB 167 SNSVSMYQGVPGTAPRLILYNNNERPSGVDRFSASKSGTSASLSGLQSEDEADYCA 226
QY 239 ANDESLNGVVFSGGRTKVTVL 258
DB 227 SWDDSLTVPVFGGGTSLTVL 246

Search completed: May 13, 2004, 15:01:00
Job time : 54.1029 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 14.1524 Seconds
(without alignments)
941.146 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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5: /cgn2_6/prodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1003.5	73.2	244	4	US-10-039-785-44 Sequence 44, Appl
2	985.5	71.9	250	4	US-10-039-785-50 Sequence 50, Appl
3	915.5	66.8	244	4	US-08-918-148-79 Sequence 79, Appl
4	815	59.4	278	3	US-09-260-527-3 Sequence 3, Appl
5	808	58.9	310	4	US-09-079-029-11 Sequence 11, Appl
6	800	58.4	258	2	US-08-665-202-5 Sequence 5, Appl
7	800	58.4	258	4	US-09-315-574-5 Sequence 5, Appl
8	728	53.1	334	4	US-09-646-028-53 Sequence 53, Appl
9	728	53.1	339	4	US-09-646-028-55 Sequence 55, Appl
10	728	53.1	348	4	US-09-646-028-51 Sequence 51, Appl
11	716	52.2	249	4	US-10-039-785-53 Sequence 53, Appl
12	698	50.9	249	4	US-08-918-148-74 Sequence 74, Appl
13	693	50.5	245	4	US-10-039-785-42 Sequence 42, Appl
14	689.5	50.3	309	4	US-09-079-029-9 Sequence 9, Appl
15	689	49.4	312	4	US-09-079-029-10 Sequence 10, Appl
16	677	49.0	245	4	US-10-039-785-46 Sequence 46, Appl
17	672	49.0	245	4	US-10-039-785-47 Sequence 47, Appl
18	672	49.0	245	4	US-10-039-785-48 Sequence 48, Appl
19	671	48.9	245	4	US-10-039-785-51 Sequence 51, Appl
20	669	48.8	245	4	US-10-039-785-49 Sequence 49, Appl
21	666	48.6	235	2	US-08-190-199A-61 Sequence 61, Appl
22	666	48.6	245	4	US-10-039-785-52 Sequence 52, Appl
23	666	48.6	280	3	US-09-260-527-1 Sequence 1, Appl
24	648	47.3	245	4	US-10-039-785-43 Sequence 43, Appl
25	643.5	46.9	248	2	US-08-887-352B-22 Sequence 22, Appl
26	643.5	46.9	248	3	US-09-109-207C-22 Sequence 22, Appl
27	643.5	46.9	248	3	US-09-296-005-22 Sequence 22, Appl

28	643.5	46.9	248	4	US-09-920-171-22 Sequence 22, Appl
29	641	46.8	245	4	US-10-039-785-45 Sequence 45, Appl
30	629	45.9	281	4	US-09-025-769B-178 Sequence 178, Appl
31	627	45.7	263	2	US-08-752-844-66 Sequence 66, Appl
32	627	45.7	263	4	US-09-293-533-66 Sequence 66, Appl
33	626.5	45.7	248	2	US-08-887-352B-23 Sequence 23, Appl
34	626.5	45.7	248	3	US-09-109-207C-23 Sequence 23, Appl
35	626.5	45.7	248	3	US-09-296-005-23 Sequence 23, Appl
36	626.5	45.7	248	4	US-09-920-171-23 Sequence 23, Appl
37	623	45.4	249	2	US-08-797-689-18 Sequence 18, Appl
38	623	45.4	249	4	US-09-984-186-18 Sequence 18, Appl
39	613	44.7	245	4	US-08-918-148-75 Sequence 75, Appl
40	610	44.5	245	4	US-08-918-148-76 Sequence 76, Appl
41	609.5	44.5	240	4	US-10-092-246-36 Sequence 36, Appl
42	609.5	44.5	240	4	US-10-092-246-37 Sequence 37, Appl
43	606.5	44.2	297	4	US-09-486-814A-2 Sequence 2, Appl
44	606.5	44.2	301	2	US-08-661-052-14 Sequence 14, Appl
45	606.5	44.2	301	3	US-09-188-082-14 Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-10-039-785-44
; Sequence 44, Application US/10039785
; Patent No. 6536938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 44
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A02 scFv
US-10-039-785-44
Query Match 73.2%; Score 1003.5; DB 4; Length 244;
Best Local Similarity 75.2%; Pred. No. 3.1e-66;
Matches 194; Conservative 18; Mismatches 31; Indels 15; Gaps 2;
QY 1 QVQLQESGPGLVKPSSETLSLCTVVGSGSIQGHYMSWIRPQEGLEWIGFIFDGSNTNN 60
DB 1 QVQLQESGPGLVKPSSETLSLCTVVGSGSIQGHYMSWIRPQEGLEWIGFIFDGSNTNN 60
QY 61 PSLNKRVITSLDTSKNOJSLRLTSYADTAIVYFCARLKGAWLSEPPYSSDGDMDVQ 120
DB 61 PSLNKRVITSLDTSKNOJSLRLTSYADTAIVYFCARLKGAWLSEPPYSSDGDMDVQ 120
QY 62 PSLNKRVITSLDTSKNOJSLRLTSYADTAIVYFCARLKGAWLSEPPYSSDGDMDVQ 120
DB 62 PSLNKRVITSLDTSKNOJSLRLTSYADTAIVYFCARLKGAWLSEPPYSSDGDMDVQ 120
QY 63 PSLNKRVITSLDTSKNOJSLRLTSYADTAIVYFCARLKGAWLSEPPYSSDGDMDVQ 120
DB 63 PSLNKRVITSLDTSKNOJSLRLTSYADTAIVYFCARLKGAWLSEPPYSSDGDMDVQ 120
```


FEATURE: Anti-homogalacturonan specific antibodies selected
OTHER INFORMATION: from a naive phage display library known as the
OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match 59.4%; Score 815; DB 3; Length 278;
Best local similarity 63.3%; Pred. No. 2, 2e-52;
Matches 164; Conservative 24; Mismatches 49; Indels 22; Gaps 5;

QY 1 QVQLQSGPGLVPSSETLSLTCTVSGGSI-GHDYMSWIRPPEGLEWIGFIFPDGSTNY 59
DB 23 QVQLQSGPGLVPSSETLSLTCTVSGGSISSNMWGWIRPPEGLEWIGIYISGTTY 82
QY 60 NPSLNRYITSLDTSKQSLRLTSTYADTAVYFCARLKGAWLSEPPFSSDGMWVG 119
DB 83 NPSLNRYITSLDTSKQSLRLTSTYADTAVYFCARLKGAWLSEPPFSSDGMWVG 119
QY 120 QGTTVTVSSGGSGSGSGSGSGSGSNFMLTOPPSAGTPGQRYISCSGSSSDIGS 179
DB 130 QGTLTVSSRGSGSGSGSGSGSGSS-----ELTPDPAVSVALGQTVRITCGDS--LRS 181
QY 180 NTVMNYQQLPGTAPKLLIYSNNQRPSPGVDPDRFSGFSGTASLVISGLQSEDEADYYCA 239
DB 182 YVASWYQQRKGAPVLVYIGKNNRPSGIPDRFSGSSSGNTASLITGAQDEADYYCNS 241
QY 240 WDESLNGVYFGGCTVTVL 258
DB 242 RDSGNHVYFGGCTVTVL 260

RESULT 5

US-09-079-029-11
Sequence 11, Application US/09079029
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chantaratpal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-079-029-11

Query Match 58.9%; Score 808; DB 4; Length 310;
Best local similarity 61.9%; Pred. No. 7, 9e-52;
Matches 161; Conservative 31; Mismatches 50; Indels 18; Gaps 4;

QY 1 QVQLQSGPGLVPSSETLSLTCTVSGGSI-GHDYMSWIRPPEGLEWIGFIFPDGSTN-Y 59
DB 40 QVQLQSGGCVVQPGSRSLRSLCAASGFIFSSYGMHWYQAPKGLLEVAVGIFDGCNKYY 99
QY 60 NPSLNRYITSLDTSKQSLRLTSTYADTAVYFCARLKGAWLSEPPFSSDGMWVG 119
DB 100 ADSVKRPFITSRNSKNITLYLQNMSLRAEDTAVYCARDRGY--MDWVG 148
QY 120 QGTTVTVSSGGSGSGSGSGSGSNFMLTOPPSAGTPGQRYISCSGSSSDIGS 179
DB 149 KGTITVVS-----SGGGSGGGSGGGSGSGLTTPPSVGARQKRTISCTGRSSNYGA 203
QY 180 -NTVMNYQQLPGTAPKLLIYSNNQRPSPGVDPDRFSGFSGTASLVISGLQSEDEADYYCA 238
DB 204 GHDVHWYQQLPGTAPKLLIYDDSNRPSGVDPDRFSGSGTASLAIITGLQADEADYYCQ 263
QY 239 AMDESLNGVYFGGCTVTVL 258
DB 264 SYDSLRSYVFGGCTVTVL 283

RESULT 6

US-08-665-202-5
Sequence 5, Application US/08665202
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-202-5
Query Match 58.4%; Score 800; DB 2; Length 258;


```

RESULT 9
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 5562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

```

```

Query Match Similarity 53.1%; Score 728; DB 4; Length 339;
Best Local Similarity 57.6%; Pred. No. 6,2e-46;
Matches 152; Conservative 30; Mismatches 60; Indels 22; Gaps 6;

QY      1 QVQLQESPGELVRPSETLSLTCTVSGSGSGISGHDSWMIROPGSGLEWIGTIFPDGSTN-Y 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      85 EVQLLESGGGLVQSGGSLRLTSCVASSGLTPSSSAITWRAQPGKGLWVGISPGDTYY 144
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 NPSLNGRVTISLDPTSKKQLSLRLTSVTAADTAIFYFCARLKGAALBLEPPYFSDG---MD 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      145 ADSYKGRFSSARSDSKNTVTYLOMNNLEPNDAIVPCAN-----NOTGAFCLD 191
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      117 VMGGGTVTVTVSS--GGGSGGGGSGGSGGGSGGSGSNFMLTOPPSASGTPGGRVSISSGSSS 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      192 NMGGGLTVTVSSRRGGSGGGSGGGSGGGSG---GSGSVLTQPPVSAAAPGQRVTISCTGSR 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      176 DLSGN-TVNNYQQQLPGTAPFKLLIYSNNQRPSTGVPDRPSGKSGTSLVYSGIQSDEAD 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      249 NIGAGYDNNYQKPEPTAPFKVLIYSNNNRPSGVDRPSGKSGTSLAITGLQLEDEGT 308
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      235 YYCAAMDESINGVVFVGSGTKVTVL 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      309 YYCQCNDSLSGLWFGSGTKLTVL 332
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-646-028-51
: Sequence 51, Application US/09646028
: Patent No. 6562347
: GENERAL INFORMATION:
: APPLICANT: Kwak, Larry
: APPLICANT: Birsayn, Arya.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
: TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
: FILE REFERENCE: 14014.0316/P
: CURRENT APPLICATION NUMBER: US/09/646.028
: PRIOR FILING DATE: 2000-09-12
: PRIOR APPLICATION NUMBER: 60/077,745
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 51
: LENGTH: 348
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

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[illegible]

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RESULT 11
US-10-039-785-53
/ Sequence 53, Application US/10039785
/ Patent No. 6538938
/ GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: PFS50
/ CURRENT APPLICATION NUMBER: US/10/039,785
/ CURRENT FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 60/369,860
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/331,310
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/331,044
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: 60/327,364
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/323,807
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/309,166
/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/294,981
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/293,473
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 53
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: T1006F07 seqv
US-10-039-785-53

Query Match 52.2%; Score 716; DB 4; Length 249;
Best Local Similarity 56.7%; Pred. No. 3,36-45;
Matches 149; Conservative 30; Mismatches 64; Indels 20; Gaps 6;

1 QVQIQESGPGIVKRSERLTSLCTWYSGSGISGHDYMSYRROPGEGLWIMIGFI-FDGSINY 59
1 EVQLLEGGGGLVQGGSGIRLSCASGFTFSYMSWRQARQKGLIEWSAISGSGSTYY 60

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CURRENT APPLICATION NUMBER: US/10/039, 785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369, 860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341, 237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331, 310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331, 044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327, 364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323, 807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309, 176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294, 981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293, 473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: T1014A04 bcfv
US-10-039-785-42

Query Match          50.5%; Score 693; DB 4; Length 245;
Best Local Similarity 53.5%; Pred. No. 1,6e-43;
Matches 139; Conservative 43; Mismatches 60; Indels 18; Gaps 5

QY      1 QVQLDSGPGELVKPSETLTCTVSGSGISGHDYMSWRROPGRGLMIGFIFD-GSTY 59
       :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 EVQLVDSGADVRRPASVYKSCIKSGSFNAYFLHWROAPGGGLMHWNPDSGTADS 60
QY      60 NPSLNRVLTISLDTSKQDLRLTSVTAADTAVYFCARLGMILSEPPYFSDDGMDVWG 119
       :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 AQRFRVLTMTDITSSSTAFLESLRNSDDTAVYCYR-----QHRGNTFAPMG 109
QY      120 QGTTVTSVSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 179
       :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      110 RGTMTVSSGGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 165
QY      180 -NTVNNYQQLPGTAPRLILYSNNQPPSGVPRFSGFGKSGTSAALVYSGQSEDEADYCA 238
       :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      166 YNYVSYQQHPKAPKAPLMYGVNRPSPGVPDRFSGSKSGNTASLVSGLADEADYCS 225
QY      239 AMDESLNGVPPGGGKTVTVL 258
       :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      226 SYAGS-NNNVFGGGTKLYLV 244

RESULT 14
US-09-079-029-9
Sequence 9, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Adan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

```

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/079,029

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mareschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1101R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-079-029-9

Query Match

Best Local Similarity 50.3%; Score 689.5; DB 4; Length 309;

Best Local Similarity 55.0%; Pred. No. 3.7e-43;

Matches 144; Conservative 32; Mismatches 63; Indels 23; Gaps 6;

QY 1 QVLOESGGLVYKPSRTSLTCTVSGSGSIGHDYMSWIRPPRGLEWMT-GTIFPDGNTNY 59

DB 40 EVOLVOSGGGVRRPGSLRLSCAASGFTPDYGMSSVVRQAPGKLEWVSGIMNNGSTGY 99

QY 60 NSLNGRVTISLDTSKNQLSLRLSTADTAVYPCARLKA---WLSEPPYFSSDGM 116

DB 100 ADVKGRVTISLDMNLSLYLQMSLRADTAVYICAKLIGAKRG-----YF-----D 148

QY 117 VWGQGTIVTVSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTFPGQRVISISCGSSSD 176

DB 149 LMGKGTIVTVSSGGGSGGGSGGGSGGGS-----ELTQDPAVSVALGQTVRITCGDS-- 200

QY 177 IGSNTVNTYQQLPGTAPKLLIYSNNORPSGVDRPSGFSGSASLVISGLQSEBDAAY 236

DB 201 LRSYASWYQKPGQAPVLYVIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADAY 260

QY 237 CAAPDESINGVYFGGQTKTVL 258

DB 261 CNSRDSGNHVYFGGQTKTVL 282

QY 237 CAAPDESINGVYFGGQTKTVL 258

DB 261 CNSRDSGNHVYFGGQTKTVL 282

RESULT 15

US-09-079-029-10

Sequence 10, Application US/09079029

Patent No. 6342369

GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Chuntharapai, Anan

APPLICANT: Kim, Kyung J.

TITLE OF INVENTION: Apo-2 Receptor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079,029

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mareschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1101R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 312 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-079-029-10

Query Match

Best Local Similarity 50.3%; Score 689; DB 4; Length 312;

Best Local Similarity 55.7%; Pred. No. 4e-43;

Matches 146; Conservative 28; Mismatches 66; Indels 22; Gaps 5;

QY 2 VLOESGGLVYKPSRTSLTCTVSGSGSIGHDYMSWIRPPRGLEWMTGTFPDGNTNY- 60

DB 41 VOLVESGGGLVQPGGSLRLSCAASGFTPSYMSVVRQAPGKLEWVANI-KODGSEKYY 100

QY 61 PSANGRTVITSLDTSKNQLSLRLSTADTAVYPCAR----LKGAWLSEPPYFSSDGM 116

DB 101 DSVKGRFTISRDNALNSLYLQMSLRADTAVYICARLKLKGS-----SSGMPD 151

QY 117 VWGQGTIVTVSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTFPGQRVISISCGSSSD 176

DB 152 PMGRGTIVTVSSGGGSGGGSGGGSGGGS-----ELTQDPAVSVALGQTVRITCGDS-- 203

QY 177 IGSNTVNTYQQLPGTAPKLLIYSNNORPSGVDRPSGFSGSASLVISGLQSEBDAAY 236

DB 204 LRSYASWYQKPGQAPVLYVIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADAY 263

QY 237 CAAPDESINGVYFGGQTKTVL 258

DB 264 CNSRDSGNHVYFGGQTKTVL 285

QY 237 CAAPDESINGVYFGGQTKTVL 258

DB 264 CNSRDSGNHVYFGGQTKTVL 285

Search completed: May 13, 2004, 15:10:49

Job time : 15.1524 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 38.199 Seconds

(without alignments)
1879.405 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....AMDESLNGVFGGKRYTVL 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :	Published Applications AA:*
1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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16:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1371	100.0	258	14	US-10-072-301-27
2	1371	100.0	258	14	US-10-071-866-27
3	1371	100.0	258	15	US-10-360-828-27
4	1340	97.7	254	14	US-10-072-301-19
5	1340	97.7	254	14	US-10-071-866-19
6	1340	97.7	254	15	US-10-360-828-19
7	1031.5	75.2	252	10	US-09-880-748-1223
8	1031.5	75.2	252	12	US-10-293-418-1223
9	1003.5	73.2	244	13	US-10-039-785-44
10	1003.5	73.2	244	14	US-10-139-785-44
11	1002	73.1	255	10	US-09-880-748-1642
12	1002	73.1	255	12	US-10-293-418-1642
13	994.5	72.5	252	10	US-09-880-748-1994
14	994.5	72.5	252	12	US-10-293-418-1994
15	987	72.0	251	10	US-09-880-748-1510

16	987	72.0	251	12	US-10-293-418-1510	Sequence 1510, Ap
17	987	72.0	255	10	US-09-880-748-1597	Sequence 1597, Ap
18	987	72.0	255	12	US-10-293-418-1597	Sequence 1597, Ap
19	985.5	71.9	250	13	US-10-039-785-50	Sequence 50, Appl
20	985.5	71.9	250	14	US-10-139-785-50	Sequence 50, Appl
21	982	71.6	251	10	US-09-880-748-1546	Sequence 1546, Ap
22	982	71.6	251	12	US-10-293-418-1546	Sequence 1546, Ap
23	966	70.5	247	10	US-09-880-748-1981	Sequence 1981, Ap
24	966	70.5	247	12	US-10-293-418-1981	Sequence 1981, Ap
25	945	68.9	247	10	US-09-880-748-1993	Sequence 1993, Ap
26	945	68.9	247	12	US-10-293-418-1993	Sequence 1993, Ap
27	939.5	68.5	254	10	US-09-880-748-1659	Sequence 1659, Ap
28	939.5	68.5	254	12	US-10-293-418-1659	Sequence 1659, Ap
29	935	68.2	249	10	US-09-880-748-1962	Sequence 1962, Ap
30	935	68.2	249	12	US-10-293-418-1962	Sequence 1962, Ap
31	929	67.8	251	14	US-10-120-414-75	Sequence 75, Appl
32	927	67.6	247	10	US-09-880-748-1998	Sequence 1998, Ap
33	927	67.6	247	12	US-10-293-418-1998	Sequence 1998, Ap
34	925.5	67.5	256	10	US-09-880-748-1607	Sequence 1607, Ap
35	925.5	67.5	256	12	US-10-293-418-1607	Sequence 1607, Ap
36	921	67.2	251	10	US-09-880-748-1538	Sequence 1538, Ap
37	921	67.2	251	12	US-10-293-418-1538	Sequence 1538, Ap
38	915.5	66.8	258	10	US-09-880-748-2083	Sequence 2083, Ap
39	915.5	66.8	258	12	US-10-293-418-2083	Sequence 2083, Ap
40	905	66.0	251	10	US-09-880-748-1990	Sequence 990, Ap
41	905	66.0	251	12	US-10-293-418-1990	Sequence 990, Ap
42	898	65.5	245	10	US-09-880-748-1864	Sequence 1864, Ap
43	898	65.5	245	12	US-10-293-418-1864	Sequence 1864, Ap
44	896	65.4	253	10	US-09-880-748-1619	Sequence 1619, Ap
45	896	65.4	253	12	US-10-293-418-1619	Sequence 1619, Ap

ALIGNMENTS

RESULT 1	
US-10-072-301-27	
Sequence 27, Application US/10072301	
Publication No. US20030152913A1	
GENERAL INFORMATION:	
APPLICANT: Hua, Shao-bing	
APPLICANT: Pauling, Michelle H.	
APPLICANT: Zhu, Li	
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODE-	
FILE REFERENCE: 25636-718	
CURRENT FILING DATE: 2002-02-08	
NUMBER OF SEQ ID NOS: 54	
SOFTWARE: PatentIn version 3.1	
SEQ ID NO 27	
LENGTH: 258	
TYPE: PRT	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Clone 15.150.11	
US-10-072-301-27	
Query Match	
Best Local Similarity 100.0%, Score 1371, DB 14; Length 258;	
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QVQLQESGPGLVKPSSETLSLTTVGGSIGHDYMWIRPPPEGLEWIGFIFPDGSTNN 60
DB	1 QVQLQESGPGLVKPSSETLSLTTVGGSIGHDYMWIRPPPEGLEWIGFIFPDGSTNN 60
QY	61 PSINRVTISLDTSKNOISLRITSTVADTAVYFCARLKGAWLSEPPYSSDGDVWQ 120
DB	61 PSINRVTISLDTSKNOISLRITSTVADTAVYFCARLKGAWLSEPPYSSDGDVWQ 120
QY	121 GTTIVTSSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG 180
DB	121 GTTIVTSSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG 180

QY 181 TNNWYQOLPGTAPKLLIYSNNQPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCAAW 240
 Db 181 TNNWYQOLPGTAPKLLIYSNNQPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCAAW 240
 QY 241 DESLNGVVFQGGTKVTVL 258
 Db 241 DESLNGVVFQGGTKVTVL 258

RESULT 2

US-10-071-866-27
 / Sequence 27, Application US/10071866
 / Publication No. US2003016598A1
 / GENERAL INFORMATION:
 / APPLICANT: Hua, Shao-bing
 / APPLICANT: Pauling, Michelle H.
 / APPLICANT: Zhu, Li
 / TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
 / FILE REFERENCE: 25636-717
 / CURRENT APPLICATION NUMBER: US/10/071,866
 / NUMBER OF SEQ ID NOS: 54
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 27
 / LENGTH: 258
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Clone 15.150.11
 US-10-071-866-27

Query Match Best Local Similarity 100.0%; Score 1371; DB 14; Length 258;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWRQPPGEGLEWIGFIFPDGSTNN 60
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWRQPPGEGLEWIGFIFPDGSTNN 60
 QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGMWLSEPPYSSDGMVWQ 120
 Db 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGMWLSEPPYSSDGMVWQ 120
 QY 121 GTTVTVSSGGGSGGGSGGGSGGSGSNFMTLPSPASGTGQORVSISSGSSSDIGSN 180
 Db 121 GTTVTVSSGGGSGGGSGGGSGGSGSNFMTLPSPASGTGQORVSISSGSSSDIGSN 180
 QY 181 TNNWYQOLPGTAPKLLIYSNNQPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCAAW 240
 Db 181 TNNWYQOLPGTAPKLLIYSNNQPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCAAW 240
 QY 241 DESLNGVVFQGGTKVTVL 258
 Db 241 DESLNGVVFQGGTKVTVL 258

RESULT 3

US-10-360-828-27
 / Sequence 27, Application US/10360828
 / Publication No. US2003020690A1
 / GENERAL INFORMATION:
 / APPLICANT: Hua, Shao-bing
 / APPLICANT: Pauling, Michelle H.
 / APPLICANT: Zhu, Li
 / TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
 / FILE REFERENCE: 25636-727
 / CURRENT APPLICATION NUMBER: US/10/360,828
 / PRIOR FILING DATE: 2002-02-07
 / PRIOR APPLICATION NUMBER: US 10/071,866
 / PRIOR FILING DATE: 2002-02-08
 / PRIOR APPLICATION NUMBER: US 10/072,301

/ PRIOR FILING DATE: 2002-02-08
 / PRIOR APPLICATION NUMBER: US 10/133,978
 / PRIOR FILING DATE: 2002-04-25
 / NUMBER OF SEQ ID NOS: 64
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 27
 / LENGTH: 258
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Clone 15.150.11 Variant
 US-10-360-828-27

Query Match Best Local Similarity 100.0%; Score 1371; DB 15; Length 258;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWRQPPGEGLEWIGFIFPDGSTNN 60
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWRQPPGEGLEWIGFIFPDGSTNN 60
 QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGMWLSEPPYSSDGMVWQ 120
 Db 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGMWLSEPPYSSDGMVWQ 120
 QY 121 GTTVTVSSGGGSGGGSGGGSGGSGSNFMTLPSPASGTGQORVSISSGSSSDIGSN 180
 Db 121 GTTVTVSSGGGSGGGSGGGSGGSGSNFMTLPSPASGTGQORVSISSGSSSDIGSN 180
 QY 181 TNNWYQOLPGTAPKLLIYSNNQPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCAAW 240
 Db 181 TNNWYQOLPGTAPKLLIYSNNQPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCAAW 240
 QY 241 DESLNGVVFQGGTKVTVL 258
 Db 241 DESLNGVVFQGGTKVTVL 258

RESULT 4

US-10-072-301-19
 / Sequence 19, Application US/10072301
 / Publication No. US20030152913A1
 / GENERAL INFORMATION:
 / APPLICANT: Hua, Shao-bing
 / APPLICANT: Pauling, Michelle H.
 / APPLICANT: Zhu, Li
 / TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
 / FILE REFERENCE: 25636-718
 / CURRENT APPLICATION NUMBER: US/10/072,301
 / PRIOR FILING DATE: 2002-02-08
 / NUMBER OF SEQ ID NOS: 54
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 19
 / LENGTH: 254
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Clone 15.150.11
 US-10-072-301-19

Query Match Best Local Similarity 97.7%; Score 1340; DB 14; Length 254;
 Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWRQPPGEGLEWIGFIFPDGSTNN 60
 Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWRQPPGEGLEWIGFIFPDGSTNN 60
 QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGMWLSEPPYSSDGMVWQ 120
 Db 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGMWLSEPPYSSDGMVWQ 120

QY 121 GTTAVSSGGGGGGGGGGGGGGGSGGSGNFMLTOPPSAGTGPORVSISSGSSSDIGSN 180
DB 122 GTTAVTPSSGGGGGGGGGGGGGGGSGGSGNFMLTOPPSAGTGPORVSISSGSSSDIGSN 180
QY 181 TNNWYQQLPGLTAPKLLIYSNNORPSGVPDRFSGFSGTASIVISGLQSEDEADYYCAAW 240
DB 181 TNNWYQQLPGLTAPKLLIYSNNORPSGVPDRFSGFSGTASIVISGLQSEDEADYYCAAW 240
QY 241 DESLNGVVFVGSGTK 254
DB 241 DESLNGVVFVGSGPR 254

RESULT 5
US-10-071-866-19

/ Sequence 19, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
/ TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 19
/ LENGTH: 254
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.11
US-10-071-866-19

Query Match 97.7%; Score 1340; DB 14; Length 254;
Best Local Similarity 98.8%; Pred. No. 9.8e-85;
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGFIFPDGSTNN 60
DB 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGFIFPDGSTNN 60
QY 61 PSINGRVITSLDTSKNQSLRLTSTADTAVYFCARLKAWLSEPPYFSSDGMVWQ 120
DB 61 PSINGRVITSLDTSKNQSLRLTSTADTAVYFCARLKAWLSEPPYFSSDGMVWQ 120
QY 121 GTTAVSSGGGGGGGGGGGGGGGSGGSGNFMLTOPPSAGTGPORVSISSGSSSDIGSN 180
DB 121 GTTAVTPSSGGGGGGGGGGGGGGGSGGSGNFMLTOPPSAGTGPORVSISSGSSSDIGSN 180
QY 181 TNNWYQQLPGLTAPKLLIYSNNORPSGVPDRFSGFSGTASIVISGLQSEDEADYYCAAW 240
DB 181 TNNWYQQLPGLTAPKLLIYSNNORPSGVPDRFSGFSGTASIVISGLQSEDEADYYCAAW 240
QY 241 DESLNGVVFVGSGTK 254
DB 241 DESLNGVVFVGSGPR 254

RESULT 6
US-10-360-828-19

/ Sequence 19, Application US/10360828
/ Publication No. US20030206909A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-727
/ CURRENT APPLICATION NUMBER: US/10/360,828
/ CURRENT FILING DATE: 2003-02-07

/ PRIOR APPLICATION NUMBER: US 10/071,866
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: US 10/072,301
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: US 10/133,978
/ PRIOR FILING DATE: 2002-04-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 19
/ LENGTH: 254
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.11
US-10-360-828-19

Query Match 97.7%; Score 1340; DB 15; Length 254;
Best Local Similarity 98.8%; Pred. No. 9.8e-85;
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGFIFPDGSTNN 60
DB 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGFIFPDGSTNN 60
QY 61 PSINGRVITSLDTSKNQSLRLTSTADTAVYFCARLKAWLSEPPYFSSDGMVWQ 120
DB 61 PSINGRVITSLDTSKNQSLRLTSTADTAVYFCARLKAWLSEPPYFSSDGMVWQ 120
QY 121 GTTAVSSGGGGGGGGGGGGGGGSGGSGNFMLTOPPSAGTGPORVSISSGSSSDIGSN 180
DB 121 GTTAVTPSSGGGGGGGGGGGGGGGSGGSGNFMLTOPPSAGTGPORVSISSGSSSDIGSN 180
QY 181 TNNWYQQLPGLTAPKLLIYSNNORPSGVPDRFSGFSGTASIVISGLQSEDEADYYCAAW 240
DB 181 TNNWYQQLPGLTAPKLLIYSNNORPSGVPDRFSGFSGTASIVISGLQSEDEADYYCAAW 240
QY 241 DESLNGVVFVGSGTK 254
DB 241 DESLNGVVFVGSGPR 254

RESULT 7

US-09-880-748-1223
/ Sequence 1223, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PFS23
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1223
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1223

Query Match 75.2%; Score 1031.5; DB 10; Length 252;
Best Local Similarity 78.1%; Pred. No. 1.7e-63;
Matches 203; Conservative 15; Mismatches 31; Indels 11; Gaps 3;

QY 1 QVQLQESGGPGLVKPSETTSLTCTVSGSGSIQH--DYWMIKROPFGLEWIGFIFFDGSNTN 58
DB 1 QVQLQESGGPGLVKPSETTSLTCTVSGSGSIQH--DYWMIKROPFGLEWIGFIFFDGSNTN 58
QY 59 YNPISLNGRTVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 118
DB 61 YSPSLKSRVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 118
QY 119 GGGTIVTVSSGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG 178
DB 116 GKGITVTVSSGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG 178
QY 179 SNTVWVYQQLPGTAPKLIYNNORPSGVPDRFSGFSKGTSGASLVISGLQSEDEADYYCA 238
DB 172 SNTVWVYQQLPGTAPKLIYNNORPSGVPDRFSGFSKGTSGASLVISGLQSEDEADYYCA 238
QY 239 AMDSLNGVVFGGGKTATVL 258
DB 232 TWDLSLNGVVFGGGKTATVL 251

RESULT 8

US-10-293-418-1223
; Sequence 1223, Application US/10293418
; Publication No. US2003023956A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS32P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1223
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1223

Query Match 75.2%; Score 1031.5; DB 12; Length 252;
Best Local Similarity 78.1%; Pred. No. 1.7e-63;

Matches 203; Conservative 15; Mismatches 31; Indels 11; Gaps 3;

QY 1 QVQLQESGGPGLVKPSETTSLTCTVSGSGSIQH--DYWMIKROPFGLEWIGFIFFDGSNTN 58
DB 1 QVQLQESGGPGLVKPSETTSLTCTVSGSGSIQH--DYWMIKROPFGLEWIGFIFFDGSNTN 58
QY 59 YNPISLNGRTVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 118
DB 61 YSPSLKSRVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 118
QY 119 GGGTIVTVSSGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG 178
DB 116 GKGITVTVSSGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG 178
QY 179 SNTVWVYQQLPGTAPKLIYNNORPSGVPDRFSGFSKGTSGASLVISGLQSEDEADYYCA 238
DB 172 SNTVWVYQQLPGTAPKLIYNNORPSGVPDRFSGFSKGTSGASLVISGLQSEDEADYYCA 238

QY 239 AMDSLNGVVFGGGKTATVL 258
DB 232 TWDLSLNGVVFGGGKTATVL 251

RESULT 9

US-10-039-785-44
; Sequence 44, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PFS50
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: T1014A02 acFv
US-10-039-785-44

Query Match 73.2%; Score 1003.5; DB 13; Length 244;
Best Local Similarity 75.2%; Pred. No. 1.4e-61;

Matches 194; Conservative 18; Mismatches 31; Indels 15; Gaps 2;

QY 1 QVQLQESGGPGLVKPSETTSLTCTVSGSGSIQH--DYWMIKROPFGLEWIGFIFFDGSNTN 60
DB 1 QVQLQESGGPGLVKPSETTSLTCTVSGSGSIQH--DYWMIKROPFGLEWIGFIFFDGSNTN 60
QY 61 YNPISLNGRTVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 120
DB 61 YNPISLNGRTVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 120
QY 121 GTTVTVSSGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG 180
DB 109 GTTVTVSSGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG 180
QY 181 YNPISLNGRTVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 240
DB 166 YNPISLNGRTVTLSDTSKNQQLSLRTSVTAADTAAYVFCARLKGAWMLSEPPYFSSDGMVDVW 240
QY 241 DESLNGVVFGGGKTATVL 258
DB 226 DESLNGVVFGGGKTATVL 258

RESULT 10
US-10-139-785-44
; Sequence 44, Application US/10139785

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RESULT 12
US-10-293-418-1642
; Sequence 1642, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bvys
; FILE REFERENCE: PFS2332
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,459
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1642
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1642

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Query Match          73.1%; Score 1002; DB 12; Length 255;
Best Local Similarity 75.7%; Pred. No. 1.8e-61;
Matches 196; Conservative 23; Mismatches 34; Indels 6; Gaps 2;

QY 1 QVQLQESGGGLVQPKSEETLSLTCTVSGSGTHGYMWMIRQPPGELRWIGIFFDGSTNYN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVQLQDMGGLTKPKSETLSLTAVYGGSGFYWMIRQSPKGLWIGELNHGISTNYN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAW-LISEPPYSSDGMVW 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 PSLKSVTISVDASKNQFSLKLSVTAADTAVYCARERSYDILTGYSPRSKYGMVW 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 QGTTVTYVSSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPQGRVTSICSGSSSDIG 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 RGLTVTVS-----SGGSGGGSGGGSGGGSGQSVLTQPPSASGTPGQKVTISCSGSSNIG 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 NTVMWYQQLPGTAPKLLIYSNNORPSGVPRFSGFSGTSASLVISGLQSEDEADYYCA 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 176 NTVMWYQRLPGAAPQLLIYNNDORPSGIFDRFSGSGTSGLSVISGLQSEDEADYYCA 235
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 WDESLNGVVFGGGKTVTL 258
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 236 WDSLNGRVFGGKTVTL 254
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-880-748-1994
; Sequence 1994, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1994
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1994

Query Match          72.5%; Score 994.5; DB 10; Length 252;
Best Local Similarity 74.6%; Pred. No. 5.9e-61;
Matches 194; Conservative 21; Mismatches 34; Indels 11; Gaps 3;

QY 1 QVQLQESGGGLVQPKSEETLSLTCTVSGSGI--GHYWMIRQPPGELRWIGIFFDGSTN 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVQLQESGGGLVQPKSETLSLTCTVSGSGISSGDYWMIRQHPGELRWIGIYTHSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 YNPISLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYSSDGMVW 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YNPISLKSRYMSVDTSKNQYSLKLSVTAADTAVYCARLR-----PDADYGDYGFYW 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 GGGTTVTYVSSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPQGRVTSICSGSSSDIG 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 GGGTWTYVSSGGGSGGGSGGGSGGGSG---ALSYVLTPPSASATPQGRVTISCSGSRNIG 171
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 SNTVMWYQQLPGTAPKLLIYSNNORPSGVPRFSGFSGTSASLVISGLQSEDEADYYCA 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 172 SNTVMWYQQLPGAAPKLLIYRSYORPSGVPRFSGSGTSASLVISGLRSEDEADYYCA 231
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 SNTVMWYQQLPGTAPKLLIYSNNORPSGVPRFSGFSGTSASLVISGLQSEDEADYYCA 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 172 SNTVMWYQQLPGAAPKLLIYRSYORPSGVPRFSGSGTSASLVISGLRSEDEADYYCA 231
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 239 AMDESLNGVVFGGGKTVTL 258
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 232 TMDRLRGLVFGGKTVTL 251
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-10-293-418-1994
; Sequence 1994, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1994
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-1994

Query Match          72.5%; Score 994.5; DB 12; Length 252;
Best Local Similarity 74.6%; Pred. No. 5.9e-61;
Matches 194; Conservative 21; Mismatches 34; Indels 11; Gaps 3;

QY 1 QVQLQESGGGLVQPKSEETLSLTCTVSGSGI--GHYWMIRQPPGELRWIGIFFDGSTN 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVQLQESGGGLVQPKSETLSLTCTVSGSGISSGDYWMIRQHPGELRWIGIYTHSGSTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 YNPISLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYSSDGMVW 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YNPISLKSRYMSVDTSKNQYSLKLSVTAADTAVYCARLR-----PDADYGDYGFYW 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 GGGTTVTYVSSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPQGRVTSICSGSSSDIG 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 GGGTWTYVSSGGGSGGGSGGGSGGGSG---ALSYVLTPPSASATPQGRVTISCSGSRNIG 171
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 SNTVMWYQQLPGTAPKLLIYSNNORPSGVPRFSGFSGTSASLVISGLQSEDEADYYCA 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 172 SNTVMWYQQLPGAAPKLLIYRSYORPSGVPRFSGSGTSASLVISGLRSEDEADYYCA 231
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 AMDESLNGVVFGGGKTVTL 258
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 232 TMDRLRGLVFGGKTVTL 251
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-09-880-748-1510
; Sequence 1510, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748

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; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1510
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1510

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Query Match      72.0%; Score 987; DB 10; Length 251;
Best Local Similarity 75.8%; Pred. No. 1.9e-60;
Matches 197; Conservative 20; Mismatches 31; Indels 12; Gaps 4;

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QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIQH--DYWSMIRPPGEGLEWIGFIFPDGSTN 58
DB      1 QVQLQESGPGVVKPSFTLSLTCTVSGGFTSSRTSYWGWIROPKGLIEWIGNIYTGKTY 60
QY      59 YNPSLNGRVTISLDTSKNQLSLRTSVTAADTAIVYFCARLKGAWLSEPPYFSSDGMVW 118
DB      61 YAPSLKSRVTISADTSKNQLSLKLSVTADTAIVYCARAGYDILLGYPFYF-----DSM 115
QY      119 GGGTIVTVSSGGGSGGGSGGGSGGGSGGSGNFMULTOPPSASGTPGGRVVISCSGSSSDIG 178
DB      116 GGGTIVTVSSGGGSGGGSGGGSGGGSGGSG--AQAVLTQPSASGTPGGRVVISCSGSSSNIG 171
QY      179 SNTVWVYQQLPGTAPRLIYSNNORPSGVDPDFSGFGSGTSASLVISGLQSEDEADYCA 238
DB      172 STTVAMVYQGVPGTAPRLIYSNDRPSGVDPDFSGFGSGTSASLVISGLQSEDEADYCA 231
QY      239 AWDESLNGVVFGGGTVTVL 258
DB      232 SWDDSPH-VVFGGTVTVL 250

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Search completed: May 13, 2004, 15:43:33
Job time : 38.199 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 13, 2004, 14:50:27 ; Search time 11.6476 Seconds
(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371

Sequence: 1 QVQLQESGPGLVKPSETLSL.....AMDESLNGVPGGKTKVTVL 258

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	575.5	42.0	268	2 A56446	Ig heavy chain V r
2	548	40.0	249	2 S41374	single chain Fv an
3	532	38.8	233	2 S25752	Ig lambda chain -
4	513	37.4	112	2 D44151	Ig lambda chain V
5	508.5	37.1	149	2 S23626	Ig lambda chain V
6	506	36.9	234	2 S25757	Ig lambda chain -
7	502	36.6	112	2 B44151	Ig lambda chain V
8	501	36.5	112	2 C44151	Ig lambda chain V
9	501	36.5	129	2 S78058	Ig lambda chain pr
10	498.5	36.4	235	2 S25754	Ig lambda chain -
11	498	36.3	110	2 S57408	Ig lambda chain V-
12	498	36.3	216	2 A42193	Ig lambda chain (B
13	497	36.3	130	2 S78057	Ig lambda chain pr
14	496	36.2	112	2 A44151	Ig lambda chain V
15	492.5	35.9	135	2 S78051	Ig heavy chain pre
16	491.5	35.8	155	2 S31511	Ig heavy chain - h
17	490	35.7	233	2 S25744	Ig lambda chain -
18	489	35.7	235	2 S25750	Ig lambda chain -
19	488.5	35.6	135	2 S31512	Ig heavy chain - h
20	488	35.6	233	2 JC5322	p53 specific singl
21	483.5	35.3	140	2 I37782	Ig variable region
22	481	35.1	117	2 S23627	Ig lambda chain pr
23	481	35.1	137	2 S31676	Ig heavy chain V r
24	479.5	35.0	130	2 S31690	Ig heavy chain V r
25	479.5	35.0	146	2 S09711	Ig heavy chain V r
26	478	34.9	110	2 S57428	Ig light chain V-J
27	478	34.9	98	2 S36047	Ig lambda chain -
28	472	34.4	130	2 S30534	Ig heavy chain V r
29	469	34.2	118	2 S20780	Ig heavy chain V r

30	465	33.9	139	2 S31586	Ig heavy chain V r
31	464	33.8	216	2 S03401	Ig lambda chain (K
32	462.5	33.7	112	2 L1H0M	Ig lambda chain V-
33	461	33.6	111	1 L1H0V	Ig lambda chain V-
34	458.5	33.4	147	2 S13519	Ig heavy chain V r
35	452	33.0	130	2 S09712	Ig lambda chain V
36	452	33.0	146	1 D3H0M2	Ig heavy chain pre
37	451.5	32.9	129	1 D3H0M2	Ig heavy chain V-I
38	449.5	32.8	121	2 S44113	Ig heavy chain V r
39	449	32.7	98	2 S36048	Ig lambda chain -
40	449	32.7	220	2 A49444	Ig gamma-1 heavy C
41	449	32.7	231	2 B23746	Ig Fab region IV-J
42	448.5	32.7	143	2 B49028	Ig heavy chain V-I
43	448	32.7	235	2 S05270	Ig lambda chain pr
44	447.5	32.6	146	2 S09710	Ig heavy chain V r
45	447	32.6	109	1 L1H0M	Ig lambda chain V-

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Yang, F.W.; Folz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TRAN>

A:Cross-references: GB:U20617

C:Keywords: heterotrimer; immunoglobulin

Query Match 42.0%; Score 575.5; DB 2; Length 268;

Best Local Similarity 47.9%; Pred. No. 1.8e-30;

Matches 124; Conservative 36; Mismatches 76; Indels 23; Gaps 6;

QY	1	QVQLQESGPGLVKPSETLSLCTVSGSGISGHDYMWIRQPGGEMWIGFIRFDGSTNY	59
DB	3	QVQLQESGAEELVKPSPASVKLSCTTSGFNKIDYTMWVQKRPQGLFWIGRIAPANGITRY	62
QY	60	NPSLNGRYTISLDTSKNQLSLRTSVTAADTAAYFCARLKGAMLLSEPPYFSSDGMWVG	119
DB	63	DPKFGKATIAADTSSNTAVYQLSLTSEDTAVYYCA-----SYLTREYNWVG	111
QY	120	QGTIVTVSSGGGGSGGGSGGGSGGSGNFMFLTPPS-ASCTPGQRYVSISSGSSSDIG	178
DB	112	QGTIVTVS-----SCGGSGGGGSDSGGSDIELTQSPAIMSASLSEKWTMSGRASS---	163
QY	179	SNTVMVGOQLPGTAPAKLLIYSNNQRPSPGVPRPFGSFGKTSASLYISGLQSEBDAVYYCA	238
DB	164	VNFIYVYQKSDASPKLVWYITSHLPQVPARFSGSGSGNLSLTISMEGDAATYYCQ	223
QY	239	AMDESLNGVPGGKTKTV 257	
DB	224	QFTS--PFTFGSGTKLEI 240	

RESULT 2

S41374
single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: S41374

R:Artbaenko, O.; Weiler, B.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv antibody

A:Reference number: S41374

A/Accession: S41374
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <ART>
A/Cross-references: EMBL:Z29480

Query Match 40.0%; Score 548; DB 2; Length 249;
Best Local Similarity 48.1%; Pred. No. 1e-28;
Matches 125; Conservative 34; Mismatches 79; Indels 22; Gaps 7;

QY 1 QVOIOESGPGVXKSESTLSLTCTVSGSGIGHYKWSIRPPGGLWIGTF-FDGSTNY 59
DB 1 QVOIQQSASLVRGASVKTSCSTASGFNFKDDYIHWYKBPKEKLEMIARIAPASGVKY 60
QY 60 NPSLNGRTVSLDPSKNOISRLTSVTAAADYVFCARLKGAMLLSPFPSSDDQWVG 119
DB 61 VPRPDKATITADISSMTAVILLSSLTSEDTAVYCAR-----RITLYTS--IGYWG 110
QY 120 QGTTVTVSSGG 177
DB 111 QGSTVTVSS-----SRGG 165
QY 178 --GSNTVWYQQLPGTAPKLLIYNNRPSGVDRPSGFGSGTSSASLVISGLQSEDEADY 235
DB 166 SDGDSYVFWLQRPQSGSPOLLITRMSMLASGVDRPSGSGSGTSLRISRVADVGY 225
QY 236 YCAAMDESLLNGVVFQGGTKV 255
DB 226 YCMQHRE--YPLTFGAQTKL 243

RESULT 3

IG lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25752
R/Combricato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25752
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-233 <COM>
A/Cross-references: EMBL:X57817; NID:g33733; PID:CAA40954.1; PID:g33734
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 38.8%; Score 532; DB 2; Length 233;
Best Local Similarity 88.6%; Pred. No. 1e-27;
Matches 101; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 145 GGSNFMLTQPPASGTPQGRVISCSSGSSSDIGSNTVWYQQLPGTAPKLLIYNNORP 204
DB 14 GSWAQSVLTQPPASGTPQGRVITISGSSSNIGSNTVWYQQLPGTAPKLLIYNNORP 73
QY 205 SGVPRFSGSGTSSASLVISGLQSEDEADYCAAMDESLLNGVVFQGGTKVTL 258
DB 74 SGVPRFSGSGTSSASLVISGLQSEDEADYCAAMDESLLNGVVFQGGTKVTL 127

RESULT 4

IG lambda chain V region (BO-12) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C/Accession: D44151
R/Zedebede, S.L.; Barbas III, C.F.; Hom, Y.L.; Gaothien, R.H.; Graff, R.; Degraw, J.; Ey
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A/Reference number: A44151; MUID:92228746; PMID:1373487

A/Accession: D44151
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-112 <ZEB>
A/Note: nucleotide translation is not given
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 37.4%; Score 513; DB 2; Length 112;
Best Local Similarity 90.7%; Pred. No. 8.1e-27;
Matches 97; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 152 LTQPPASGTPQGRVISCSSGSSSDIGSNTVWYQQLPGTAPKLLIYNNORPSGVPRF 211
DB 3 LTQPPASGTPQGRVITISGSSSNIGSNTVWYQQLPGTAPKLLIYNNORPSGVPRF 62
QY 212 SGFKSGTSSASLVISGLQSEDEADYCAAMDESLLNGVVFQGGTKVTL 258
DB 63 SASKSGTSSASLVISGLQSEDEADYCAAMDESLLNGVVFQGGTKVTL 109

RESULT 5

IG lambda chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S23626
R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deflor, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A/Reference number: S23623; MUID:92156804; PMID:11740665
A/Accession: S23626
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-149 <OLE>
A/Cross-references: EMBL:X59706; NID:g34404; PID:CAA42227.1; PID:g34205
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 37.1%; Score 508.5; DB 2; Length 149;
Best Local Similarity 85.2%; Pred. No. 2.1e-26;
Matches 98; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 145 GGSNFMLTQPPASGTPQGRVISCSSGSSSDIGSNTVWYQQLPGTAPKLLIYNNORP 204
DB 16 GSWAQSVLTQPPASGTPQGRVITISGSSSNIGSNTVWYQQLPGTAPKLLIYNNORP 75
QY 205 SGVPRFSGSGTSSASLVISGLQSEDEADYCAAMDESLLNGVVFQGGTKVTL 258
DB 76 SGVPRFSGSGTSSASLVISGLQSEDEADYCAAMDESLLNGVVFQGGTKVTL 130

RESULT 6

IG lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25757
R/Combricato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25757
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-234 <COM>
A/Cross-references: EMBL:X57822; NID:g33743; PID:CAA40959.1; PID:g33744
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:149-217/Domain: immunoglobulin homology <IMM>

Db 63 SGSKSGTASLAIISGLSEDEAEATYCEAMPDSDLGPFPGGKTATVL 109

RESULT 9

Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)
S78058
CISpecies: Homo sapiens (man)
CDate: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
CAccession: S78058; S23723
R.Harindranath, N.
submitted to the EMBL Data Library, August 1990
A.Reference number: S78051
A.Accession: S78058
A.Molecule type: mRNA
A.Residues: 1-129 <HAM>
A.Cross-References: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
R.Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Bursatero, S.E.; Wilder, R.L.; Nokin
Int. Immunol. 3, 865-875, 1991
A.Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient
A.Reference number: S23716; MUID:92031262; PMID:11784404
A.Accession: S23723
A.Molecule type: mRNA
A.Residues: 19-129 <HAM>
A.Cross-References: EMBL:X54446
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F11-18/Domain: signal sequence (fragment) #status predicted <SIG>
F19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F13-109/Domain: immunoglobulin homology <IMM>

```
Query Match Similarity      36.5%; Score 501; DB 2; Length 129;
Beet Local Similarity      84.2%; Pred. No. 5.6e-26;
Matches 96; Conservative   8; Mismatches 10; Indels 0; Gaps 0;

Oy      145 GGGSFMFLTROPESASGTPGCQRVVISCGSGSSDDIGSNTVMYQQLPGTA PKLLIYSNNRP 204
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      15 GSMAGSVLTQPFSASGTPGQRVTISCSGSSNIGSNVYVYQQLPGTAPKLLIRNNR 74

Oy      205 SGVPDRFSGFKSGTSASLVISGLQSEDEADYYCAAMDESINGVFGGTKXTVL 258
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      75 SGVPDRFSGSKSGTSASLAIISGLRSEDEADYYCAAMDLSLGWVGGGTKTLVL 128

RESULT 10

S25754
Ig lambda chain - human (Bregment)
C|Species: Homo sapiens (man)
C|Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C|Accession: S25754
C|Combiarto. G ; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A|Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A|Reference number: S16439; MWID:91257162; PMID:1904362
A|Accession: S25754
A|Status: preliminary; translation not shown
A|Molecule type: mRNA
A|Residues: 1-235 <COM>

A|Cross-references: EMBL.X57819; NID:g33737; PIDN.CAA0956.1; PID:g33738
C|Superfamily: Immunoglobulin V region; immunoglobulin homology
C|Keywords: heterotetramer; immunoglobulin homology <IMM>
P.1150-218/Domain: immunoglobulin homology
```

Query Match	36.4%;	Score	498.5;	DB 2;	Length	235;
Best Local Similarity	85.2%;	Pred. No.	1.5e-25;			
Matches	98;	Conservative	5;	Mismatches	11;	Indels
						Gaps
QY	145	GGGNSPMLTOPRSPASGTPGQGVVSSICGSSSDISNNVYNNYQOOLPGTAPKLLIYSSNNORP	204			
	:				
Db	15	GSMASQVITOPPSASGTPGQGVVSSICGSSSSNNIGNTVNNYQOOLPGRAKLLIYSSNNORP	74			
QY	205	SGVDRFRSGFGKSGTSASLVISGLQSEEDADYYCAMEDSLNG-VVFGGQGTATVVL	258			

R;Harindranath, N.

submitted to the EMBL Data Library, August 1990
A-Reference number: S78051

A;Reference number: S78051

A; Accession: S78051

A;Molecule type: mRNA

A;Residues: 1-135 <HAR>

A; Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117

R; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkine

Int. Immunol. 3, 865-875, 1991

patient.

A:Reference number: S23716; MUID:92031262; PMID:1718404

A;Accession: S23716

A;Molecule type: mRNA

A;Residues: 13-111 <HAW>

A;Cross-references: EMBL:X54437

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: immunoglobulin

F:1-13/Domain: signal sequence (Fragment) #status predicted <SIG>

F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
E:37-111/Domains: immunoglobulin heavy chain <IMM>

F;27-111/Domain: immunoglobulin homology <IMM>

Query Match	35.9%	Score 492.5;	DB 2;	Length 135;
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Best Local Similarity 73.8%; Pred. No. 2.1e-25;

Matches 96; Conservative 12; Mismatches 13; Indels 9; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--GHDYWSMIRQPPGEGLEWIGFIFFDGSTN 58

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Db 13 QLQLGESGPGLVKPSSETLSLCTVSGGISRGSHYWGWIQPPGKGLEWIGSIYYSGNTY 72

QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCARLKGAWLLSEPPYFSSDGMVW 11

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GGGTTTSS 128

Db 126 GGGTTTVSS 135

Search completed: May 13, 2004, 15:08:43
Job time : 11.6476 secs

Job time : 11.6476 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.26408 Seconds
(without alignments)
1849.388 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371

Sequence: 1 QVQLQESGPGGLVKKPSETSL.....AMDSESLNGVFCGGRKVTYL 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462.5	33.7	112	1	LV1A_HUMAN
2	461	33.6	111	1	LV1A_HUMAN
3	452	33.0	146	1	HV2I_HUMAN
4	451.5	32.9	129	1	HV2F_HUMAN
5	447	32.6	109	1	LV1F_HUMAN
6	441	32.2	130	1	LV1G_HUMAN
7	436	31.8	111	1	LV1D_HUMAN
8	433.5	31.6	112	1	LV1B_HUMAN
9	426	31.1	111	1	LV1C_HUMAN
10	413	30.1	109	1	LV1I_HUMAN
11	408.5	29.8	117	1	HV2G_HUMAN
12	382	27.9	111	1	LV2G_HUMAN
13	372	27.1	111	1	LV2F_HUMAN
14	370.5	27.0	137	1	HV4G_MOUSE
15	367.5	26.8	113	1	HV4F_MOUSE
16	360.5	26.3	112	1	LV2K_HUMAN
17	360	26.3	103	1	LV1E_HUMAN
18	360	26.3	111	1	LV2B_HUMAN
19	358	26.1	111	1	LV2D_HUMAN
20	357	26.0	111	1	LV2H_HUMAN
21	356	26.0	111	1	LV2B_HUMAN
22	352	25.7	111	1	LV2C_HUMAN
23	347.5	25.3	110	1	LV2I_HUMAN
24	347.5	25.3	131	1	LV6E_HUMAN
25	347	25.3	111	1	LV2I_HUMAN
26	346.5	25.3	112	1	LV6I_HUMAN
27	346.5	25.3	144	1	HV4J_MOUSE
28	344.5	25.1	116	1	HV6F_MOUSE
29	344	25.1	109	1	LV2E_HUMAN
30	342	24.9	111	1	LV3B_HUMAN
31	336	24.5	106	1	LV4A_HUMAN
32	336	24.5	111	1	LV2A_HUMAN
33	335	24.4	106	1	LV4B_HUMAN

34	332	24.2	106	1	LV4E_HUMAN	P06689 homo sapien
35	329.5	24.0	116	1	HV6I_MOUSE	P18532 mus musculu
36	328	23.9	108	1	LV5A_HUMAN	P01719 homo sapien
37	324	23.6	107	1	LV4C_HUMAN	P01717 homo sapien
38	324	23.6	111	1	LV6C_HUMAN	P06317 homo sapien
39	324	23.6	117	1	HV6C_MOUSE	P18533 mus musculu
40	321	23.4	135	1	HV02_XENLA	P20957 xenopus lae
41	313.5	22.9	112	1	LV6B_HUMAN	P01722 homo sapien
42	310	22.6	120	1	HV2B_HUMAN	P01815 homo sapien
43	307.5	22.4	125	1	HV2D_HUMAN	P01817 homo sapien
44	305	22.2	108	1	LV3A_HUMAN	P01714 homo sapien
45	304	22.2	111	1	LV7A_HUMAN	P01720 homo sapien

ALIGNMENTS

RESULT 1	ID	LV1H_HUMAN	STANDARD	PRT	112 AA.
AC	P06687				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Ig lambda chain V-I region MEM.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=85257662; PubMed=2410269;				
RA	Mihaseo E., Roy J.P., Congy N., Peran-Rivat L., Mihaseo C.;				
RT	"The amino acid sequence of a lambda light chain presenting abnormal				
RT	physicochemical and antigenic features."				
RL	Eur. J. Biochem. 150:349-357(1985).				
CC	-1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES				
CC	WERE POSITIONED BY HOMOLOGY.				
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+				
CC	MARKERS.				
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A25479; LIHUM.				
DR	HSSP; P01703; 7PAB.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; P:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV_1.				
DR	PROSITE; PS00835; Ig_LIKE; 1.				
KW	Immunoglobulin V region; Monoclonal antibody;				
KW	Pyroglutamate carboxylic acid.				
FT	DOMAIN 1 106				
FT	MOD RES 1 1				
FT	MOD RES 22 90				
FT	DISTRID 112 112				
FT	NON_TER 112 112				
FT	BY SIMILARITY.				
SQ	SEQUENCE 112 AA; 11789 MW; 748124F079CFB84 CRC64;				
Query Match					
Best local similarity 82.6%; Pred. No. 3.5e-26;					
Matches 90; Conservative 8; Mismatches 10; Indels 1; Gaps 1;					
QY	151	MTTPPSASGTPGQVSVISGSSSSSDIGSN-TVMNYQQLPGTAPKLLITSNNQPSGVD	209		
DB	3	VITQPPASGTPGQVSVISGSSSSSDIGSN-TVMNYQQLPGTAPKLLITSNNQPSGVD	62		
QY	210	RSSGKSGTSASIVTSGLOSEADYVCAAMDSESLNGVFCGGRKVTYL 258			
DB	63	RFSASRSGTSASIVTSGLOSEADYVCAAMDSESLNGVFCGGRKVTYL 111			

RESULT 2

LVIA_HUMAN
ID LVIA_HUMAN STANDARD; PRT; 111 AA.
AC P01699;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region VOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023790; PubMed=809332;
RA Engelhard M., Hilschmann N.;
RT "Pattern of antibody structure. The amino acid sequence of a
RT monoclonal immunoglobulin L-chain of lambda-type, subgroup I
RT (Bence-Jones-protein Vor.) A contribution to the elucidation of the
RT origin of antibody specificity.";
RL Hoppe-seyler's Z. Physiol. Chem. 356:1413-1444(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01962; LHMVO.
DR HSSP: P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 105
FT MOD_RES 1 1
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11514 MW; 21D9F64250DFC8E0 CRC64;
Query Match 33.0%; Score 461; DB 1; Length 111;
Best Local Similarity 80.6%; Pred. No. 4,4e-26;
Matches 87; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
QY 151 MLTPPSASGTGPGQRVSISSGSSSDIGNTVMYQQLFGTAPKLLIYSNNRPSGVDR 210
DB 3 VLIQPPSASGTGPGQRVSISSGSSSDIGNTVMYQQLFGTAPKLLIYSNNRPSGVDR 62
QY 211 FSGFKSGTASLIVISGLQSEADADYCAAMDSLNGVVGSGTXYTL 258
DB 63 FSGFKSGTASLIVISGLQSEADADYCAAMDSLNGVVGSGTXYTL 110
RESULT 3
ID HVZ1_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1998 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).

PIR; A02101; G1H0H2.
DR HSSP: P01825; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 1 146
FT DOMAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;
Query Match 33.0%; Score 452; DB 1; Length 146;
Best Local Similarity 71.5%; Pred. No. 2,6e-25;
Matches 93; Conservative 8; Mismatches 23; Indels 6; Gaps 3;
QY 1 QVQLQESGPGLVKISSETLTCTVSGSGISGHDYMSWIRQPGEGLEWIGFIFPDGSTNYN 60
DB 21 QVQLQESGPGLVKISSETLTCTVSGSGISGHDYMSWIRQPGEGLEWIGFIFPDGSTNYN 80
QY 61 PSINGRVTISLDTKSNQLSLRTSTADTAADTVYFCAR--LKQAWLSEPPYFSSDGDVW 118
DB 81 TSLSKRVITISLDTSKNLFSLKSSVTAADTAADTVYFCARGLRGW--NDVDVYY--QMDVW 136
QY 119 GQGTTTVYS 128
DB 137 GQGTTTVYS 146
RESULT 4
ID HVZ2_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WHH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=8222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2H0WA.
DR HSSP: P01825; 7PAB.
DR GLYCOSITEDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129 IG-LIKE.

SEQUENCE 129 AA; 14117 MW; D5D53D47ABE5119 CRC64;
Query Match 32.9%; Score 451.5; DB 1; Length 129;
Best Local Similarity 65.9%; Pred. No. 2.4e-25;
Matches 89; Conservative 15; Mismatches 18; Indels 13; Gaps 3;
QY 1 QVLOESGGLVLPKSETSLTCTVSGSGSIGHD--YMSWIRPPGEGLEWIGFIFPGSTN 58
DB 1 RQLOESGGLVLPKSETSLTCTVSGSGPIRRGTYGWRROPGKLEWIGVYTYGSIY 60
QY 59 YNPSLNGRVTISLDTSKQSLRLTSVTADTAVFCAFLKCAWLLSEPPYF-----SSD 113
DB 61 YNPSLRGRVTISVDSIRNQPSLNRSMASADTAMYYCAR-----GNPPPYDIDIGSD 114
QY 114 GMDWVGQGTYYVSS 128
DB 115 GIDWVGQGTYYVSS 129
RESULT 5
ID LVIF_HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region MAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=83221661; PubMed=6407018;
RA Takehashi Y., Takehashi N., Terae T., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain."
RU Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690 (1983).
DR PIR; A01967; LIHWA.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003596; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IgV.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;
Query Match 32.6%; Score 447; DB 1; Length 109;
Best Local Similarity 81.5%; Pred. No. 4.2e-25;
Matches 88; Conservative 7; Mismatches 11; Indels 2; Gaps 1;
QY 151 MLTOPPSASGTPGORVYSICSGSSSDIGSNTVMYQQLPGTAPKLIYNNRPPSGVPR 210
DB 3 VLTQPPSASGTPGORVYTISCFSSSSNIGIYYWYQQLPGTAPKLIYNNRPPSGVPR 62
QY 211 FSGFKSGTSASLVISGLQSEADADYCAAMDSLNGVFGGKTATVL 258
DB 63 FSGFKSGTSASLVISGLQSEADADYCAAMDSL--WVFGGKTATVL 108
RESULT 6
ID LVIG_HUMAN STANDARD; PRT; 130 AA.
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85062823; PubMed=6095199;
RA Teuimeto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
sequence."
RU Nucleic Acids Res. 12:8407-8414 (1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; X01147; CAA25598.1; -.
DR PIR; A01966; LIHBL.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG-like.
DR Pfam; PF00047; IgV.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON TER 130 130
SQ SEQUENCE 130 AA; 13564 MW; FA44B817D3A55EBF CRC64;
Query Match 32.2%; Score 441; DB 1; Length 130;
Best Local Similarity 71.1%; Pred. No. 1.3e-24;
Matches 81; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
QY 145 GGSNFMLTOPPSASGTPGORVYSICSGSSSDIGSNTVMYQQLPGTAPKLIYNNRPP 204
DB 16 GSMASVLTQPPSVSAARQKVTISCSGSSSSNIGNDYVSWYQVGTAPKLIYNNRPP 75
QY 205 SGVPRFSGFKSGTSASLVISGLQSEADADYCAAMDSLNGVFGGKTATVL 258
DB 76 SGVPRFSGFKSGTSATLTGTLQGTDEADYCGTWNNSLSGWFVFGGKTATVL 129
RESULT 7
ID LVLD_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shintzu A.;

RT "Comparative studies on the structure of the light chains of human
 immunoglobulins. IV. Assignment of a subgroup.",
 RL J. Biochem. 93:421-429(1983).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A01965; LIHUNG.
 DR HSSP: P01703; 7FAB.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Pyroliidone carboxylic acid.
 KM Immunoglobulin V region; Bence-Jones protein;
 PYROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 105
 FT MOD RES 22 89
 FT NON TER 111 111
 FT BY SIMILARITY.
 SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;
 Query Match 31.8%; Score 436; DB 1; Length 111;
 Best Local Similarity 75.0%; Pred. No. 2.5e-24;
 Matches 81; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
 OY 151 MLTOPPSASGTPGQGVISICSGSSSDIGSNTVMYQQLPGTAPKLLIYNNQPSGVPDR 210
 DB 3 VLTQPPSVSAPGQAVTISCGSSNGTNNVYVYQQLPGTAPKLLIYNNQPSGVPDR 62
 OY 211 FSGFGSGTSASLVISGLSEDEADYYCAAMDESINGVFGGKTAVTL 258
 DB 63 FSGSGSGTSATLTGTGTGTGDEADYYCGTWDSLSLVGFGGKTAVTL 110
 RESULT 8
 LV1B HUMAN STANDARD; PRT; 112 AA.
 ID LV1B HUMAN
 AC P01700;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-1 region HA.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71103824; PubMed=5532227;
 RA Shindoda T., Titeani K., Putnam F.W.;
 RT "Amino acid sequence of human lambda chains. II. Chymotryptic
 RT peptides and sequence of protein Ha.",
 RL J. Biol. Chem. 245:4475-4487(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A01963; LIHUNG.
 DR HSSP: P01703; 7FAB.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein;
 PYROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 106
 FT MOD RES 22 90
 FT NON TER 112 112
 FT BY SIMILARITY.
 SQ SEQUENCE 112 AA; 11896 MW; 8D73378F3F5CD039 CRC64;

Query Match 31.6%; Score 433.5; DB 1; Length 112;
 Best Local Similarity 77.1%; Pred. No. 3.8e-24;
 Matches 84; Conservative 12; Mismatches 12; Indels 1; Gaps 1;
 OY 151 MLTOPPSASGTPGQGVISICSGSSSDIGSNTVMYQQLPGTAPKLLIYNNQPSGVPDR 209
 DB 3 VLTQPPSVSAPGQAVTISCGSSNGTNNVYVYQQLPGTAPKLLIYNNQPSGVPDR 62
 OY 210 FSGFGSGTSASLVISGLSEDEADYYCAAMDESINGVFGGKTAVTL 258
 DB 63 FSGSGSGTSATLTGTGTGTGDEADYYCAAMDESINGVFGGKTAVTL 111
 RESULT 9
 LV1C HUMAN STANDARD; PRT; 111 AA.
 ID LV1C HUMAN
 AC P01701;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-1 region NEW.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69060892; PubMed=4177823;
 RA Langer B., Steinmetz-Kayne M., Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein New (lambda-
 RT type). Subgroups in the variable part of immunoglobulin L-chains of
 RT the lambda-type.",
 RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A01964; LIHUNG.
 DR HSSP: P01703; 7FAB.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein;
 PYROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 105
 FT MOD RES 22 89
 FT NON TER 111 111
 FT BY SIMILARITY.
 SQ SEQUENCE 111 AA; 11453 MW; AABCBCA3C49F2AD3 CRC64;
 Query Match 31.1%; Score 426; DB 1; Length 111;
 Best Local Similarity 72.2%; Pred. No. 1.3e-23;
 Matches 78; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
 OY 151 MLTOPPSASGTPGQGVISICSGSSSDIGSNTVMYQQLPGTAPKLLIYNNQPSGVPDR 210
 DB 3 VLTQPPSVSAPGQAVTISCGSSNGTNNVYVYQQLPGTAPKLLIYNNQPSGVPDR 62
 OY 211 FSGFGSGTSASLVISGLSEDEADYYCAAMDESINGVFGGKTAVTL 258
 DB 63 ISASGSGTSATLTGTGTGTGDEADYYCAAMDESINGVFGGKTAVTL 110
 RESULT 10
 LV1I HUMAN STANDARD; PRT; 109 AA.
 ID LV1I HUMAN
 AC P06888;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB Ig lambda chain V-I region EPS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_Taxid=9606;
 RX MEDLINE=86000126; PubMed=3929803;
 RA Toff K.G., Sletten K., Husby G.;
 RT "The amino-acid sequence of the variable region of a carbohydrate-
 containing amyloid fibril protein EPS (immunoglobulin light chain,
 type lambda)." ;
 RL Biochem. Hoppe-Seyler 366:617-625(1985).
 CC -1- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
 PEPTIDES WERE POSITIONED BY HOMOLOGY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A24656; L1HUBP.
 DR HSSP; P01703; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0005955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Amyloid; Glycoprotein.
 FT DOMAIN 1 105 IG-LIKE.
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .).
 FT DISULFID 22 89 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;
 Query Match 30.1%; Score 413; DB 1; Length 109;
 Best Local Similarity 73.1%; Pred. No. 1e-22;
 Matches 79; Conservative 12; Mismatches 15; Indels 2; Gaps 1;
 QY 151 MLOTPSASGTCGCVSTSCSSGSSDICTNTMYQOGLPTAKLIYSNNRPGVPR 210
 DB 3 VLTQPPSIAAPGQRVSTSCSSSSNIGKVVWYQQLGTAPKLIFFNNRPSGIPDR 62
 QY 211 FSGFSGTSASIVIGLQSEDEADYCYCAMDESLNGVFGGKTATVL 258
 DB 63 FEGSGSGHSATIGITGLGTDEAIYICGWMNR--VFGGNTATV 108
 RESULT 11
 HV2G_HUMAN STANDARD; PRT; 117 AA.
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region NEMM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_Taxid=9606;
 RX MEDLINE=7742302; PubMed=407927;
 RA Poljak R.U., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the VH region of a human myeloma
 immunoglobulin (IgG New)." ;
 RL Biochemistry 16:3412-3420(1977).
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE=7806916; PubMed=618887;
 RA Saul F.A., Amzel L.M., Poljak R.U.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 from human immunoglobulin new at 2.0-A resolution." ;
 RL J. Biol. Chem. 253:585-597(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA

CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A30404; G1HNM.
 DR PDB; 7FAB; 31-JAN-94.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0005955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 111 IG-LIKE.
 FT MOD RES 1 111 PYRROLIDONE CARBOXYLIC ACID.
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59
 FT TURN 61 63
 FT HELIX 64 66
 FT TURN 67 72
 FT TURN 73 76
 FT STRAND 77 82
 FT HELIX 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
 Query Match 29.8%; Score 408.5; DB 1; Length 117;
 Best Local Similarity 59.2%; Pred. No. 2.2e-22;
 Matches 77; Conservative 22; Mismatches 16; Indels 15; Gaps 2;
 QY 1 QVQLQESGPGLVKPSSETLTCTVSGSGISGHDYMSWIRPQSGLEWIGFIPFGSTVYN 60
 DB 1 QVQLQESGPGLVKPSSETLTCTVSGSGSTFNSDYTWVQPPRGLWIGYVYHGTSDT 60
 QY 61 PSLNGRVTSIDTSSKNQSLRTSVTAADTAVYFCAR--LKGAWLLSEPPYFSSDGMVY 118
 DB 61 TPLRSRYTMLVDTSKNQPSLRISVTAADTAVYFCARLLIAGC-----IDW 107
 QY 119 GQGITVYVSS 128
 DB 108 GQGSIVTVSS 117
 RESULT 12
 LV2G_HUMAN STANDARD; PRT; 111 AA.
 AC P01710;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-II region BO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_Taxid=9606;
 RX MEDLINE=71103825; PubMed=5532228;
 RA Wikler M., Putnam F.W.;
 RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
 RT chymotryptic peptides, and sequence of protein Bo." ;
 RL J. Biol. Chem. 245:4488-4507(1970).

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CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01976; L2HUBO.
DR HSBP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KM Pyridoxaldehyde carboxylic acid.
FT DOMAIN 1 106
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 27.9%; Score 382; DB 1; Length 111;
Best Local Similarity 67.6%; Pred. No. 1.5e-20;
Matches 73; Conservative 19; Mismatches 14; Indels 2; Gaps 2;

QY 152 LTQPPSAGTGPQGRVSISSGSSSDIGSNT-VNMYQQLPGTAPKLLIYSNNORPSGVDR 210
DB 4 LTQPPSAGSPEQSVTISCTGTSDDVGNKYVSWYQOHFGAPKLVIFEVSGRPSGVDR 63
QY 211 FSGFGSGTASLVISGLQSEDEADYCCAMDESLNGVFGGRTVTVL 258
DB 64 FSGSKSDNTASLTVSGLRARDEADYCCSYSDN-NNFVFGGRTVTVL 110

RESULT 13
LV2F_HUMAN STANDARD; PRT; 111 AA.
AC P01709;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Ig lambda chain V-II region MGC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75013804; Pubmed=4415202;
RA Felt J.W.; Deutsch H.F.;
RT "Primary structure of the Mcg lambda chain.";
RL Biochemistry 13:4102-4114(1974).
RN [2]
RP LAMBDA CHAIN GENES.
RX MEDLINE=76093781; Pubmed=812801;
RA Felt J.W.; Deutsch H.F.;
RT "A new lambda-chain gene.";
RL Immunochimistry 12:643-652(1975).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Edmundson A.B.; Ely K.R.; Abola E.E.; Schiffer M.;
RX Panagiotopoulos N.;
RT "Rotational allomerism and divergent evolution of domains in
RL immunoglobulin light chain.";
RN Biochemistry 14:3953-3961(1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=90133913; Pubmed=2515285;
RA Ely K.R.; Herron J.N.; Harker M.; Edmundson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
RT water. Conformational flexibility of a molecule in two crystal
RT forms.";
RN J. Mol. Biol. 210:601-615(1988).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY.
CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KENN+ AND MCG+
CC MARKERS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90381; L2HUMC.
DR PDB; 2MCG; 15-JUL-92.
DR PDB; 1ABJ; 17-JUN-98.
DR PDB; 1DCU; 15-MAY-97.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure;
KM Pyridoxaldehyde carboxylic acid.
FT DOMAIN 1 108
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT STRAND 5 5
FT STRAND 10 12
FT STRAND 18 23
FT TURN 26 32
FT STRAND 36 40
FT TURN 42 43
FT STRAND 45 50
FT TURN 52 54
FT STRAND 55 55
FT TURN 58 62
FT STRAND 62 63
FT STRAND 66 68
FT STRAND 72 77
FT HELIX 82 84
FT STRAND 86 93
FT STRAND 99 101
FT STRAND 105 109
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11558 MW; 7CC1D6B2FA3377BA CRC64;

Query Match 27.1%; Score 372; DB 1; Length 111;
Best Local Similarity 68.5%; Pred. No. 7.7e-20;
Matches 74; Conservative 16; Mismatches 16; Indels 2; Gaps 2;

QY 152 LTQPPSAGTGPQGRVSISSGSSSDIGS-NTVNYQQLPGTAPKLLIYSNNORPSGVDR 210
DB 4 LTQPPSAGSLDQSVTISCTGTSDDVGNKYVSWYQOHAGKAPKLVIFEVNKRPSGVDR 63
QY 211 FSGFGSGTASLVISGLQSEDEADYCCAMDESLNGVFGGRTVTVL 258
DB 64 FSGSKSDNTASLTVSGLRARDEADYCCSYSDN-FVFGGRTVTVL 110

RESULT 14
HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; Pubmed=2497341;
RA Rinfret A.; Horne C.; Dorrington K.J.; Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment.";
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Db 40 QVQLQSGGGLVKGPGSLIKLSCAASGDSFRYWMWVRQAPGKGLIEWIGINPDSSITNY 99
 QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKGMILSEPPFSSDGMVWG 119
 Db 100 TPLSKDKFTISRDAKNTLYLQMSKVSEDPALYYCARA-----YGHSA--YWG 148
 QY 120 QGTTVTVSSGGGGSGGGSGGGSGGGSGNFMLTQ-PPSASGTPGQVSISSGSSSDIG 178
 Db 149 QGTTVTVS-----SGGGSGGGSGGGSGGGSDIELQSPASLSASVGETVITTCASAGNI-- 201
 QY 179 SNTVNWYQOLPGTAPKLLIYSNNORPSGVDPDRSGFGSGTSASLIVISGLQSEDBADYYCA 238
 Db 202 HNYYIAWYQKQKSPQLLYNNAKTLDADGVPFRSGSGSTQYSLKINSIQPEDFGSYCQ 261
 QY 239 -AMDESINGVFGGGTKVTV 257
 Db 262 HFW---TTPYTFGGGTLEI 278

RESULT 2

ID Q7TOM2 PRELIMINARY; PRT; 243 AA.
 AC Q7TOM2;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE SCFV 6H8 protein (Fragment).
 GN SCFV 6H8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/C;
 RA Peter J.C., Eftekhari P., Billalid P., Wallukat G.;
 RT "scfv single chain antibody variable fragment as inverse agonist for
 the beta-2 adrenergic receptor."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A0574851; CAB00495.1; -
 FT NON_TER 1
 SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;

Query Match 38.8%; Score 531.5; DB 11; Length 243;
 Best Local Similarity 45.0%; Pred. No. 8e-34;
 Matches 117; Conservative 40; Mismatches 76; Indels 27; Gaps 8;

QY 1 QVQLQSGGGLVKGPGSLIKLSCAASGDSFRYWMWVRQAPGKGLIEWIGINPDSSITNY 59
 Db 1 QVQLQSGGGLVKGPGSLIKLSCAASGDSFRYWMWVRQAPGKGLIEWIGINPDSSITNY 60
 QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKGMILSEPPFSSDGMVWG 119
 Db 61 DEKFKKKGILTVDTSSSTAYMHLISLASBDAVYYCAR-----GGRGLDVGW 107
 QY 120 QGTTVTVSSGGGGSGGGSGGGSGGGSGNFMLTQPPSA-SGTGQKRVISICSGSSSDIG 178
 Db 108 AGTTLTVS-----SGGGSGGGSGGGSGGGSDIPTQSSSFVSLDRLVITTC-ASEBI- 160
 QY 179 SNTVNWYQOLPGTAPKLLIYSNNORPSGVDPDRSGFGSGTSASLIVISGLQSEDBADYYCA 238
 Db 161 YNRILAWYQKQKSPQLLYNNAKTLDADGVPFRSGSGSTQYSLKINSIQPEDFGSYCQ 261
 QY 239 A-WDESINGVFGGGTKVTV 257
 Db 221 QYWSTR---TFGGGTLEI 236

RESULT 3

ID Q921A6 PRELIMINARY; PRT; 241 AA.
 AC Q921A6;
 DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Anti-CEA 79 single chain Fv fragment (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98170165; PubMed=9509426;
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
 RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
 RT "Cloning and characterization of cDNAs encoding VH and VL of a
 RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
 generation of a single-chain Fv molecule (SCFV).";
 RL Mol. Cells 7:816-819(1997).
 DR EMBL; U68067; AAB48044.1; -
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00406; IGv_2.
 DR PROSITE; PS00835; IG_LIKE, 2.
 FT NON_TER 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C71 CRC64;

Query Match 37.1%; Score 508.5; DB 11; Length 241;
 Best Local Similarity 46.0%; Pred. No. 5e-32;
 Matches 120; Conservative 34; Mismatches 76; Indels 31; Gaps 11;

QY 1 QVQLQSGGGLVKGPGSLIKLSCAASGDSFRYWMWVRQAPGKGLIEWIGINPDSSITNY 59
 Db 1 QVQLQSGGGLVKGPGSLIKLSCAASGDSFRYWMWVRQAPGKGLIEWIGINPDSSITNY 60
 QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAAYFCARLKGMILSEPPFSSDGMVWG 119
 Db 61 ADDEKGFAPSLIETSSASTAYLQINNKNEDATATFCARKD---LLR---YE-----DYG 109
 QY 120 QGTTVTVSSGGGGSGGGSGGGSGGGSGNFMLTQPPSA-SGTGQKRVISICSGSSSDIG 178
 Db 110 QGTTVTVS-----SGGGSGGGSGGGSGGGSDIELQSPASLSASLGKVTITTC-AQDI- 162
 QY 179 SNTVNWYQOLPGTAPK-----LLIYSNNORPSGVDPDRSGFGSGTSASLIVISGLQSEDBAD 234
 Db 163 NKYIAWYQKQKSPQLLYNNAKTLDADGVPFRSGSGSTQYSLKINSIQPEDFGSYCQ 261
 QY 235 YYCAAMDESINGVFGGGTKV 255
 Db 219 YYCLHYD---NLATFGGTLEI 236

RESULT 4

ID Q96EYO PRELIMINARY; PRT; 613 AA.
 AC Q96EYO;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AA011857.1; -
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003065; IG_MHC.
 DR InterPro; IPR003596; IG_v.

DR pfam; PF00047; ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_5.
DR SMART; SM0046; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW

Query Match	34.6%;	Score 474.5;	DB 4;	Length 597;
Best Local Similarity	47.1%;	Pred. No. 6.6e-29;		
Matches 113;	Conservative 19;	Mismatches 69;	Indels 39;	Gaps 5

QY 1 QVQLSSGPELVKPSERTSLTCTVSGSGTGHYMWNIQPPQEGLEMTGTFIPDGSNTYN 60
Db 20 QVQLQMGAGLAKPSERTSLTCTGVYGGSSGYWMNIQPPQEGLEMTGFINHSGSNTYN 79
QY 61 PSLINGVITSLDTSKNQSLRLTVTAADTAVYFCARLEKAGMLLSEPPYFSSDGMVWGQ 120
Db 80 PSLKSRVITSLVDTSKQSLKSLSTVNAADTAIYYCARV---ITRASPTDGRYAMDWGQ 136
QY 121 GTTAVTVSSGGGSGGGGSGGGSGGGGGSFNLTOPSLASGTPGRVSIISCGSSSDISGN 180
Db 137 GTTAVTVSSG-----SASAPTLFPIVSCENSPSDTSV 168
QY 181 TNNMTQQ--LPSTAPKLILYNNRPS---GVDRFSFGKGTASLIVSG---LQSEDE 232
Db 169 AVGCLADQLPDSITFSWYKNNNDISSTRFPSVLRGKGKAAITSQVLLPSKDWQGTDE 228

RESULT 8

ID	Q96AA6	PRELIMINARY:	PRT:	618 AA.
AC	Q96AA6;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
IDE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
NCBI	NCBI_TaxId=9606;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RA	TISUS=LympH;			
RRL	Strausberg R.;			
EMBL	Submitted (NCV-2001) to the EMBL/GenBank/DBD databases.			
PIR	EMBL; BC017356; AAH7356.1; -			
PIR	PIR, S15590; S15590			
InterPro	InterPro: IPR007110, IG-like.			
InterPro	InterPro: IPR003006, IG_MHC.			
InterPro	InterPro: IPR003596, IG_v.			
Pfam	Pfam: PF00047, IG, 5.			
SMART	SMART; SM00406, IGV, 1.			
PROSITE	PROSITE; PS50835, IG_LIKE, 5.			
PROSITE	PROSITE; PS00290, IG_MHC, 3.			
TM	Hypothetical protein.			
SEQUENCE	618 AA, 67758 MW, 96D6D4C7C696E0A6 CRC64;			

Query Match	34.6%	Score 474.5;	DB 4;	Length 618;
Best Local Similarity	47.1%	Pred. No. 6,9e-29;		
Matches 113; Conservative	19;	Mismatches 69;	Indels 39;	Covs 5

[illegible]

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Db      137 GTTATVSSG-----SASAPTLFPIVSCENSPDTSV 168
Qy      181 TNAWYQQ--LPGPAPKLLYSNNQRP---GYDPAFSGFSKGTASLVISG---LQGEDE 232
Db      169 AVGCLAQDFLPDISITFSWKYKNNSDISSTRGPPSVLRGKXAALASQVLLPSKVMQGTDE 228

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RESULT AND

ID	GENE/JI	PRELIMINARY	PRT	236 AA.
AD	GNBEJ1			
DT	01-OCT-2002 (TREMBL)	22, Created		
DT	01-OCT-2002 (TREMBL)	22, Last sequence update)		
DT	01-OCT-2003 (TREMBL)	25, Last annotation update)		
DR	Hypochemical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	Strausberg R;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL, BC030984; AAH30984.1; -.			
DR	InterPro; IPR003599; IG_1.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003597; IG_c1.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG_2.			
DR	SMART; SM00409; IG_2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; 1.			
DR	Hypothetical protein			
SW	SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;			

Query Match	34.5%	Score 472.5;	DB 4;	Length 236;
Best Local Similarity	80.0%;	Pred. No. 3.2e-29;		
Matches 92;	Conservative 11;	Mismatches 11;	Indels 1;	Gaps 1

[illegible]

RESULT 10

ID Q9BQ8 PRELIMINARY; PRT; 597 AA.
 AC Q9BQ8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DS Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eularchia; Primates; Catarrhini; Homnidae; Homo.
 NC [1]
 NC TextID=9606;
 PP
 PP SEQUENCE FROM N.A.
 CC TISSUE=Muscle, and Lymph;
 CC Straussberg R.;
 LA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 LR EMBL; BC006180; AAH06180.1; -
 LR EMBL; BC001872; AAH01872.1; -
 LR HSSP; P01825; 7FEA.
 LR InterPro; IPR007110; Ig-1like.

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
DR Hypothetical protein.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 34.2%; Score 468.5; DB 4; Length 597;
Best Local Similarity 46.7%; Pred. No. 1.9e-28;
Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRPPGEGLEWIGIFPDGSTNN 60
DB 20 QVQLQEQMGAGLKPSETLSLTCTGVGSGFSGYWMIROPPKGLHWIGIINHSGITNN 79
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYSSDGMVWQ 120
DB 80 PSLKSRVTISVDTSKQSLSLKSSVNAADTAVYCARV---ITRASPGTDGRYGMVWQ 136
QY 121 GTTVTVSSGGGGSGGGSGGGSGGNFMLTPPSASGTPGQRVISICSGSSDIGN 180
DB 137 GTTVTVSSG-----SASAPTLPLPVGCENSPSDTSV 168
QY 181 TVNWYQO--LPGTAPKLLIYSNNQRP---GVDPFRSGKSGTSASIVISG---LQSEDE 232
DB 169 AVGCLAQPLPDSITFSWKYKNNSDISSTRGFPVLRGGKATVATQVLLPSKDVWQGTDE 228

RESULT 11

ID 0925S1 PRELIMINARY; PRT; 218 AA.
AC 0925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RA "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice";
RN World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain";
RN Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR NON TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 33.6%; Score 460; DB 11; Length 218;
Best Local Similarity 45.2%; Pred. No. 2.7e-28;
Matches 103; Conservative 33; Mismatches 72; Indels 20; Gaps 5;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRPPGEGLEWIGIFPDGSTNN 59

DB 3 QVQLQESGPGLVKPSETLRISCKASGYFTTQAGMGMVQMPKGLKGIWINTHSGVPKY 62
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYSSDGMVWQ 119
DB 63 AEEFKRPAFSLSTASAYVLIQISNLKNEIDATYVCMR-----WDYDGFPAWG 111
QY 120 QGTVTVSSGGGGSGGGSGGGSGGNFMLTPPSASGTPGQRVISICSGSS--D 176
DB 112 QGTVTVS-----SGGGSGGGSGGSDIVLTQSPASLAVSLQQRATISCRABESVDN 166
QY 177 IGSNTVNWYQO-LPGTAPKLLIYSNNQRPSPGVDPFRSGKSGTSASLVI 224
DB 167 IGISPMNMFQKRGQGPPLLIYAASKQSGVPAGLLAGSGGTDFSLNI 214

RESULT 12

ID 072379 PRELIMINARY; PRT; 478 AA.
AC 072379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZP686K04218 (Fragment).
GN DKFZP686K04218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Kewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 33.5%; Score 459; DB 4; Length 478;
Best Local Similarity 45.0%; Pred. No. 8.3e-28;
Matches 113; Conservative 18; Mismatches 60; Indels 60; Gaps 8;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRPPGEGLEWIGIFPDGSTN 58
DB 19 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQHDYMSWIRPPGEGLEWIGIYVSGSY 78
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYSSDGMVW 118
DB 79 YNPSLSESLISLDTSKNQLSLRLTSLTAADTAVYFCARVGL-----GTAFDIW 128
QY 119 QGTVTVTVSSGGGGSGGGSGGGSGGNFMLTPPSASGTPGQ-RVYSISC----- 170
DB 129 QGTVTVTVSSASPS-----PKVPLSLDSTPDGDANVAVACLVQGFPP 171
QY 171 ----SGSSSDIGSNTVNWYQO-LPGTAPKLLIYSNNQRPSPGVDPFRSGKSGTSASLVI 226
DB 172 QEPISLVTSSESGQN-----VTARPPPS---QDASGDIYTTSSQTLTIPA 212
QY 227 LQSEADADYVC 237
DB 213 TQCPDGKSVTC 223

RESULT 13

ID 096S80 PRELIMINARY; PRT; 108 AA.
AC 096S80;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-mysin immunoglobulin lambda light chain

DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AAB68783.1; -.
DR PDB; 1KU4; 29-MAY-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 32.5%; Score 445; DB 4; Length 108;
Best Local Similarity 84.8%; Pred. No. 1.8e-27;
Matches 84; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 151 MLTPPSASGTGPGQVRSISCGSSSDIGSNVTVMYQQLPQTAPKLLIYSNNRPSGVPR 210
DB 3 VLTQPPSASGTGPGQVRSISCGSSSDIGSNVTVMYQQLPQTAPKLLIYSNNRPSGVPR 62

QY 211 FSGFSGTSASLVISGLQSEDEADYCAAMDESLNGVVF 249
DB 63 FSGSFGTSASLVISGLQSEDEADYCAAMDESLNGVVF 101

RESULT 14
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CSDDL004YMI9 of B cells (Ramos cell line)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE=B-cell;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization."
RL EMBL; BX248300; CAD62627.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 32.3%; Score 443; DB 4; Length 139;
Best Local Similarity 84.5%; Pred. No. 3.4e-27;
Matches 82; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 QYLOESGPGVYKPEETSLTCTVSGSGTGHYMSWIRQPEEGLEWIGFIFPDSTYNN 60
DB 33 QYLOESGPGVYKPEETSLTCTVSGSGTGHYMSWIRQPEEGLEWIGFIFPDSTYNN 92

QY 61 PSLNGRVITSLDTSKNQSLRLTSTYADTAAYFCAR 97
DB 93 PSLKRVITSLDTSKNQSLRLTSTYADTAAYFCAR 129

RESULT 15
Q8WUK4 PRELIMINARY; PRT; 237 AA.
ID Q8WUK4
AC Q8WUK4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020233; AAH20233.1; -.
DR PIR; S12441; S12441.
DR PIR; S12627; S12627.
DR PIR; S29258; S29258.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IGV_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 32.1%; Score 440; DB 4; Length 237;
Best Local Similarity 74.1%; Pred. No. 1.1e-26;
Matches 86; Conservative 14; Mismatches 14; Indels 2; Gaps 2;

QY 145 GGSNFMLTQPPSASGTGPGQVRSISCGSSSDIGSN-TVMYQQLPQTAPKLLIYSNNR 203
DB 16 GSWAQSGLTQPPSASGTGPGQVRSISCGSSSDIGSN-TVMYQQLPQTAPKLLIYSNNR 75

QY 204 PSGVPRDFSGFSGTSASLVISGLQSEDEADYCAAMDESLNG-VVFGGSTRVTVL 258
DB 76 PSGVPRDFSGFSGTSASLVISGLQSEDEADYCAAMDESLNG-VVFGGSTRVTVL 131

Search completed: May 13, 2004, 15:06:59
Job time : 34.6922 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 51.4563 Seconds
(without alignments)
1372.754 Million cell updates/sec

Title: US-10-072-301-29

Perfect score: 1336

Sequence: 1 QVQLQDQMGAGLLKSWGTSL.....CLQHNDPFLTGGTKVEIK 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838	63.7	249	5	ABP45310 Human Bly
2	820.5	63.4	249	5	AAU75150 Amino aci
3	774.5	58.0	256	3	AAV55072 Interleuk
4	774.5	58.0	260	3	AAV55075 Single ch
5	774.5	58.0	367	3	AAV55078 Single ch
6	774.5	58.0	381	3	AAV55079 Single ch
7	774.5	58.0	519	3	AAV55080 Single ch
8	774.5	58.0	546	3	AAV55074 Single ch
9	774.5	58.0	626	3	AAV55081 Single ch
10	774.5	58.0	640	3	AAV55082 Single ch
11	760	56.9	251	5	ABP45038 Human Bly
12	741.5	55.5	248	5	ABP45349 Human Bly
13	741.5	55.5	252	5	ABP45315 Human Bly
14	739.5	55.4	250	5	ABP45402 Human Bly
15	736	55.1	255	5	ABP45631 Human Bly
16	734.5	55.0	250	5	ABP45634 Human Bly
17	734.5	55.0	253	5	AAU72867 PS-9 sing
18	731	54.7	253	5	ABP45332 Human Bly
19	730.5	54.7	254	5	ABP45648 Human Bly
20	729.5	54.6	244	4	AAV21883 Amino aci
21	719	53.8	241	4	AAV46061 Human TF
22	719	53.8	909	2	AAV50092 Humanised
23	717.5	53.7	240	4	AAV46020 Human MOC
24	716	53.6	253	5	ABP44943 Human Bly
25	715.5	53.6	241	7	ADc64791 Hu-B-A5 C

26	714.5	53.5	241	7	ADc64785 Hu-E4-1 C
27	713	53.4	249	5	ABP44946 Human Bly
28	711.5	53.3	240	4	ABP45992 Human MOC
29	710	53.1	255	5	ABP45586 Human Bly
30	709.5	53.1	242	3	AAV58236 Interleuk
31	705	52.8	253	5	ABP45591 Human Bly
32	703.5	52.7	240	4	AAV46039 Human TF
33	702.5	52.6	240	4	AAV46021 Human MOC
34	702	52.5	239	5	ABP45871 Human Bly
35	702	52.5	245	5	AAV06714 Antibody
36	701	52.5	237	5	ABP45895 Human Bly
37	699.5	52.4	251	4	AAV46018 Human MOC
38	699.5	52.4	240	5	AAU72868 PS-10 sin
39	699	52.3	239	5	ABP45911 Human Bly
40	698.5	52.3	241	7	ADc64788 Hu-A-B5 C
41	698	52.2	255	5	ABP45615 Human Bly
42	697.5	52.2	240	4	AAV45993 Human MOC
43	697.5	52.2	240	4	AAV45991 Human MOC
44	696.5	52.1	241	7	ADc64787 Hu-A-D2 C
45	696	52.1	255	5	ABP45592 Human Bly

ALIGNMENTS

RESULT 1
ID ABP45310 standard; protein; 249 AA.
XX
AC ABP45310;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1321.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; Rheumatoid arthritis; COVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
PS Claim 1, Page 1979-1980; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antineumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

Sequence 249 AA;

Query Match 62.7%; Score 838; DB 5; Length 249;
 Best Local Similarity 63.8%; Pred. No. 7,6e-45;
 Matches 166; Conservative 27; Mismatches 45; Indels 22; Gaps 3;

QY 1 QVQLQQWAGLILKSGTSLTCAVSGASFGSYWMIROPKGLKLEWIGENIRGSTYN 60
 Db 1 QVQLQQWAGLILKSGTSLTCAVSGASFGSYWMIROPKGLKLEWIGENIRGSTYN 60
 QY 61 PSIDGRVTISLDTSTNOISLKTSMTPADTAVYYCAR-----TVAGTS----DYWGQGT 110
 Db 61 PSIDGRVTISLDTSTNOISLKTSMTPADTAVYYCAR-----TVAGTS----DYWGQGT 110
 QY 111 LVTWSSGSASAPITGGGSGGSGGSGGSETTLTQSPAFMSATPDGKVISICKASR 170
 Db 121 LVTWSSGSASAPITGGGSGGSGGSGGSETTLTQSPAFMSATPDGKVISICKASR 170
 QY 171 DVDDVVMYQORPEAPFIETEDATTLVPGISPRFSGSGYGTDFTLTINNISEDAAYF 230
 Db 169 GISSWLMYQORPEAPFIETEDATTLVPGISPRFSGSGYGTDFTLTINNISEDAAYF 230
 QY 231 CLQHDNPLTFGGGTVEIK 250
 Db 229 CQGSSTPMTFGQGTLEIK 248

RESULT 2

AAU75150 standard; protein; 249 AA.

AC AAU75150;
 DT 23-APR-2002 (first entry)

DE Amino acid sequence of human anti-IL8 scFv clone 123-57.

KW Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;
 KW variable light-chain; VL; anti-IL8; interleukin-8; scFv clone.

OS Homo sapiens.
 OS Synthetic.

PN WO200200729-A2.

PD 03-JAN-2002.

PF 25-JUN-2001; 2001WO-US020542.

PR 23-JUN-2000; 2000US-00602373.

PR 23-JUN-2000; 2000US-00602972.

PR 23-JUN-2000; 2000US-00603658.

PR 23-JUN-2000; 2000US-00603663.

PA (GENE-) GENETASTIX CORP.

PI Zhu L, Hua SB;

DR WPI; 2002-090521/12.

DR N-PSDB; ABK32984.

XX Screening libraries of tester proteins against protein, peptide or
 PT nucleic acid target(s) using a two-hybrid method in yeast, useful for
 PT generating recombinant human antibodies and screening for their affinity
 PT binding with target antigens.

PS Example 8; Fig 16; 251pp; English.

XX The present invention relates to compositions and methods for high
 CC throughput generation and screening of a human antibody or immunoglobulin
 CC (Ig) library in yeast. The method comprises expressing a library of
 CC tester fusion proteins in yeast cells, each tester fusion protein of
 CC comprising either an activation domain or a DNA binding domain of a
 CC transcription activator and a tester protein having a large diversity
 CC subunit (e.g. human variable heavy-chain, VH) whose sequence varies
 CC within the library. The tester protein comprises a first polypeptide
 CC light-chain, VL) whose sequence varies within the library independently
 CC of the first polypeptide, and a linker peptide which links the first and
 CC second polypeptide subunits. The method is useful for generating
 CC recombinant human antibodies and screening for their affinity binding
 CC with target antigens. The present sequence represents the amino acid
 CC sequence for an anti-IL8 scFv clone as described in the methods of the
 CC present invention

Sequence 249 AA;

Query Match 61.4%; Score 820.5; DB 5; Length 249;
 Best Local Similarity 62.8%; Pred. No. 9,4e-44;
 Matches 157; Conservative 32; Mismatches 60; Indels 1; Gaps 1;

QY 1 QVQLQQWAGLILKSGTSLTCAVSGASFGSYWMIROPKGLKLEWIGENIRGSTYN 60
 Db 1 QVQLQQWAGLILKSGTSLTCAVSGASFGSYWMIROPKGLKLEWIGENIRGSTYN 60
 QY 61 PSIDGRVTISLDTSTNOISLKTSMTPADTAVYYCAR-----TVAGTS----DYWGQGT 110
 Db 61 PSIDGRVTISLDTSTNOISLKTSMTPADTAVYYCAR-----TVAGTS----DYWGQGT 110
 QY 121 LVTWSSGSASAPITGGGSGGSGGSGGSETTLTQSPAFMSATPDGKVISICKASR 170
 Db 120 LVTWSSGSASAPITGGGSGGSGGSGGSETTLTQSPAFMSATPDGKVISICKASR 170
 QY 181 QRPGEAPFIETEDATTLVPGISPRFSGSGYGTDFTLTINNISEDAAYFCLQHDNPLT 240
 Db 180 QRPGEAPFIETEDATTLVPGISPRFSGSGYGTDFTLTINNISEDAAYFCLQHDNPLT 240
 QY 241 FGGGTVEIK 250
 Db 240 FGGGTVEIK 249

RESULT 3

AAV55072 standard; protein; 256 AA.

AC AAV55072;

DT 25-FEB-2000 (first entry)

DE Interleukin-6 specific scFv protein sequence.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secreted functional protein; antigenic protein;
 KW protein isolation; diagnosis; interleukin-6; scFv.

OS Homo sapiens.

OS Synthetic.

PN WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.
 XX
 XX 20-MAY-1998; 98JP-00138652.
 PR 01-OCT-1998; 98JP-00279876.
 XX
 XX (CHUS) CHUGAI SEIRYAKU KK.
 PI Tsuchiya M, Saito M, Ohtomo T;
 DR WPI; 2000-039382/03.
 DR N-PSDB; AA240291.
 XX
 XX Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.
 XX
 XX Example 1; Page 54-56; 120pp; Japanese.
 XX
 XX This sequence represents a ScFv specific for human interleukin-6. The
 CC invention relates to a method for isolating a gene encoding a membrane-
 CC bound protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein
 XX

SQ Sequence 256 AA;

Query Match 58.0%; Score 774.5; DB 3; Length 256;
 Best Local Similarity 59.7%; Pred. No. 7.1e-41;
 Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQOMGAGLKSNGTSLTCAVSGASF-SGYTSMWIRPQPKGLEWIGELINHGSTTY 59
 DB 1 QVQLQESGPGLVPRPSQTLSTCTVSGYSTITSDHAWSMWVRPGRGLEWIGYISYGITTY 60
 QY 60 NSLQGRVTISLDTSTNOISLKLTSMTADTAIVYVCARTVAGTS--DYWGQGLTVTVSSG 117
 DB 61 NSLSKRVTLMDRTSKNPSTLRSLSSVTADTAIVYCARSLARTAMDYWGQSLTVVS-- 118
 QY 118 SASAPFTGGGSGGSGGSGGSGGSETTLTQSPAFMSATPDGKYSISCKASRDVDDVN 177
 DB 119 -----SGGSGSGGSGGSGGSGSDIQMTQSPSLASVGDRTVITTCRAQDISSYLN 168
 QY 178 WTQQRPGAPFIITIEDATTLVPGISPRSGSGYGTDFLTINNIDSEDAAYFCLQDNF 237
 DB 169 WTQQRPGKAPKLLIYTSRLHSGVSPRFGSGGTDFTTISLQPEDIATAYYCOQGNLT 228
 QY 238 PLTGGGTRKVEIK 250
 DB 229 PTFPGGTRKVEIK 241

RESULT 4

ID AAY55075 standard; protein; 260 AA.

AC AAY55075;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1(deltaatl).

KW Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; ScFv.

XX

OS Synthetic.

PN MO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIRYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AA240305.

PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.

XX Example 7; Page 80-82; 120pp; Japanese.

CC This sequence represents a single chain Fv (ScFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an
 CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein
 XX

SQ Sequence 260 AA;

Query Match 58.0%; Score 774.5; DB 3; Length 260;
 Best Local Similarity 59.7%; Pred. No. 7.2e-41;
 Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQOMGAGLKSNGTSLTCAVSGASF-SGYTSMWIRPQPKGLEWIGELINHGSTTY 59
 DB 20 QVQLQESGPGLVPRPSQTLSTCTVSGYSTITSDHAWSMWVRPGRGLEWIGYISYGITTY 79
 QY 60 NSLQGRVTISLDTSTNOISLKLTSMTADTAIVYVCARTVAGTS--DYWGQGLTVTVSSG 117
 DB 80 NSLSKRVTLMDRTSKNPSTLRSLSSVTADTAIVYCARSLARTAMDYWGQSLTVVS-- 137
 QY 118 SASAPFTGGGSGGSGGSGGSGGSETTLTQSPAFMSATPDGKYSISCKASRDVDDVN 177
 DB 138 -----SGGSGSGGSGGSGGSGSDIQMTQSPSLASVGDRTVITTCRAQDISSYLN 187
 QY 178 WTQQRPGAPFIITIEDATTLVPGISPRSGSGYGTDFLTINNIDSEDAAYFCLQDNF 237
 DB 188 WTQQRPGKAPKLLIYTSRLHSGVSPRFGSGGTDFTTISLQPEDIATAYYCOQGNLT 247
 QY 238 PLTGGGTRKVEIK 250
 DB 248 PTFPGGTRKVEIK 260

RESULT 5

ID AAY55078 standard; protein; 367 AA.

AC AAY55078;

DT 25-FEB-2000 (first entry)

XX

DE Single chain Fv protein sequence shPM1-Kappa.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KM antigen-binding cell; secretable functional protein; antigenic protein;
XX protein isolation; diagnosis; ScFv.

OS Synthetic.

PN MO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AA240308.

XX Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
XX production of drugs treating abnormal functions of the protein.

Example 7; Page 86-89; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the CDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a CDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein

XX Sequence 367 AA;

Query Match 58.0%; Score 774.5; DB 3; Length 367;
Best Local Similarity 59.7%; Pred. No. 1e-40;

Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQOMGAGLTKSWGTLTLTCAVSGASF-SGYVMSWIRPQPKGLEWIGETINHRGTTY 59
DB 20 QVQLQSGGGLVAPSPGTLITCTVSGYSTISHAMSWRQPGRLGIWIGYISYGITTY 79
QY 60 NPSLDGRVTISLDTSTNQISLKLTMATAADTAIVVYCAITVAGTS--DYWGQGLTVTVSSG 117
DB 80 NPSLKSRYTMLDTSKQPSLRSLSVTAADTAIVVYCAISLARTTMDYWGQGLTVTVSSG 137
QY 118 SASAPRTGGSGGGSGGGSGGGSETTLTQSPAFMGATPDGKYSISCKASRDVDDVN 177
DB 138 -----SGGGSGGGSGGGSGGGSDIQMTQSPSLASVGDRTVITICRASQDISSYLN 187
QY 178 WYQORPGEAPFIIEADATLVPGISPRFSGGYGDTFTLTINNIIDSEDAAYFCLQDNF 237
DB 188 WYQOKPKGAPKLLIYTSRLHSGVPSRFSGSGSDIFTTITSSIQPEDIAITYCOQGNLT 247
QY 238 PLTFGGGTKEIK 250
DB 248 PLTFGGGTKEIK 260

RESULT 6
AAVS5079

ID AAVS5079 standard; protein; 381 AA.

XX AAVS5079;

XX 25-FEB-2000 (first entry)

XX Single chain Fv protein sequence shPM1-MCH4.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KM antigen-binding cell; secretable functional protein; antigenic protein;
XX protein isolation; diagnosis; ScFv.

OS Synthetic.

PN MO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AA240309.

XX Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
XX production of drugs treating abnormal functions of the protein.

Example 7; Page 90-94; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the CDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a CDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein

XX Sequence 381 AA;

Query Match 58.0%; Score 774.5; DB 3; Length 381;
Best Local Similarity 59.7%; Pred. No. 1e-40;

Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQOMGAGLTKSWGTLTLTCAVSGASF-SGYVMSWIRPQPKGLEWIGETINHRGTTY 59
DB 20 QVQLQSGGGLVAPSPGTLITCTVSGYSTISHAMSWRQPGRLGIWIGYISYGITTY 79
QY 60 NPSLDGRVTISLDTSTNQISLKLTMATAADTAIVVYCAITVAGTS--DYWGQGLTVTVSSG 117
DB 80 NPSLKSRYTMLDTSKQPSLRSLSVTAADTAIVVYCAISLARTTMDYWGQGLTVTVSSG 137
QY 118 SASAPRTGGSGGGSGGGSGGGSETTLTQSPAFMGATPDGKYSISCKASRDVDDVN 177
DB 138 -----SGGGSGGGSGGGSGGGSDIQMTQSPSLASVGDRTVITICRASQDISSYLN 187
QY 178 WYQORPGEAPFIIEADATLVPGISPRFSGGYGDTFTLTINNIIDSEDAAYFCLQDNF 237
DB 188 WYQOKPKGAPKLLIYTSRLHSGVPSRFSGSGSDIFTTITSSIQPEDIAITYCOQGNLT 247
QY 238 PLTFGGGTKEIK 250

DB 248 PTFEGGKVEIK 260

RESULT 7

ID AAY55080 standard; protein; 519 AA.

XX AAY55080;

XX 25-FEB-2000 (first entry)

XX Single chain Fv protein sequence shPM1(deltaE1)-BVGS3.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 XX antigen-binding cell; secretable functional protein; antigenic protein;
 XX protein isolation; diagnosis; ScFv.

XX Synthetic.

XX WO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Saico M, Ohtomo T;

XX WPI; 2000-039382/03.

XX N-PSDB; AAZ40312.

XX Efficient and selective isolation of a gene encoding membrane protein
 XX with low or no antigenic binding activity, for diagnosis, study of, and
 XX production of drugs treating abnormal functions of the protein.

XX Example 7; Page 95-100; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
 XX relates to a method for isolating a gene encoding a membrane-bound
 XX protein, comprising introducing a vector into a cell, contacting an
 XX antigen with the cell expressing the fused protein encoded by the vector
 XX on its surface to select an antigen-binding cell, and isolating the cDNA.
 XX The vector contains DNA encoding a secretable functional protein with
 XX antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 XX of the 3' end of the coding sequence. The method can be used to isolate a
 XX membrane-bound protein for diagnosis and study. It can also be used for
 XX producing drugs treating abnormal functions of the protein. Such a
 XX technique is efficient and selective, which is different from the prior-
 XX art transmembrane trap (TMT) method wherein an epitope recognised by an
 XX antibody is carried in a fused protein

XX Sequence 519 AA;

XX Query Match 58.0%; Score 774.5; DB 3; Length 519;

XX Best Local Similarity 59.7%; Pred. No. 1.4e-40;

XX Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQDQWAGLLSKGTLSTLCAVSGASP-SGYWYMWIRPPGKLEWIGELINRGSTTY 59

DB 20 QVQLQDQWAGLLSKGTLSTLCAVSGASP-SGYWYMWIRPPGKLEWIGELINRGSTTY 79

QY 60 NPSLDGRITISLDISTNGLSKLTSMATADVAVYVCARVAAGTS--DYMGGQTLVTYSSG 117

DB 80 NPSLDGRITISLDISTNGLSKLTSMATADVAVYVCARVAAGTS--DYMGGQTLVTYSSG 137

QY 118 SASAPRTGGSGGGSGGGSGGGSETLITQSPAFMSATPPDKYSISCKASRDVDDVN 177

DB 138 -----SGGGSGGGSGGGSGGGSDIOMTOSPSLSASVDRITITRABQDISSYLN 187

QY 178 WYQORPGAPIFITIEDATTLVPGISPRPSGGYGTDFLTINNIDSEDAAYVFCLOHNF 237

DB 188 WYQORPGAPILYISRLHSVPSRPSGGSGTDFLTISSLOPEDIATYICQCGNTL 247

QY 238 PTFEGGKVEIK 250

DB 248 PTFEGGKVEIK 260

RESULT 8

ID AAY55074 standard; protein; 546 AA.

XX AAY55074;

XX 25-FEB-2000 (first entry)

XX Single chain Fv protein sequence hPM1-BVGS3.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 XX antigen-binding cell; secretable functional protein; antigenic protein;
 XX protein isolation; diagnosis; ScFv.

XX Synthetic.

XX WO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Saico M, Ohtomo T;

XX WPI; 2000-039382/03.

XX N-PSDB; AAZ40303.

XX Efficient and selective isolation of a gene encoding membrane protein
 XX with low or no antigenic binding activity, for diagnosis, study of, and
 XX production of drugs treating abnormal functions of the protein.

XX Example 5; Page 73-78; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
 XX relates to a method for isolating a gene encoding a membrane-bound
 XX protein, comprising introducing a vector into a cell, contacting an
 XX antigen with the cell expressing the fused protein encoded by the vector
 XX on its surface to select an antigen-binding cell, and isolating the cDNA.
 XX The vector contains DNA encoding a secretable functional protein with
 XX antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 XX of the 3' end of the coding sequence. The method can be used to isolate a
 XX membrane-bound protein for diagnosis and study. It can also be used for
 XX producing drugs treating abnormal functions of the protein. Such a
 XX technique is efficient and selective, which is different from the prior-
 XX art transmembrane trap (TMT) method wherein an epitope recognised by an
 XX antibody is carried in a fused protein

XX Sequence 546 AA;

XX Query Match 58.0%; Score 774.5; DB 3; Length 546;

XX Best Local Similarity 59.7%; Pred. No. 1.5e-40;

XX Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQDQWAGLLSKGTLSTLCAVSGASP-SGYWYMWIRPPGKLEWIGELINRGSTTY 59

DB 20 QVQLQDQWAGLLSKGTLSTLCAVSGASP-SGYWYMWIRPPGKLEWIGELINRGSTTY 79

QY 60 NPSLDGRITISLDISTNGLSKLTSMATADVAVYVCARVAAGTS--DYMGGQTLVTYSSG 117

```

Db      80  NPSLKSRYTLMRDTSKNOFSLRLSSVTAADTAIVVYCARSLARTTAMMYMGQSLVTVS-- 137
QY      118 SASAPVTGGGGGGGGGGGGGGGGGGSETTTQSPAFMSATPGDVKVSIICRARSDDVDVN 177
Db      138 -----SGGGGGGGGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 187
QY      178 WYQQRPGRAPFIITEDATTVPGISPRPSGGSGYGTDFLTITNNIDSEDAAYFCTQHDFN 237
Db      188 WYQQRPGRAPKLLIYYTSRLHSGVPSRPSGGSGTDFLTITSLQPEDIAITYCCQGNL 247
QY      238 PLTGGGGRKVEIK 250
Db      248 PYTFGGGTVEIK 260

RESULT 9
ID      AAY55081
AC      AAY55081;
XX      25-FEB-2000 (first entry)
XX      DE      Single chain Fv protein sequence shPM1-kappa-BVGS3.
XX      KW      Gene isolation; membrane-bound protein; fusion protein; drug production;
XX      KM      antigen-binding cell; secretable functional protein; antigenic protein;
XX      OS      protein isolation; diagnosis; ScFv.
XX      OS      Synthetic.
XX      PN      MO9960113-A1.
XX      PD      25-NOV-1999.
XX      PF      30-APR-1999; 99MO-JP002341.
XX      PR      20-MAY-1998; 98JP-00138652.
XX      PR      01-OCT-1998; 98JP-00279876.
XX      PA      (CHUS ) CHUGAI SEIYAKU KK.
XX      PI      Teuchiya M, Saito M, Ohtomo T;
XX      DR      WPI: 2000-039382/03.
XX      DR      N-PSDB; AAZ40316.
XX      PT      Efficient and selective isolation of a gene encoding membrane protein
XX      PT      with low or no antigenic binding activity, for diagnosis, study of, and
XX      PT      production of drugs treating abnormal functions of the protein.
XX      PS      Example 7; Page 103-109; 120pp; Japanese.
CC      This sequence represents a single chain Fv (ScFv) sequence. The invention
CC      relates to a method for isolating a gene encoding a membrane-bound
CC      protein, comprising introducing a vector into a cell, contacting an
CC      antigen with the cell expressing the fused protein encoded by the vector
CC      on its surface to select an antigen-binding cell, and isolating the cDNA.
CC      The vector contains DNA encoding a secretable functional protein with
CC      antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC      of the 3' end of the coding sequence. The method can be used to isolate a
CC      membrane-bound protein for diagnosis and study. It can also be used for
CC      producing drugs treating abnormal functions of the protein. Such a
CC      technique is efficient and selective, which is different from the prior-
CC      art transmembrane trap (TMT) method wherein an epitope recognised by an
CC      antibody is carried in a fused protein
XX      SO      Sequence 626 AA;

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Query Match 58.0%; Score 774.5; DB 3; Length 626;
 Best Local Similarity 59.7%; Pred. No. 1.7e-40;
 Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

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QY      1  QVQLQDQWGAFLKSWGTLISLTCAVSGASF-SGYIWSMIRPPGKGLMEIGIINHGSITY 59
Db      20  QVQLQDSGPGVLRPQGLTSLTCTVSGYISITSHANSMWRQPPGRLEWIGIYSIGITTY 79
QY      60  NPSLGRVITSLDITSTNOISLKLTSMTAADAIVVYCARTVAGTS--DYMGQGTIVTVSSG 117
Db      80  NPSLKSRYTLMRDTSKNOFSLRLSSVTAADTAIVVYCARSLARTTAMDYMGQSLVTVS-- 137
QY      118 SASAPVTGGGGGGGGGGGGGGGGGGSETTTQSPAFMSATPGDKVSIICRARSDDVDVN 177
Db      138 -----SGGGGGGGGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 187
QY      178 WYQQRPGRAPFIITEDATTVPGISPRPSGGSGYGTDFLTITNNIDSEDAAYFCTQHDFN 237
Db      188 WYQQRPGRAPKLLIYYTSRLHSGVPSRPSGGSGTDFLTITSLQPEDIAITYCCQGNL 247
QY      238 PLTGGGGRKVEIK 250
Db      248 PYTFGGGTVEIK 260

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RESULT 10
ID      AAY55082
AC      AAY55082 standard; protein; 640 AA.
XX      25-FEB-2000 (first entry)
XX      DE      Single chain Fv protein sequence shPM1-MCH4-BVGS3.
XX      KW      Gene isolation; membrane-bound protein; fusion protein; drug production;
XX      KM      antigen-binding cell; secretable functional protein; antigenic protein;
XX      OS      protein isolation; diagnosis; ScFv.
XX      OS      Synthetic.
XX      PN      MO9960113-A1.
XX      PD      25-NOV-1999.
XX      PF      30-APR-1999; 99MO-JP002341.
XX      PR      20-MAY-1998; 98JP-00138652.
XX      PR      01-OCT-1998; 98JP-00279876.
XX      PA      (CHUS ) CHUGAI SEIYAKU KK.
XX      PI      Teuchiya M, Saito M, Ohtomo T;
XX      DR      WPI: 2000-039382/03.
XX      DR      N-PSDB; AAZ40321.
XX      PT      Efficient and selective isolation of a gene encoding membrane protein
XX      PT      with low or no antigenic binding activity, for diagnosis, study of, and
XX      PT      production of drugs treating abnormal functions of the protein.
XX      PS      Example 7; Page 111-117; 120pp; Japanese.

```

This sequence represents a single chain Fv (ScFv) sequence. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused protein

XX Sequence 640 AA;
SQ
Query Match 58.0%; Score 774.5; DB 3; Length 640;
Best Local Similarity 59.7%; Pred. No. 1.7e-40;
Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;
QY 1 QVQLQQMGAGLTKSGTSLTCAVSGASG--SGYWMGIRPPKGLWIGINHRGSTR 59
DB 20 QVQLQSGRGLVPSQTLSTCTVSGFISRTSYGWIRPPKGLWIGINYSGITTY 79
QY 60 NPSLDGRVTLSDTSTNQISLKLTSMTADTAIVYVCARTVAGTS--DYWGCGTLVTVSSG 117
DB 80 NPSLSRVTLMDTSGNQPSLRSLSSVTADTAIVYCARSLARTADNDYGGQSLVTVS-- 137
QY 118 SASAPLTGGSGSGSGSGSGSGSETTLTOSPAFMSATPPGDKVISISCKASRDVDDVN 177
DB 138 -----SGSGSGSGSGSGSGSGSDIQMTQSPSSLSASVGPRTVITCRASQDISSYLN 187
QY 178 WYQORPGEAPRIIEDATTLVPGISPRFSGSGVGTDFLTINNIDSEDAAYPCLOHNP 237
DB 188 WYQORPGEAPRIIEDATTLVPGISPRFSGSGVGTDFLTINNIDSEDAAYPCLOHNP 247
QY 238 PLTFGGGTVEIK 250
DB 248 PLTFGGGTVEIK 260
RESULT 11
ABP45038
ID ABP45038 standard; protein; 251 AA.
XX AC ABP45038;
XX 19-AUG-2002 (first entry)
DE Human Blys binding scFv SEQ ID 1049.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
PD
XX 15-JUN-2001; 2001WO-US019110.
PF
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
XX
XX Antbodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 1654-1655; 3148pp; English.
PS
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
SQ Sequence 251 AA;
Query Match 56.9%; Score 760; DB 5; Length 251;
Best Local Similarity 59.9%; Pred. No. 5.6e-40;
Matches 157; Conservative 28; Mismatches 53; Indels 24; Gaps 6;
QY 1 QVQLQQMGAGLTKSGTSLTCAVSGASG--YYWMIRPPKGLWIGINHRGSTR 58
DB 1 QVQLQSGRGLVPSQTLSTCTVSGFISRTSYGWIRPPKGLWIGINYSGITTY 60
QY 59 NPSLDGRVTLSDTSTNQISLKLTSMTADTAIVYVCARTVAGTS-----DYWGCG 109
DB 61 YSPSLKSRVTLSDTSTNQISLKLTSMTADTAIVYVCARTVAGTS-----DYWGCG 118
QY 110 TLVTVSSGASAPTPGSGSGSGSGSGSGSETTLTOSPAFMSATPPGDKVISISCKAS 169
DB 119 TLVTVSS-----GGSGSGSGSGSGSGSGS--ALRVLTSRATLSLSEBDAAY 168
QY 170 RDVDDVWYQORPGEAPRIIEDATTLVPGISPRFSGSGVGTDFLTINNIDSEDAAY 229
DB 169 QSVSYLAWYQORPGEAPRIIEDATTLVPGISPRFSGSGVGTDFLTINNIDSEDAAY 228
QY 230 PCLQNDNP-LTFGGGTVEIK 250
DB 229 YQQRSMNPFPLTFGGGTVEIK 250
RESULT 12
ABP45349
ID ABP45349 standard; protein; 248 AA.
XX AC ABP45349;
XX 19-AUG-2002 (first entry)
DE Human Blys binding scFv SEQ ID 1360.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
PD
XX 15-JUN-2001; 2001WO-US019110.
PF
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
DR
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1, Page 2025-2026; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;
XX
Query Match 55.5%; Score 741.5; DB 5; Length 248;
Best Local Similarity 58.9%; Pred. No. 7.9e-39;
Matches 152; Conservative 31; Mismatches 56; Indels 19; Gaps 5;
QY 1 QVQLQWAGLGLKSWGTLSITCAVSGASFSGYYMSWIRQPGKGLWIGINHRGSTTYN 60
DB 1 QVQLQSGPGLVLPSELTLSICTVSGSIRSYMSWIRQPGKGLWIGITHVSGSTVDN 60
QY 61 PSIDGRTVTSIDSTNOISLKLSTMAADTAAYVYCAR-----IVAGT-----SYWGQGTIV 112
DB 61 PSIRSRVTVMSIDTSKQFSLNLTSTVTAADTAAYVYCARHDYDVLTSQYLAQAFVWQGTIV 120
QY 113 TVSSGSASAPTGSGSGSGSGSGSGSGSETTLTQSPAPMSATPGDKVSIKSCASRDV 172
DB 121 TVSS-----GGGSGSGSGSGSGSGSGS---ALDIQLTQSPSSISASVGRVTTTCASQGI 170
QY 173 DDDVMMYQORPGEAPFIETEDATTLVPGISPRPSGSGYGTDTTLTINNIDSEDAAYFCL 232
DB 171 GRLMMYQOKPRAAPLILFVTSLSHSDVSRFSGSGSGTDLTSLTINLQPEDATYYCQ 230
QY 233 QHDFPLTFGGGTKEIK 250
DB 231 QSYTDP-TTGGGTRELEIK 247
RESULT 13
ID ABP45315
AC ABP45315 standard; protein; 252 AA.
XX
XX
DT 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1326.
DE
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX
XX WO200202641-A1.
PN
XX
XX 10-JAN-2002.
PD
XX
XX 15-JUN-2001; 2001WO-US019110.
PF
XX
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0273799P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
DR WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
PT
XX
XX Claim 1, Page 1985-1986; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 252 AA;
XX
Query Match 55.5%; Score 741.5; DB 5; Length 252;
Best Local Similarity 58.6%; Pred. No. 8e-39;
Matches 154; Conservative 26; Mismatches 56; Indels 27; Gaps 6;
QY 1 QVQLQWAGLGLKSWGTLSITCAVSGASFSGYYMSWIRQPGKGLWIGINHRGSTTYN 60
DB 1 QVQLQSGPGLVLPSELTLSICTVSGSIRSYMSWIRQPGKGLWIGITHVSGSTVDN 60
QY 61 PSIDGRTVTSIDSTNOISLKLSTMAADTAAYVYCARVAGT-----DYWGQGT 110
DB 61 PSLSKRVTVMSIDTSNLFSLKNSVTAADTAAYVYCARERADYDILGYYFYGMVWQGT 120
QY 111 LTVSSGSASAPTGSGSGSGSGSGSGSETTLTQSPAPMSATPGDKVSIKSCASRDV 169
DB 121 MVTVS-----SGGSGSGSGSGSGSGSGSVLTQ-PASVSGSPGSIITISCTGNS 167
QY 170 RDVY--DDVMMYQORPGEAPFIETEDATTLVPGISPRPSGSGYGTDTTLTINNIDSEDA 227
DB 168 SDVGIVYVSWYQOHGKAPKLMITEGSKRPSGVNRFSGSKGNATSLTISGLQAEDEA 227
QY 228 YFCLQH-DNFPPLTFGGGTKEI 249
DB 228 DYCCSYTTRSTRVFGGKTIV 250

RESULT 14
 ABP45402
 ID ABP45402 standard; protein; 250 AA.
 XX
 AC ABP45402;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1413.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 2088-2089; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 250 AA;
 XX
 QY Query Match 55.4%; Score 739.5; DB 5; Length 250;
 Db Best Local Similarity 59.0%; Pred. No. 1.1e-38;
 Matches 154; Conservative 26; Mismatches 56; Indels 25; Gaps 7;
 QY 1 QVQLQQGKGLKSGTSTLTCAVSGASGSGYTWMIROPPKKGLEWIGRIHRSSTYN 60
 1 QAOIQDQMGAGLKLPSTSLTLVVGSGPGSYGWMIROPPKKGLEWIGRIHRSSTYN 60
 61 PSIDGRVTSLDSTINQISLKLSTMTAAPTAVYYCAR-----TVAG-----TSDYWGQGLTV 112

Db 61 PSLSKRVTVISDVTSKNQPSLKLSTVTAADTAVYYCARGERDILNGYLDGMDWGKGTWV 120
 QY 113 TVSSGSAAPPTGGSGSGSGSGSGSETTLTQSPAFMSTAPRGKVSICK-ASRD 171
 Db 121 TVSS-----SSGSGSGSGSGSGSGSQSVLTQPPS-VSAPPGQVTVISCTGTSSD 167
 QY 172 VD--DDVMVYQORPGEAPIFILEDATTVLPGISPPSGSGGYGTDFTLTINNIDSEDAVY 229
 Db 168 VGGYTVSMYQOHRKAPKLMITYEGSKRPSGVSNSRFSKSGKNTASLTISGLQADEADY 227
 QY 230 FCLQH-DNPPALTGGGTVEI 249
 Db 228 YCSSYTTSTRTVFGGGLTV 248
 RESULT 15
 ABP45631
 ID ABP45631 standard; protein; 255 AA.
 XX
 AC ABP45631;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1642.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 2362-2363; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of
CC the invention
yy

XX Sequence 255 AA;
SQ

50

Sequence 255 AA;

Query Match	55.1%	Score 736;	DB 5;	Length 255;
Best Local Similarity	58.6%	Pred. No. 1	Re-38.	

Best Local Similarity 58.6%; Pred. No. 1.8e-38;
Matches 156; Conservative 21. Mismatches 50

Matches 156; Conservative 21; Mismatches 59; Indels 30; Gaps 6;

QY 1 QVQLQQMGAGLLSKMGLSTITCAVSAASASGYMMWMIQPKKLEWIGELINHGSTTNN 60

Db 1 QVQLQQMGAGLLPSETLSTCAVYGGSSGYMMWMIQSPKGLEWIGELINHGSTNN 60

QY 61 PSLDGRVTTLSLDTSTNQISLKLSTMTADTAVYYCAR-----TVAGTS-----DYWG 107

Db 61 PSLKSRVTTISVDASKNQPSLKLSSVTAATAVYYCARRSRYDILTVGSPRSKQMDVWG 120

QY 108 QGTLTVYSSGSAAPATGGGSGGGSGGGSGGGSSFTLLTQSPAFMATITGDKVYISCK 167

Db 121 RGLTVLVYS-----SGGGSGGGSGGGSGGGSGVLTQPPS-ASGTPGQRVYISCS 167

QY 168 ASQD--VDDVNMVYQQRPEGAPFIIEBATLLVLPQISIRFSGSGYGTDFTLTINNIDSE 225

Db 168 GSSSNIGSTVYMWYQRLPFGAAPQLLIYNNDDQPSGIPRFGSGISGTSGLVVISGLQSD 227

QY 226 AAYYFCLQHDNF--PLTGGGKTKVMI 249

Db 228 EADYICASWDSDSLNGRVFGGGTKLTV 253

Search completed: May 13, 2004, 15:01:00
Job time : 51.4563 sec


```

; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Syoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-22

Query Match      51.8%; Score 691.5; DB 2; Length 248;
Best Local Similarity 54.4%; Pred. No. 2.1e-46;
Matches 143; Conservative 34; Mismatches 57; Indels 29; Gaps 5;

QY 1 OVOLQOMGAGLLKSMGTLSTLTCVAGSASF-SGYWMSWTROPKGLWIGETINRGSTTY 59
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVQPGGSLRLSCAVSQSYSTSGSNMWRQAPGKLEWVASITYDGSTNY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTSDY-----WGQGT 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NPSVKGRTITSRDSSKNTFYIQMNSLRABDTAVYICAR-----GSHYFGHMHPAWMGQ 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 112 VTVSSGSASAPTPGGSGSGGSGGGSGGSETTLTQSPAFMSATPDGKVISCKASRD 171
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 117 VTVS-----SEGGSGEGGSGEGGSGDQLTQSPSLSASVGDRTVITCRASKP 164
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1172 VDDD-----VNWYQQRPGAPFIPIEDATTLVPGISPRFSGSGYCDFTLTINNISEDA 227
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 165 VDGEQSYLNMWYQKPKKLLIYAASYLESGVPSRSGSGTDFTLTISLQPEDFA 224
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 228 YVFCLOHDFPLTFGGGTVEIK 250
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 225 TYCCQSHEDPYTFGGGTVEIK 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-09-109-207C-22
; Sequence 22, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44

```

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; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-248
; OTHER INFORMATION: sFv sequence derived from MAb11
;
US-09-109-207C-22

Query Match      51.8%; Score 691.5; DB 3; Length 248;
Best Local Similarity 54.4%; Pred. No. 2.1e-46;
Matches 143; Conservative 34; Mismatches 57; Indels 29; Gaps 5;

QY 1 OVOLQOMGAGLLKSMGTLSTLTCVAGSASF-SGYWMSWTROPKGLWIGETINRGSTTY 59
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVOLVESGGGLVQPGGSLRLSCAVSQSYSTSGSNMWRQAPGKLEWVASITYDGSTNY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTSDY-----WGQGT 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NPSVKGRTITSRDSSKNTFYIQMNSLRABDTAVYICAR-----GSHYFGHMHPAWMGQ 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 112 VTVSSGSASAPTPGGSGSGGSGGGSGGSETTLTQSPAFMSATPDGKVISCKASRD 171
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 117 VTVS-----SEGGSGEGGSGEGGSGDQLTQSPSLSASVGDRTVITCRASKP 164
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1172 VDDD-----VNWYQQRPGAPFIPIEDATTLVPGISPRFSGSGYCDFTLTINNISEDA 227
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 165 VDGEQSYLNMWYQKPKKLLIYAASYLESGVPSRSGSGSGTDFTLTISLQPEDFA 224
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 228 YVFCLOHDFPLTFGGGTVEIK 250
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 225 TYCCQSHEDPYTFGGGTVEIK 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-09-296-005-22
; Sequence 22, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1R
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-248
; OTHER INFORMATION: sFv sequence derived from MAb11
;
US-09-296-005-22

Query Match      51.8%; Score 691.5; DB 3; Length 248;
Best Local Similarity 54.4%; Pred. No. 2.1e-46;
Matches 143; Conservative 34; Mismatches 57; Indels 29; Gaps 5;

QY 1 OVOLQOMGAGLLKSMGTLSTLTCVAGSASF-SGYWMSWTROPKGLWIGETINRGSTTY 59
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVOLVESGGGLVQPGGSLRLSCAVSQSYSTSGSNMWRQAPGKLEWVASITYDGSTNY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTSDY-----WGQGT 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NPSVKGRTITSRDSSKNTFYIQMNSLRABDTAVYICAR-----GSHYFGHMHPAWMGQ 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 112 VTVSSGSASAPTPGGSGSGGSGGGSGGSETTLTQSPAFMSATPDGKVISCKASRD 171
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 117 VTVS-----SEGGSGEGGSGEGGSGDQLTQSPSLSASVGDRTVITCRASKP 164
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1172 VDDD-----VNWYQQRPGAPFIPIEDATTLVPGISPRFSGSGYCDFTLTINNISEDA 227
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 165 VDGEQSYLNMWYQKPKKLLIYAASYLESGVPSRSGSGSGTDFTLTISLQPEDFA 224
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 228 YVFCLOHDFPLTFGGGTVEIK 250
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 225 TYCCQSHEDPYTFGGGTVEIK 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


US-09-109-207C-23

Query Match	51.5%;	Score 687.5;	DB 3;	Length 248;
Best Local Similarity	54.0%;	Pred. No. 4.3e-46;		
Matches 142;	Conservative 34;	Mismatches 58;	Indels 29;	Gaps 5

QY	1	IVVLIQDMAGLLKMSGTSLITCAVSGASF-SGIYWSWIRQPPGKLEWIGELNHRGSTTY	59
Db	1	EVOLVESGGGLVQPEGGSLRLSCAASGYSITISCSYNNMWIRQAGKGLIEWASIKYSGETKY	60
QY	60	NPSLDGRVTISLDTSTNOISLKLTSMTAADZAVVYCAITVACTSDY-----WGQGLT	111
Db	61	NPSYKGRITISRDSKNTFYLQMNSLRAEDTAVVYCAR-----GSHYGHMHAHWGQGLT	116
QY	112	VTVSSGSAASATYGGGSGGGSGGGSGGGSEITLLTQSPAFMSATPEDKVASISCKASRD	171
Db	117	VTVS-----SEGGSGSEGGSGSGGSDIQLTSPSSLASVSGRVTITCRASKP	164
QY	172	VDDD-----VMNYQORPGEARFIIEEDATTVLGISPRPSGSGYGFDTLLTINISEBAA	227
Db	165	VDGSGDSYLVNMYQKPKRAFLTLITAAASYLSSGVSRISGSGSGIDFTLLTISLQPEDFA	224
QY	228	YTFCLQNDNFLTITGGGKTVKIK	250
Db	225	TYICQQSHEDPYTFGGKTVKIK	247

US-09-920-171-23

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US-09-296-005-23 / Sequence 23, Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IGE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 23
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-248
OTHER INFORMATION: sfv sequence derived from MAR11
US-09-296-005-23

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Query Match	51.5%	Score 687.5	DB 3	Length 248									
Best Local Similarity	54.0%	Pred. No. 4,3e-46											
Matches 142	Conservative 34	Mismatches 58	Indels 29	Gaps 5									
1	QVQLQWQWGA	LLKSWG	TLSTLTC	AVSGASF-SGYIWSMI	RPQPKGI	EWIGRI	NHRS	STTY 59					
1	EVQLVESGGGL	LVQP	GGSLRLSC	AVSGYSIT	SGYSMM	IRGAP	KGLEWVAS	ITYSGETKY 60					
60	NSLDRV	VTISL	DTSTNQ	SLKLT	SMTADT	AYYCA	RYAG	TSDY-----WGQGLT 111					
61	NSVAKR	ITIS	DRDS	KNNT	FYLLQNN	SLRA	BDTAY	YCAR---GSHYFGHMFAWVGQTL 116					
112	VTWSSGSAS	APITGG	GGSGGG	GGSGGG	GGGSE	FTLLTQ	SPAFMS	ATPGD	RVYSIS	CKASRD 171			
117	VTVS-----	SEGGSG	SEGGSG	SEGGSG	SDIQ	LQ	TPSP	SLAS	AVGR	VTITTC	ASKP 164		
172	VDD-----	VNMYQ	ORPGE	APFI	IEDA	TLTV	PGIS	PSRG	SGVGT	FTLIT	INNISE	DDA 227	
165	VDGED	SYLNM	YQQR	PKAP	PKLIT	YAS	YLSE	GVPER	FGSG	SGTD	FTLIT	SLQPED	FA 224
228	YIFCL	QHDN	FLP	ITFG	GGIT	VEIK 250							
225	TYV	COQ	SHED	PYTF	GGIT	VEIK 247							

RESULT 9
US-09-920-171-23
; Sequence 23, Application US/09920171

```

1  / GENERAL INFORMATION:
2  / APPLICANT: Lowman, Henry B.
3  / APPLICANT: Presta, Leonard G.
4  / APPLICANT: Jardieu, Paula M.
5  / APPLICANT: Lowe, John
6  / TITLE OR INVENTION: Improved Anti-IgE Antibodies (as amended)
7  / FILE REFERENCE: P123C2US
8  / CURRENT APPLICATION NUMBER: US/09/920.171
9  / CURRENT FILING DATE: 2001-08-01
10 / PRIOR APPLICATION NUMBER: US 08/887,352
11 / PRIOR FILING DATE: 1997-07-02
12 / PRIOR APPLICATION NUMBER: US 09/296,005
13 / PRIOR FILING DATE: 1999-04-21
14 / NUMBER OF SEQ ID NOS: 44
15 / SEQ ID NO 23
16 / LENGTH: 248
17 / TYPE: PRT
18 / ORGANISM: Artificial Sequence
19 / FEATURE:
20 / OTHER INFORMATION: sfv sequence derived from MAE11
21 / US-09-920-171-23
22
23 Query Match
24 Best Local Similarity 51.5%; Score 687.5; DB 4; Length 248;
25 Matches 142; Conservative 34; Mismatches 58; Indels 29; Gaps 5

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[illegible]

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RESULT 10
US-08-918-148-79
: Sequence 79, Application US/08918148A
: Patent No. 6342220
: GENERAL INFORMATION:
: APPLICANT: Adams, Camellia
: APPLICANT: W.
: APPLICANT: Carter, Paul J.
: APPLICANT: Fendly, Brian M.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Agonist Antibodies
: FILE REFERENCE: P0979
: CURRENT APPLICATION NUMBER: US/08/918,148A
: CURRENT FILING DATE: 1997-08-25
: NUMBER OF SEQ ID NOS: 79
: SEQ ID NO 79
: LENGTH: 244
: TYPE: PRT
: ORGANISM: artificial
US-08-918-148-79

```


QY	181	QRGGAAPFIIEBATTLVPGISPRFGSGSYGDFLTNNIDSEDAAYFCLQDNEP	240
Db	181	QRGGAAPFIIEBATTLVPGISPRFGSGSYGDFLTNNIDSEDAAYFCLQDNEP	240
QY	241	FGGGTVEIK	250
Db	241	FGGGTVEIK	250

```

RESULT 2
US-10-071-866-29
/ Sequence 29, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST
/ TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 29
/ LENGTH: 250
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.12 variant
/ US-10-071-866-29

```

Query Match	100.0%	Score 1336;	DB 14;	Length 250;
Best Local Similarity	100.0%	Pred. No. 2.5e-84;		
Matches 250; Conservative	0;	Mismatches	0;	Indels 0

QY	1	QYVLQOMGAGLLKSNWTTLSLTCAVSGASPSGYVMGMINQPGKGLIEWTGEINHHGSTTYN	60
Db	1	QYVLQOMGAGLLKSNWTTLSLTCAVSGASPSGYVMGMINQPGKGLIEWTGEINHHGSTTYN	60
QY	61	PSLDGRVTIISLDTSTNIOISLKLTSMTADTAIVYVCARTVAGTSDYWGQTLVTVSSGSAS	120
Db	61	PSLDGRVTIISLDTSTNIOISLKLTSMTADTAIVYVCARTVAGTSDYWGQTLVTVSSGSAS	120
QY	121	APTGGGSGSGSGSGSGSGSETTTLTQSPAFMATPGDKVYSISCRASRPVDDVNMWQ	180
Db	121	APTGGGSGSGSGSGSGSGSETTTLTQSPAFMATPGDKVYSISCRASRPVDDVNMWQ	180
QY	181	QRPGEAPFPIIEDATTLVPGISPRFSGSGYGTDFLLTINNIDSDAAYVFCLOHNPFLT	240
Db	181	QRPGEAPFPIIEDATTLVPGISPRFSGSGYGTDFLLTINNIDSDAAYVFCLOHNPFLT	240
QY	241	FGGGTKTVEIK 250	
Db	241	FGGGTKTVEIK 250	

```

RESULT 3
US-10-360-828-29
/ Sequence 29, Application US/10360828
/ Publication No. US20030206909A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shaobing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu Li
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-727
/ CURRENT APPLICATION NUMBER: US/10/360,828
/ CURRENT FILING DATE: 2003-02-07
/ PRIOR APPLICATION NUMBER: US 10/071,866
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: US 10/072,301

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/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: US 10/133,978
/ PRIOR FILING DATE: 2002-04-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 29
/ LENGTH: 250
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: clone 15.150.12 Variant
US-10-360-828-29

Query Match      100.0%; Score 1336; DB 15; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.5e-84;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

	Query Match	Best Local Similarity	Matches	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	QVQLVQDQAGLLSGVSTLTCAVSGAS	100.0%;	Score 1336;	DB 15;	Length 250;					
Db	1	QVQLVQDQAGLLSGVSTLTCAVSGAS	100.0%;	Pred. No. 2.5e-84;							
QY	61	PSLDGRVTISLDSTSTNQISLKTSTMTADPTAVVYCAITVAGTSDYWGQGLVTVSSGGAS									
Db	61	PSLDGRVTISLDSTSTNQISLKTSTMTADPTAVVYCAITVAGTSDYWGQGLVTVSSGGAS									
QY	121	APFGGGSGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVSISSCARSDVDDVVMYQ									
Db	121	APFGGGSGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVSISSCARSDVDDVVMYQ									
QY	181	QRPGKAPFIPIEDATTLVPGISIPFSSGGYDPTTLTINNIDSEDAAYFCLQHDNPLT									
Db	181	QRPGKAPFIPIEDATTLVPGISIPFSSGGYDPTTLTINNIDSEDAAYFCLQHDNPLT									
QY	241	FGGGTKVEIK	250								
Db	241	FGGGTKVEIK	250								

```

1      RESULT 4
2      US-10-072-301-21
3      ; Sequence 21, Application US/10072301
4      ; Publication No. US20030152913A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Hua, Shao-bing
7      ; APPLICANT: Pauling, Michelle H.
8      ; APPLICANT: Zhu, Li
9      ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
10     ; TITLE OF INVENTION: VIRUS
11     ; FILE REFERENCE: 25636-718
12     ; CURRENT APPLICATION NUMBER: US/10/072,301
13     ; CURRENT FILING DATE: 2002-02-08
14     ; NUMBER OF SEQ ID NOS: 54
15     ; SOFTWARE: PatentIn version 3.1
16     ; SEQ ID NO 21
17     ; LENGTH: 250
18     ; TYPE: PRT
19     ; ORGANISM: Artificial Sequence
20     ; FEATURE:
21     ; OTHER INFORMATION: Clone 15.150.12
22     ; US-10-072-301-21

```

Query Match	99.7%	Score 1332	DB 14	Length 250
Best Local Similarity	99.6%	Pred. No. 4,86-84		
Matches	249	Conservative 1	Mismatches 0	Indels 0
QY	1	QVQLQDQWAGLLKSGMTGLSTLTCAVSGASPGSGYYMSWIRPDPKGLFEMTGEINHRSGTNN	60	
Db	1	QVQLQDQWAGLLKSGMTGLSTLTCAVSGASPGSGYYMSWIRPDPKGLFEMTGEINHRSGTNN	60	
QY	61	PSLDGRVTISLDPTSTNIOISLKLTSMTAPADTAVYYCCARTAGTSDYWGQGLTVTVSSGSAS	120	
Db	61	PSLDGRVTISLDPTSTNIOISLKLTSMTAPADTAVYYCCARTAGTSDYWGQGLTVTVSSGSAS	120	

CURRENT FILING DATE: 2003-02-07

US-09-880-748-1321

Query Match	62.7%	Score 838;	DB 10;	Length 249;
Best Local Similarity	63.8%;	Pred. NO. 4.2e-50;		
Matches 166;	Conservative 27;	Mismatches 45;	Indels 22;	Gaps 3;

Qy	1	OYVOLQOMGGLIKSMGTSILTCAVSASISGYWSMIROPKGKLEMGIEINRGSTTN	60
Db	1	QVOLQOMGGLIKSPSTTSLTCVAVCGSSGYWSMIROPKGKLEMGIEINRGSTTN	60
Qy	61	PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCAR-----TVAGTS----	DYWGQGT 110
Db	61	PSLKRVTISVPTSKNQFSLKLTSVTAADTAVYYCARGPRYYIDILGYRNMFDPMGRGT	120
Qy	111	LVTVSSGASAPITGGGSGGGGSGGGSGGGSETTLTOSPAPMSATPGDPKXVISCASR	170
Db	121	LVTVS-----SGGGSGGGGSGGGSGGGSDIYMTOSPSTLSASVGKRVITLCASQ	168
Qy	171	DVDDDVNMYQQRPEGAIPFIIEBDATTLVPGISDRFSGSGYGTDFTLTINNIDSEDAAYF	230
Db	169	GISSMLAWYQKRPGRAPKVLIIKASLTLSGVPSPRFGSGSGGTFTLITLSLQEDFATYY	228
Qy	231	CLQHNDPFLITPBGGTVEIK 250	
Db	229	COOSYSTPMTFQGTLEIK 248	

RESULT 8
US-10-293-418-1321

Query Match	62.7%;	Score 838;	DB 12;	Length 249;
Best Local Similarity	63.8%;	Pred. No. 4.2e-50;		
Matches 166; Conservative	27;	Mismatches 45;	Indels 22;	Gaps 3

```
QY      231 CLQHDNFPLTFGGTKEIK 250
      | | : | | | | | | |
Db      229 CQQSSTPWTFGGQTKLEIK 248
```

```

RESULT 9
US-10-406-830-8
/ Sequence 8, Application US/10406830
/ Publication No. US20040071696A1
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, GREGORY P.
/ APPLICANT: HORAK, EVA M.
/ APPLICANT: WEINER, LOUIS M.
/ APPLICANT: JAMES, MARKS D.
/ TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 407T-000410US
/ CURRENT APPLICATION NUMBER: US/10/406,830
/ CURRENT FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: US 60/370,276
/ PRIOR FILING DATE: 2002-04-05
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 8
/ LENGTH: 286
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic antibody.
US-10-406-830-8

```

[illegible]

PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1049
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1049

Query Match 56.9%; Score 760; DB 10; Length 251;
Best Local Similarity 59.9%; Pred. No. 9.6e-45;
Matches 157; Conservative 28; Mismatches 53; Indels 24; Gaps 6;

QY 1 QVLOQWAGLILKSWGTLSTCAVSGASFG--YYMSWIRPPGKLEWIGIHRGSGTT 58
DB 1 QVLOQWAGLILKSWGTLSTCAVSGASFG--YYMSWIRPPGKLEWIGIHRGSGTT 60
QY 59 YNPSLDGRVITSLDTSTNQISLKLSTMTADTAVYVCARTVAGTS-----DYWGOG 109
DB 61 YSPSLKSRVITSLDTSTNQISLKLSTMTADTAVYVCARTVAGTS-----DYWGOG 118
QY 110 TLVTYSSGASAPFTGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 169
DB 119 TLVTYSSGASAPFTGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 168
QY 170 RDVDDVWVWQORPEAPFIIEADTTLVPGISPRFSGSGYGTDTLTINNIDSDAAY 229
DB 169 QSVSYLWYQKPEARPLIYDASNRATGIPARFSGSGGSDTTLTISLLEPDAVY 228
QY 230 FCLQHDNFP-LTFGGGTVEIK 250
DB 229 YCQGRSNWPLTFGGGTVEIK 250

RESULT 11

US-10-293-418-1049
Sequence 1049, Application US/10293418
Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1049
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1049

Query Match 56.9%; Score 760; DB 12; Length 251;
Best Local Similarity 59.9%; Pred. No. 9.6e-45;
Matches 157; Conservative 28; Mismatches 53; Indels 24; Gaps 6;

QY 1 QVLOQWAGLILKSWGTLSTCAVSGASFG--YYMSWIRPPGKLEWIGIHRGSGTT 58
DB 1 QVLOQWAGLILKSWGTLSTCAVSGASFG--YYMSWIRPPGKLEWIGIHRGSGTT 60
QY 59 YNPSLDGRVITSLDTSTNQISLKLSTMTADTAVYVCARTVAGTS-----DYWGOG 109
DB 61 YSPSLKSRVITSLDTSTNQISLKLSTMTADTAVYVCARTVAGTS-----DYWGOG 118
QY 110 TLVTYSSGASAPFTGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 169
DB 119 TLVTYSSGASAPFTGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 168
QY 170 RDVDDVWVWQORPEAPFIIEADTTLVPGISPRFSGSGYGTDTLTINNIDSDAAY 229
DB 169 QSVSYLWYQKPEARPLIYDASNRATGIPARFSGSGGSDTTLTISLLEPDAVY 228
QY 230 FCLQHDNFP-LTFGGGTVEIK 250
DB 229 YCQGRSNWPLTFGGGTVEIK 250

RESULT 12

US-09-880-748-1360
Sequence 1360, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1360
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1360

Query Match 55.5%; Score 741.5; DB 10; Length 248;
Best Local Similarity 58.9%; Pred. No. 1.8e-43;
Matches 152; Conservative 31; Mismatches 56; Indels 19; Gaps 5;

QY 1 QVLOQWAGLILKSWGTLSTCAVSGASFG--YYMSWIRPPGKLEWIGIHRGSGTT 60
DB 1 QVLOQWAGLILKSWGTLSTCAVSGASFG--YYMSWIRPPGKLEWIGIHRGSGTT 60
QY 61 YNPSLDGRVITSLDTSTNQISLKLSTMTADTAVYVCARTVAGTS-----DYWGOG 112
DB 61 YNPSLDGRVITSLDTSTNQISLKLSTMTADTAVYVCARTVAGTS-----DYWGOG 120
QY 113 TVSSGASAPFTGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 172
DB 121 TVSSGASAPFTGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 170
QY 173 DDDVWVWQORPEAPFIIEADTTLVPGISPRFSGSGYGTDTLTINNIDSDAAY 232
DB 171 GRYLWYQKPEARPLIYDASNRATGIPARFSGSGGSDTTLTISLLEPDAVY 230
QY 233 QHDNFP-LTFGGGTVEIK 250
DB 231 QSYDTP-LTFGGGTVEIK 247

```
RESULT 13
US-10-293-418-1360
/ Sequence 1360, Application US/10293418
/ Publication No. US20030223996A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P2
/ CURRENT APPLICATION NUMBER: US/10/293,418
/ PRIOR FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1360
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-1360

Query Match
Best Local Similarity 55.5%; Score 741.5; DB 12; Length 248;
Matches 152; Conservative 31; Mismatches 56; Indels 19; Gaps 5;

QY 1 QVQLQQGAGLLKSGWGLSLTCAVSGASFSGYVSWIRPPGKGLWIGINHRGSTTYN 60
DB 1 QVQLQSGSGPGLVPRSELTLSCTVSGSGSIRSYWMSWIRSPGKGLWIGHITHSSTIDN 60
QY 61 PSIDGRVTISLDTSTNQISLKLSTMTADTAAYVYCAR-----TVAGT-----SYWQGTIV 112
DB 61 PSLRSKRVTVMSIDTISKQFSLNLSVTADTAAYVYCARHDYDVLITGSIYQAFVWQGTIV 120
QY 113 TVSSGSASAPRTGGSGSGGSGSGSGSETTLTQSPAFMSATPGDKVSISSCKASRDV 172
DB 121 TVSS-----GGGSGSGSGSGSGSGS---ALDIQLTQSPSSLSASVGRVITTCASQSI 170
QY 173 DDVWNYQQRPGAPRFITIEDATTLVPGISPRFSGSGYGTDTTLTINNIDSEDAAYVFC 232
DB 171 GRLTNYQQKPGAPRLIFVTSSLSHSDVSRFSGSGCTDPSLTISNLQEDFATYYCQ 230
QY 233 QHDFPLRTFGGRTKVEIK 250
DB 231 QSTYDP-TFGGRTLEIK 247

RESULT 14
US-09-880-748-1326
/ Sequence 1326, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
```

```
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1326
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1326

Query Match
Best Local Similarity 55.5%; Score 741.5; DB 10; Length 252;
Matches 154; Conservative 26; Mismatches 56; Indels 27; Gaps 6;

QY 1 QVQLQQGAGLLKSGWGLSLTCAVSGASFSGYVSWIRPPGKGLWIGINHRGSTTYN 60
DB 1 QVQLQSGSGPGLVPRSELTLSCTVSGSGSIRSYWMSWIRPPGKGLWIGHITHSSTIDN 60
QY 61 PSIDGRVTISLDTSTNQISLKLSTMTADTAAYVYCARVAGTS-----DYWQGT 110
DB 61 PSLRSKRVTVMSIDTISKQFSLNLSVTADTAAYVYCARHDYDVLITGSIYQAFVWQGTIV 120
QY 111 LVTVSSGSASAPRTGGSGSGGSGSGSGSETTLTQSPAFMSATPGDKVSISSCKASRDV 169
DB 121 MVTVS-----SGGSGSGSGSGSGSGS---ALDIQLTQSPSSLSASVGRVITTCASQSI 167
QY 170 RDVD--DDVWNYQQRPGAPRFITIEDATTLVPGISPRFSGSGYGTDTTLTINNIDSEDA 227
DB 168 SDVGIVTVMSYQQHPKAPRLMIVESKRPVSGVSNFSGSKSGNTATISLQAEDEA 227
QY 228 YFELQH-DNFPLRTFGGRTKVEI 249
DB 228 DYCSSTYTRTFGGRTLEIK 250

RESULT 15
US-10-293-418-1326
/ Sequence 1326, Application US/10293418
/ Publication No. US20030223996A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P2
/ CURRENT APPLICATION NUMBER: US/10/293,418
/ PRIOR FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1326
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-1326
```


Query Match 55.5%; Score 741.5; DB 12; Length 252;
 Best Local Similarity 58.6%; Pred. No. 1.8e-43;
 Matches 154; Conservative 26; Mismatches 56; Indels 27; Gaps 6;

```

QY 1 QVQLQOMGAGLLKSMGTLSLTCAVSGASFSGYTWSWIRPPGKGLEWIGELNHRSSTYN 60
   |||||
DB 1 QVQLQOMGAGLLKPSSETLSLTCAVYGGSFSGYWSWIRQPPGKGPWIGIKITHSGSTYN 60
   |||||
QY 61 PSLDGRVTISLPTSTNQISLKLTSMTAAPTAVYYCARTVAGTS-----DYGQGT 110
   |||||
DB 61 PSLKSRVTISVDTSTNQISLKLNSVTAAADTAVYYCARERADYDILTGYFFGMDYWGQGT 120
   |||||
QY 111 LVTVSSGSAAPPTGGSGSGSGSGSGSETTLTQSPAFMSATPGDKVISCK-AS 169
   |||||
DB 121 MVTVS-----SGGSGSGSGSGSGSGSVLTQ-PASVSGSPGQSTISCTGS 167
   |||||
QY 170 RDVD--DVNMYQQRPGAPFIPIEDATTLPGISPRFSGSGYGTDFLTINNIDSEDA 227
   |||||
DB 168 SDVGGYNVYSWYQOHFGKAPKLMIEGSRPSGVSNRFSGSKSGNTASLTISGLQADEA 227
   |||||
QY 228 YFECLQH--DNFPLTFGGGTKEI 249
   |||||
DB 228 DYICSSYTRSTRVFGGGTKLTV 250
   |||||
    
```

Search completed: May 13, 2004, 15:43:34
 Job time : 38.016 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.2864 Seconds

(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-29

Perfect score: 1336
Sequence: 1 QVQLQOMGAGLLKSWGTLSTL.....CLQHDNPLTFGGTKVEIK 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	46.0	249	S41374	single chain Fv an
2	604.5	45.2	268	A56446	Ig heavy chain V r
3	535	40.0	233	JCS322	p53 specific singl
4	506	37.9	231	B23746	Ig Fab region IV-J
5	502.5	37.6	140	A49045	Ig heavy chain V r
6	498.5	37.3	143	B49028	Ig heavy chain V-I
7	490	36.7	140	S78052	Ig heavy chain pre
8	478	35.8	126	S47010	Ig heavy chain Va
9	472	35.3	115	K3H015	Ig kappa chain pre
10	452	33.8	146	1 GHU02	Ig heavy chain pre
11	442.5	33.1	122	JL0047	Ig heavy chain V r
12	439	32.9	97	S26898	Ig heavy chain V r
13	436.5	32.7	140	I37782	Ig variable region
14	431.5	32.3	130	S31690	Ig heavy chain V r
15	431	32.3	129	S44114	Ig heavy chain V r
16	430	32.2	97	S14474	Ig heavy chain V r
17	429	32.1	97	G34964	Ig heavy chain V-I
18	429	32.1	145	S78055	Ig heavy chain pre
19	425.5	31.8	114	I72667	cold agglutinin FS
20	420	31.4	118	S24443	Ig heavy chain V r
21	419.5	31.4	147	S13519	Ig heavy chain V r
22	418	31.3	139	S31586	Ig heavy chain V r
23	416	31.1	220	A49444	Ig gamma-1 heavy c
24	415.5	31.1	155	S31511	Ig heavy chain - h
25	414	31.0	97	S26805	Ig heavy chain V r
26	413.5	31.0	155	S31512	Ig heavy chain - h
27	411.5	30.8	123	S30530	Ig heavy chain V r
28	410	30.7	137	S31676	Ig heavy chain V r
29	409.5	30.7	134	S54906	Ig heavy chain V r

30	409	30.6	97	2	JH0428	Ig gamma chain V r
31	408	30.5	130	2	S30534	Ig heavy chain V r
32	406	30.4	118	2	S20780	Ig heavy chain V r
33	405.5	30.4	121	2	S44113	Ig heavy chain V r
34	404	30.2	97	2	S26806	Ig heavy chain V r
35	401.5	30.1	139	2	S31696	Ig heavy chain V r
36	400.5	30.0	127	2	S19668	Ig heavy chain V r
37	398.5	29.8	135	2	S78051	Ig heavy chain pre
38	396.5	29.7	146	2	S09711	Ig heavy chain V r
39	393	29.4	97	2	S26808	Ig heavy chain V r
40	391.5	29.3	123	2	S30529	Ig heavy chain V r
41	385.5	28.9	146	2	S09710	Ig heavy chain V r
42	385	28.8	106	2	S37454	Ig mu chain - huma
43	385	28.8	139	2	A41287	Ig heavy chain pre
44	384	28.7	97	2	S12416	Ig heavy chain V r
45	383.5	28.7	140	2	A24770	hypothetical hybr

ALIGNMENTS

RESULT 1

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artseenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv antibod

A:Reference number: S41374

A:Accession: S41374

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <ART>

A:Cross-references: EMBL:Z29480

Query Match 46.0%; Score 614; DB 2; Length 249;

Best Local Similarity 48.1%; Pred. No. 1.6e-32;

Matches 124; Conservative 40; Mismatches 74; Indels 20; Gaps 4;

QY	1	QVQLQOMGAGLLKSWGTLSTLTCVAGSFGSYGWSMIRPOPKGGLWIGEI-NHRGSTTY	59
DB	1	QVQLQOSGAEIVRPASVYKSLCTAGFNFKODIHWVQRPEKGLWIAIPAGSNVYK	60
QY	60	NPSLDGRVTISLDTSTNOISLKLSTMTADTAIVYCAR--IVAGTSDYWGCGTLVTVSSG	117
DB	61	VRPFQDKATITPADTSSNTAYVLLSLTSEDPDAVYVCARDTLVTSIGYWGCGSTVTVS--	118
QY	118	SASAPYGGGSGGSGGSGGSGGSGGSETTLTOSPAFMATPDCKYSICKAKR-----DV	172
DB	119	-----SRGSGSGGSGGSGGSGGSDLELTQSPSVAVITPEESVISCRSSKSLVSDG	168
QY	173	DDDVNMVQORPEAFIFIEBDATLVPGISPRFSSGSGGTDTLTINNIDSEDAVYFCL	232
DB	169	DSYLWFLQRFQGSQQLLYRMSNLASGVPRFSSGSGTSTTLNISRVEADGVYICM	228
QY	233	QHDFNPLTFGGTKVEIK 250	
DB	229	QHREYPLTFGAGTKLELK 246	
RESULT 2			
A56446			
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)			
C:Species: Mus musculus (house mouse)			
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996			
C:Accession: A56446			
R:Yang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.			
J. Biol. Chem. 270, 7829-7835, 1995			
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identic			
A:Reference number: A56446; MUID:95329583; PMID:7713873			
A:Accession: A56446			

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-268 <TRAN>
 A:Cross-references: GB:U20617
 C:Keywords: heterotetramer; immunoglobulin

Query Match 45.2%; Score 604.5; DB 2; Length 268;
 Best Local Similarity 48.8%; Pred. No. 6.9e-32;
 Matches 123; Conservative 42; Mismatches 72; Indels 15; Gaps 4;

QY 1 OVLOQMGAGLLKSMGTLSTLCAVSGASFSGYWMSIRQPPGKLEWIGETINHRGSTTYN 59
 DB 3 OVLOQMGAGLLKSPSTLSTLCAVSGASFSGYWMSIRQPPGKLEWIGETINHRGSTTYN 62
 QY 60 NSLDRVTISLDTSTNQISLKLTSMTADTAVYYCAR-TVAGTSDYMGQGLTVTVSSG 118
 DB 63 DRFGOKATITADTSSNTAVLQSLTSEDTAVYYCASTYLRREYMGQGLTVTVSSG 119
 QY 119 ASAPRTGGSGGGSGGGSGGGSETTLTQSPAFMSATPPGDKVISICRASRDVDDVNM 178
 DB 120 -----SGGGSGGGSGGGSGGGSDIELTQSPAFMSATISGEKVTWSCRASSSV-NFIYM 169
 QY 179 YQORPEARPIFIETEDATTLVPGISPRFSGSGYGTDTLTINNDSDAAYRCLQHDNRP 238
 DB 170 YQKSDASPKLWYTYTSHLPQVPARFSGSGSGNSYSLTISMEGSDAATYCCQPTSSP 229
 QY 239 LTFGGGTKEIK 250
 DB 230 FTFGSGTKLEIK 241

RESULT 3
 JC5322
 p53 specific single-chain antibody Fab421 - human

C:Species: Homo sapiens (man)
 C>Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
 C:Accession: JC5322
 R:Jannot, C.B.; Hynes, N.E.
 Biochem. Biophys. Res. Commun. 230, 242-246, 1997
 A>Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
 A:Reference number: JC5322; MUID:97168950; PMID:9016757
 A:Accession: JC5322
 A:Molecule type: mRNA
 A:Residues: 1-233 <TRAN>
 A:Experimental source: hybridoma cell
 C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 40.0%; Score 535; DB 2; Length 233;
 Best Local Similarity 45.6%; Pred. No. 1.6e-27;
 Matches 114; Conservative 41; Mismatches 73; Indels 22; Gaps 6;

QY 5 OQMGAGLLKSMGTLSTLCAVSGASFSGYWMSIRQPPGKLEWIGETINHRGSTTYNPSL 63
 DB 1 QSSGAEIVASGASVKLSCTTSGFNINDYTMHWKKEGEGLEWIGETINHRGSDADMTNRS 60
 QY 64 DGRVTISLDTSTNQISLKLTSMTADTAVYYCARIVAGTSDYMGQGLTVTVSSGASAPT 123
 DB 61 GYKATWTADTSSNTAVLQSLTSEDTAVYYCA--AG-MDYMGQGLTVTVS----- 108
 QY 124 GGGSGGGSGGGSGGGSETTLTQSPAFMSATPPGDKVISICRASRDVDD---VNMV 179
 DB 109 ----SGGGSGGGSGGGSGGGSDIELTQSPAFMSATISCRASKSVTSQSYSMHN 164
 QY 180 QORPEARPIFIETEDATTLVPGISPRFSGSGYGTDTLTINNDSDAAYRCLQHDNRP 239
 DB 165 QKPGQPPRLIYLVNLSGVPARFSGSGSDTFLNIHPVEEDAAATYCC-QHIRELT 223
 QY 240 TFGGGTKEIK 249
 DB 224 RSEGGTKLEI 233

RESULT 4

B23746
 Ig Fab region IV-J(H4)-C (KAV cold agglutinin) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
 C:Accession: B23746
 R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
 J. Biol. Chem. 266, 2836-2842, 1991
 A>Title: The primary structure of the Fab fragment of protein KAV, a monoclonal immunogl
 A:Reference number: A23746; MUID:91131575; PMID:1992660
 A:Accession: B23746
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-231 <LEO>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:140-209/Domain: immunoglobulin homology <IMM>

Query Match 37.9%; Score 506; DB 2; Length 231;
 Best Local Similarity 80.2%; Pred. No. 1.2e-25;
 Matches 101; Conservative 4; Mismatches 17; Indels 4; Gaps 1;

QY 2 VOLQMGAGLLKSMGTLSTLCAVSGASFSGYWMSIRQPPGKLEWIGETINHRGSTTYN 61
 DB 1 VOLQMGAGLLKSPSTLSTLCAVSGASFSGYWMSIRQPPGKLEWIGETINHRGSTTYN 60
 QY 62 SLDRVTISLDTSTNQISLKLTSMTADTAVYYCARIVAGTSDYMGQGLTVTVSSG 117
 DB 61 SLKSRVTISVDTSKNQFLKLSVTADTAVYYCARPPHDSGHYWMYMGQGLTVTVSSG 120
 QY 118 SASAPT 123
 DB 121 SASAPT 126

RESULT 5

A49045
 Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
 C:Accession: A49045
 R:Grillencour, C.; Brunet, J.C.; Piller, F.; Rasseant, L.Z.; Labaume, S.; Silverma
 Eur. J. Immunol. 22, 1781-1788, 1992
 A>Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes a bl
 A:Reference number: A49045; MUID:92324290; PMID:1623923
 A:Accession: A49045
 A:Molecule type: DNA
 A>Status: preliminary
 A:Residues: 1-140 <GRI>
 A:Cross-references: GB:S39381; NID:9250899; PID:AA822441.1; PID:9250900
 A>Note: sequence extracted from NCBI Backbone (NCBI:108088, NCBI:108089)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 37.6%; Score 502.5; DB 2; Length 140;
 Best Local Similarity 80.2%; Pred. No. 1.1e-25;
 Matches 97; Conservative 5; Mismatches 14; Indels 5; Gaps 1;

QY 1 OVLOQMGAGLLKSMGTLSTLCAVSGASFSGYWMSIRQPPGKLEWIGETINHRGSTTYN 60
 DB 20 OVLOQMGAGLLKSPSTLSTLCAVSGASFSGYWMSIRQPPGKLEWIGETINHRGSTTYN 79
 QY 61 PSLDRVTISLDTSTNQISLKLTSMTADTAVYYCAR-----TVAGTSDYMGQGLTVTVSS 115
 DB 80 PSLSKRVITISVDTSKNQSLKLSVTADTAVYYCARGGPAATIVESPDYMGQGLTVTVSS 139
 QY 116 S 116
 DB 140 S 140

RESULT 6

B49028
 Ig heavy chain V-IV region - human (fragment)

C.Species: Homo sapiens (man)
C.Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C.Accession: B49028
R.Timers, E.; Kerner, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schur
Eur. J. Immunol. 21, 2355-2363, 1991
A.Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A.Reference number: A49028; MUID:92008140; PMID:1915549
A.Accession: B49028
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-143 <TIM>
A.Cross-references: GB:S64473; NID:9236906; PID:AA820012.1; PID:9236907
A.Experimental source: X-linked agammaglobulinemia patients; B lymphoblastoid cell lines
C.Note: sequence extracted from NCBI backbone (NCBI:64473, NCBI:64472)
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotrimer; immunoglobulin
F.15-97/Domain: immunoglobulin homology <IMM>

Query Match 37.3%; Score 498.5; DB 2; Length 143;
Best Local Similarity 73.5%; Pred. No. 2, 1e-25;
Matches 100; Conservative 4; Mismatches 19; Indels 13; Gaps 2;

Qy 1 OVQLOQWAGGLKSGTSLTCAVSGASFSGYWMIROPPKGGEMWIGEHNRGSTYN 60
1 OVQLOQWAGGLKSGTSLTCAVSGASFSGYWMIROPPKGGEMWIGEHNRGSTYN 60

Qy 61 PSLDGRVTISLDTSTNOISLKLTSMTADTAVYYCAR-----TVAGTS-----DWG 107
61 PSLSKRVITISVDTSGNQFSLKLSTVTAADTAVYYCARGPVVVPAAMRGMDYGDWVG 120

Db 108 OGTLVTVSSGSASAP 123
121 OGTLVTVSSGSASAP 136

RESULT 7

S78052

Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)

C.Species: Homo sapiens (man)

C.Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C.Accession: S78052; S23717

R.Harindranath, N.

submitted to the EMBL Data Library, August 1990

A.Reference number: S78051

A.Accession: S78052

A.Molecule type: mRNA

A.Residues: 1-140 <HAR>

A.Cross-references: EMBL:X54441; NID:937815; PID:CAA8308.1; PID:9930118

R.Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burasero, S.E.; Wilder, R.L.; Nocklin

Int. Immunol. 3, 865-875, 1991

A>Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h

patient.

A.Reference number: S23716; MUID:92031262; PMID:1718404

A.Accession: S23717

A.Molecule type: mRNA

A.Residues: 15-111 <HAR>

A.Cross-references: EMBL:X54441

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: immunoglobulin

F.1-14/Domain: signal sequence (fragment) #status predicted <SIG>

F.15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>

F.29-111/Domain: immunoglobulin homology <IMM>

Query Match 36.7%; Score 490; DB 2; Length 140;

Best Local Similarity 76.0%; Pred. No. 7, 2e-25;

Matches 98; Conservative 3; Mismatches 12; Indels 16; Gaps 2;

Qy 1 OVQLOQWAGGLKSGTSLTCAVSGASFSGYWMIROPPKGGEMWIGEHNRGSTYN 60

15 OVQLOQWAGGLKSGTSLTCAVSGASFSGYWMIROPPKGGEMWIGEHNRGSTYN 74

Qy 61 PSLDGRVTISLDTSTNOISLKLTSMTADTAVYYCARVAGTS-----DWG 107

11 PSLSKRVITISVDTSGNQFSLKLSTVTAADTAVYYCARGPVVVPAAMRGMDYGDWVG 120

121 OGTLVTVSSGSASAP 136

Db 75 PSLSKRVITISVDTSGNQFSLKLSTVTAADTAVYYCAR---GGSVLRFILEMLYPADWVG 131
Qy 108 OGTLVTVSS 116
132 OGTLVTVSS 140

RESULT 8

S47010

Ig heavy chain V4.21-UniqueD-J5 region - human

C.Species: Homo sapiens (man)

C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C.Accession: S47010

R.Mahmoudi, M.; Geyrhofer, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.

submitted to the EMBL Data Library, July 1994

A.Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin

A.Reference number: S47009

A.Accession: S47010

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-126 <MAT>

A.Cross-references: EMBL:Z35492; NID:9517254; PID:CAA84625.1; PID:9517255

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: heterotrimer; immunoglobulin

F.15-97/Domain: immunoglobulin homology <IMM>

Query Match 35.8%; Score 478; DB 2; Length 126;
Best Local Similarity 75.4%; Pred. No. 3, 8e-24;
Matches 95; Conservative 3; Mismatches 18; Indels 10; Gaps 1;

Qy 1 OVQLOQWAGGLKSGTSLTCAVSGASFSGYWMIROPPKGGEMWIGEHNRGSTYN 60
1 OVQLOQWAGGLKSGTSLTCAVSGASFSGYWMIROPPKGGEMWIGEHNRGSTYN 60

Qy 61 PSLDGRVTISLDTSTNOISLKLTSMTADTAVYYCAR-----TVAGTSYDYGCT 110
61 PSLSKRVITISVDTSGNQFSLKLSTVTAADTAVYYCARGGQCPKASCYTKMFPDYGCT 120

Db 111 LVTYSS 116
121 LVTYSS 126

RESULT 9

K3H015

Ig kappa chain precursor V region (EV15) - human

C.Species: Homo sapiens (man)

C.Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000

C.Accession: A01906

R.Stavnezer, J.; Kekish, O.; Batter, D.; Grenier, J.; Balazs, I.; Henderson, E.; Zegers,

Nucleic Acids Res. 13, 3495-3514, 1985

A>Title: Aberrant recombination events in B cell lines derived from a kappa-deficient hu

A.Reference number: A01906; MUID:85242052; PMID:3925437

A.Accession: A01906

A.Molecule type: DNA

A.Residues: 1-115 <STA>

A.Note: the sequence was determined from the germline gene

C.Comment: This sequence does not belong to any of the previously described V-kappa subg

its type.

C.Comment: The gene was found to be aberrantly rearranged in an individual who does not

C.Genetics:

A.Gene: GDB:IGKV

A.Cross-references: GDB:119341; OMIM:146980

A.Map position: 2p12-2p12

A.Introns: 17/1

C.Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: heterotrimer; immunoglobulin

F.21-115/Product: signal sequence #status predicted <SIG>

F.21-43/Region: Ig kappa chain V region (EV15) #status predicted <MAT>

F.36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1
 F:55-69/Region: framework 2
 F:70-76/Region: complementarity-determining 2
 F:77-108/Region: framework 3
 F:109-115/Region: complementarity-determining 3
 F:143-108/Diulfide bonds: #status predicted

Query Match 35.3%; Score 472; DB 1; Length 115;
 Best Local Similarity 88.5%; Pred. No. 8.3e-24;
 Matches 85; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 143 SETTLTQSPAFMSATPGKVSISCKASRDVDDVMYQORGEAFIFIEPATLVPGIS 202
 Db 20 AETTLTQSPAFMSATPGKVNISCKASQDIDDMVMYQORGEAFIFIEPATLVPGIP 79

QY 203 PFGSGGYGTDTFTLTINNISEDAAYYFCLOHDFP 238
 Db 80 PFGSGGYGTDTFTLTINNISEDAAYYFCLOHDFP 115

RESULT 10

GIH0H2
 Ig heavy chain precursor V-II region (ARR-77) - human

C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
 C:Accession: A02101
 R:Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
 Gene 33, 181-189, 1985
 A:Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence
 A:Reference number: A02101; MUID:85205332; PMID:3922855
 A:Accession: A02101

A:Molecule type: mRNA
 A:Residues: 1-146 <KUD>
 A>Note: the sequence was determined from the differentiated gene
 A>Note: the authors translated the codon GGG for residue 17 as Arg
 C:Genetics:

A:Gene: GDB:IGHV8
 A:Cross-references: GDB:128528; OMIM:147070
 A:Map position: 14q32.33-14q32.33

A:Insertions: 16/3
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-146/Product: Ig heavy chain V-II region (ARR-77) #status predicted <MAR>
 F:20-117/Region: V segment
 F:35-117/Domain: immunoglobulin homology <IMM>
 F:118-127/Region: D segment
 F:128-146/Region: J segment
 F:42-115/Diulfide bonds: #status predicted

Query Match 33.8%; Score 452; DB 1; Length 146;
 Best Local Similarity 72.4%; Pred. No. 2e-22;
 Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;

QY 1 QVQLQQMGAGLLKSWGTLSTCAVSGASPSGYWMIRPPKGLGIEWIGETINHRGSTTYN 60
 Db 21 QVQLQQMGAGLVKPSFTLSLTCAVSGSFGSYWMIRPPKGLGIEWIGETINHRGSTNYK 80

QY 61 PSLDGRVTISLDTSTNQISLKTSTMTADTAVYTCARV--AGTS-----DYMGQGT 110
 Db 81 TSLKSRVTISLDTSTNQISLKTSTMTADTAVYTCARV--AGTS-----DYMGQGT 140

QY 111 LTVVSS 116
 Db 141 LTVVSS 146

RESULT 11

JI0047
 Ig heavy chain V region precursor (clone CR18) - human

C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
 C:Accession: JI0047

R:Baer, R.; Forster, A.; Lavenir, I.; Rabblite, T.H.

J. Exp. Med. 167, 2011-2016, 1988
 A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new
 A:Reference number: JI0047; MUID:88258392; PMID:3133445
 A:Accession: JI0047

A:Molecule type: mRNA
 A:Residues: 1-122 <BAE>
 A:Experimental source: T-cell line RPMI 8402

A>Note: the authors translated the reading frame which extends to the stop codon; the s
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:23-105/Domain: immunoglobulin homology <IMM>

Query Match 33.1%; Score 442.5; DB 2; Length 122;
 Best Local Similarity 84.3%; Pred. No. 6.8e-22;
 Matches 86; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLQQMGAGLLKSWGTLSTCAVSGASPSGYWMIRPPKGLGIEWIGETINHRGSTTYN 60
 Db 9 QVQLQQMGAGLLKPSFTLSLTCAVYGSFSGSYWMIRPPKGLGIEWIGETINHRGSTTYN 68

QY 61 PSLDGRVTISLDTSTNQISLKTSTMTADTAVYTCAR--TVAG 101
 Db 69 PSLKSRVTISVDTSKNQPSLKLSSVTADTAVYTCARGTARG 110

RESULT 12

S26898
 Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26898; S12420
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117; PMID:11404388
 A:Accession: S26898

A:Molecule type: DNA
 A:Residues: 1-97 <TON>

A:Cross-references: EMBL:212363; NID:G32944; PID:CAA78233.1; PID:G32945
 A:Experimental source: clone DP-63
 R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.

EMBO J. 8, 3741-3748, 1989
 A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
 A:Reference number: S09421; MUID:90059975; PMID:2511001
 A:Accession: S12420

A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-97 <SAN>

A:Cross-references: EMBL:X56364
 A:Experimental source: V(H)4.2
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 439; DB 2; Length 97;
 Best Local Similarity 85.6%; Pred. No. 8.9e-22;
 Matches 83; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLQQMGAGLLKSWGTLSTCAVSGASPSGYWMIRPPKGLGIEWIGETINHRGSTTYN 60
 Db 1 QVQLQQMGAGLLKPSFTLSLTCAVYGSFSGSYWMIRPPKGLGIEWIGETINHRGSTTYN 60

QY 61 PSLDGRVTISLDTSTNQISLKTSTMTADTAVYTCAR 97
 Db 61 PSLKSRVTISVDTSKNQPSLKLSSVTADTAVYTCAR 97

RESULT 13

I37782
 Ig variable region (VDJ) (clone T23-9) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: J37782; S25476
R:Dematston, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by T
A:Reference number: A36876; MUID:9411917; PMID:829056
A:Accession: J37782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <RES>
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
A:Superfamily: immunoglobulin V region; immunoglobulin homology
F:46-128/Domain: immunoglobulin homology <Im>

Query Match	32.7%	Score 436.5	DB 2	Length 140
Best Local Similarity	71.9%	Pred. No. 1.9e-21		
Matches	87	Conservative	8	Mismatches 21; Indels 5; Gaps 1

QY	1	QVQLQDQMGAGLLKSGVLTSLTCAVSGASGFSGYGWSMIRPPGKGLIEWIGELINHRG	STYN	60
Db	20	QVQLQESGPGLVKPSSETLSLTCTVSGGSSISYWMIRPPGKGLIEWIGIYISGS	TNN	79
QY	61	PSLDGRVTISLDTSTNOISLKITSMATDVTANYCARFYAGT-----SDYWGCGITLV	YWS	115
Db	80	PSLSKRVTVISDTSKNOFSLKLTSSYAADVTANYCARHNSSSSWGRYPDYWGCGITLV	YWS	139
QY	116	\$	116	
Db	140	\$	140	

RESULT 14
S31690
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31690
R:Contributor: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
A:Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31690
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <EMBL>
A:Cross-references: CMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
J:20-102/Domain: immunoglobulin homology <IMM>

	Query Match	32.3%	Score 431.5;	DB 2;	Length 130;	
	Best Local Similarity	68.8%	Pred. No. 3.6e-21;			
	Matches	88;	Conservative	7;	Mismatches	18; Indels 15; Gaps 2
Qy	1 QVQLQQMGAGLLKSWGTLSTLCAVSGASPSGYMSMIRPPCKGLEWIGELINHRSTTYN	60				
Dd	6 QVQLQESPGLVKRPEETLSLTCTVGSGGISYYWMNSRQPKCKGLEWIGIYITSSNTYN	65				
Qy	61 PSLDGRVTISLDTSTNQISLKITSMTADTAVYICARIVAGTS-----DYMQQ	108				
Dd	66 PSLSKRVITISVDTSNGQFSKLKISTYADTAVYICAR---GSSVLMEFGEILLYPDYMQQ	122				
Qy	109 GTILVTSSS	116				
Dd	123 GTILVTSSS	130				

RESULT 15
S44114
I9 heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44114

R: Hakkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamlin, T.J.; Stevenson, F.K.
 submitted to the EMBL data library, March 1994
 A: Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
 A: Reference number: S44105
 A: Accession: S44114
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-129 <HAW>
 A: Cross-references: EMBL:Z31579; NID:G472968; PIDN:CA84351.1; PID:G940525
 C: Superfamily: immunoglobulin V region; immunoglobulin homology
 C: Keywords: heterotrimer; immunoglobulin
 F: 15-98/Domain: immunoglobulin homology <Imm>

[illegible]

Search completed: May 13, 2004, 15:08:44
Job time : 12.2864 secs

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DB 20 AETTLTQSPAFNSATPGDKVNISCKASQIDDDMMNYQKPGBAFLTIQEAATLVGIP 79

QY 203 PRSSGSGYGDFTLTNNIDSEDAAYFCLOHNP 238

DB 80 PRSSGSGYGDFTLTNNIDSEDAAYFCLOHNP 115

RESULT 2

HV2I HUMAN STANDARD; PRT; 146 AA.

AC P06331;

DT 01-JUN-1988 (Rel. 06, Created)

DT 01-JUN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-II region ARH-77 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85205332; PubMed=3922855;

RA Kudo A., Iehizara T., Nishimura Y., Matanabe T.;

RT "A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region.";

RL Gene 33:181-189 (1985).

DR PIR; A02101; GIH02.

DR HSSP; P01825; 7FAB.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IG_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.

FT DOMAIN 20 117 D SEGMENT.

FT DOMAIN 118 127 D SEGMENT.

FT DOMAIN 128 146 J SEGMENT.

FT DISULFID 42 115 BY SIMILARITY.

FT NON TER 146 146

SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52B2B18171F CRC64;

Query Match 33.8%; Score 452; DB 1; Length 146;

Best Local Similarity 72.2%; Pred. No. 1.6e-26;

Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;

QY 1 QVQLQQWAGLILKSGTSLTCAVSGASPSGYWNIROPKGLRWIGIEINHRGSTTN 60

DB 21 QVQLQQWAGLILKSGTSLTCAVSGASPSGYWNIROPKGLRWIGIEINHRGSTTN 80

QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYCARV--AGTS-----DYWGQT 110

DB 81 TSLKSRVTISLDTSTNQISLKLTSMTADTAVYCARV--AGTS-----DYWGQT 140

QY 111 LTVSS 116

DB 141 TTVSS 146

RESULT 3

HV2F HUMAN STANDARD; PRT; 129 AA.

AC P01824;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-II region WAH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=8222235; PubMed=6806818;

RA Takahashi N., Tetsert D., Debure B., Lin L.-C., Putnam F.W.;

RT "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02099; D2HWA.

DR HSSP; P01825; 7FAB.

DR GlycositeDB; P01824; -

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG_V.

DR InterPro; IPR003596; IG_LIKE.

DR Pfam; PF00047; IG_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT DOMAIN 1 113 IG-LIKE.

FT NON TER 129 129

SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 28.0%; Score 374.5; DB 1; Length 129;

Best Local Similarity 61.2%; Pred. No. 6.3e-21;

Matches 79; Conservative 10; Mismatches 27; Indels 13; Gaps 3;

QY 1 QVQLQQWAGLILKSGTSLTCAVSGASF--SGYWSNIROPKGLRWIGIEINHRGSTT 58

DB 1 RQLQDSGPGVLPKSETISLTCLIVSGSPRRTGYWNIROPKGLRWIGIVYTSIY 60

QY 59 YNPISLGRVTISLDTSTNQISLKLTSMTADTAVYCAR-----TVAGTS-----DYWG 107

DB 61 YNPISLGRVTISLDTSTNQISLKLTSMTADTAVYCAR-----TVAGTS-----DYWG 120

QY 108 QGTLTVSS 116

DB 121 QGTLTVSS 129

RESULT 4

HV2G HUMAN STANDARD; PRT; 117 AA.

AC P01825;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-II region NEMM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=77242302; PubMed=407927;

RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;

RT "Amino acid sequence of the VH region of a human myeloma immunoglobulin (IGG New).";

RL Biochemistry 16:3412-3420 (1977).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.

RX MEDLINE=78066916; PubMed=618887;

RA Saul F.A., Amzel L.M., Poljak R.J.;

RT "Preliminary refinement and structural analysis of the Fab fragment from human immunoglobulin new at 2.0-A resolution.";

RL J. Biol. Chem. 253:585-597 (1978).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.

Query Match	23.7%	Score 316.5;	DB 1;	Length 144;
Best Local Similarity	52.0%;	Pred. No. 1.2e-16;		
Matches 65;	Conservative 16;	Mismatches 35;	Indels 9;	Gaps 1

RESULT 11	
KV1A_HUMAN	
ID_KV1A_HUMAN	STANDARD;
	PRT; 108 AA.

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FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT FT 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT FT 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT FT 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C1BF0CAF CRC64;

Query Match 23.7%; Score 316; DB 1; Length 108;
Best Local Similarity 54.8%; Pred. No. 9,5e-17;
Matches 57; Conservative 22; Mismatches 25; Indels 0; Gaps 0

QY 147 LTQSFAFMASAPDGDVNSISCSKSRVDVVNMYOQRPGEPALPFIETADATTVLGISPRFS 206
DB 4 MTQSSSSIASAGVGDRVTTCASQSDINHYLMWYQQGPKKAPRILTYDASNLETGVSPRFS 63
QY 207 GSGYGTDFTLTINNIDSEDAAYVFCLQHDNFPLTPGGGKNVEIK 250
DB 64 GSGFGTDTFTIISGLQPEDIAITYCOQYDITLPTRTGGTKLEIK 107

RESULT 12
KVSA_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-V region MPCII precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=628267;
RA Kelley D.B., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RL 5'-terminal regions of immunoglobulin variable-region genes.";
Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbits T.H., Hamlyn P.H., Matthyseens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RL genes"; Can. J. Biochem. 58:1176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RL myeloma MPC 11."; Biochem. J. 171:1337-347(1978).
CC -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEN DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00561; AAA83776.1; -.
DR PIR; A90823; KVMS11.
DR HSSP; P80362; IWTU.
DR InterPro; IPR007110; Ig-1/Ike.

```

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 129 FRAMEWORK-3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 FRAMEWORK-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 23.7%; Score 316; DB 1; Length 149;
Best Local Similarity 53.2%; Pred. No. 1.3e-16;
Matches 59; Conservative 20; Mismatches 32; Indels 0; Gaps 0;

QY 140 GGGSETTLTQSPAFMSATPGDKVYSISCKASRDVDDVNMVYQQRPGEPAPFIIEDATTLVPGISPRS 199
DB 38 GVDGDIWMTQSHKFMSTSVGDRVSIITCKASQDVSTTVAMVYQQRPGSPFLILYSASYRT 97
QY 200 GISPRFSGSGYGTDTFTLTINMIDSEDAAYFCLQHDNFPFLTGGGTXKVIK 250
DB 98 GVPDRFTSGSGSDFTFTLTISVQABDLAVYCOQHYSTPRTGGTKLEIK 148

RESULT 13
KV1B_HUMAN STANDARD; PRT; 108 AA.
ID KV1B_HUMAN
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-1 region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schleich H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RX X-RAY CRYSTALLOGRAPHY.
RP MEDLINE=77022433; PubMed=1234024;
RA Schwaeger H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
DR PIR; A91653; KIHUAV.
DR PDB; 1JVS; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_v.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 FRAMEWORK-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E801187BE6F6FB9 CRC64;

Query Match 23.6%; Score 315; DB 1; Length 108;
Best Local Similarity 54.8%; Pred. No. 1.1e-16;
Matches 57; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

QY 147 LTQSPAFMSATPGDKVYSISCKASRDVDDVNMVYQQRPGEPAPFIIEDATTLVPGISPRS 206
DB 4 MTQSPSSLSASVGRVITTCQASQDISYLMVYQQRPGKAPFLILYDASNLSEGVSRRS 63
QY 207 GSGYGTDTLTINMIDSEDAAYFCLQHDNFPFLTGGGTXKVIK 250
DB 64 GGGSGAHFTFTLTISLQPEDIAAYVCOQDYLPWTFGGGTXKVIK 107

RESULT 14
KV5S_MOUSE STANDARD; PRT; 108 AA.
ID KV5S_MOUSE
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Stankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-I)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR; A92811; KVM506.
DR HSP; P01607; IRR1.
DR InterPro; IPR007110; Ig_v-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11810 MW; 8DE4DD31076F2AFB CRC64;

Query Match 23.5%; Score 314; DB 1; Length 108;
Best Local Similarity 53.3%; Pred. No. 1.3e-16;
Matches 57; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 144 ETTLTQSPAFMSATPGDKVYSISCKASRDVDDVNMVYQQRPGEPAPFIIEDATTLVPGISPR 203
DB 4 ETTLTQSPAFMSATPGDKVYSISCKASRDVDDVNMVYQQRPGEPAPFIIEDATTLVPGISPR 203

Db 1 DVQMIOSSPSLSASIGDIVTMTQASOGTSININMFWQKPGKAPKLLIYGASNLSDGVPS 60
QY 204 RPSGGYGTDFLTITINNIDSEDAAYFCLQHDNFPPLTFGGGTRKVEIK 250
Db 61 RPSGSRVGTDFLTITISLEDEDMATYFCLQHSYLPYTFGGGTRKLEIK 107

RESULT 15

KVSQ_MOUSE
ID KVSQ_MOUSE STANDARD; PRT; 108 AA.
AC P01650;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Ig kappa chain V-V region UPC 61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxId=10090;
RN [1]
RP SEQUENCE.

RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype."; J. Immunol. 122:1905-1910(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR; A92808; KYM61.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.

KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11809 MW; FAE4DA36076F2AFE CRC64;

Query Match 23.4%; Score 313; DB 1; Length 108;
Best Local Similarity 53.3%; Pred. No. 1.6e-16;
Matches 57; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 144 ETTLQSPAFMGATPGDKYSISCKASRDVDDVNWYQQRPGRAPFIIEDATTIVPGISF 203
Db 1 DVQMIOSSPSLSASIGDIVTMTQASOGTSININMFWQKPGKAPKLLIYGASNLSDGVPS 60
QY 204 RPSGGYGTDFLTITINNIDSEDAAYFCLQHDNFPPLTFGGGTRKVEIK 250
Db 61 RPSGSRVGTDFLTITISLEDEDMATYFCLQHSYLPYTFGGGTRKLEIK 107

Search completed: May 13, 2004, 15:02:06
Job time : 8.03884 secs


```
Db 40 QVLAQSGGGLVPGGSLKLSGASGSDPSRYMAGWROAPGKLEWIGETINPDSSTNY 99
Qy 60 NPSLDGRVITISLDTSTNOISLKLTSMTAADIAVYCAR-TVAGTSDYWGQGLTVYSSGS 118
Db 100 TSLADKFTISRDNAKNTLYLQMSKVRSEDTALYACASAYGHSAVWGQGLTVYSSGS 156
Qy 119 ASAPTGGGSGGGGSGGGGSETTLTOSPAFMSATPDQKYSISCKASRDVDDVNW 178
Db 157 -----SGGGGSGGGGSGGGGSDIELTOSPAFMSASVETVITTCRASGNTIHWLAW 207
Qy 179 YQARGAPFIIEADATLVPGISPRFSGSGYGTDPFTLTINNIDSEDAAYFCLQHNF 238
Db 208 YQKQKSPOLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLSQEDPFGSYCCQHFVTP 267
Qy 239 LTFGGGTVEIK 250
Db 268 YTFGGGTLEIK 279
```

RESULT 2

```
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.H., Lee S.D.,
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U08067; AAB48044.1; -.
DR InterPro; IPR001110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SMO0406; IG; 2.
DR PROSITE; PSS0835; IG_Like; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;
```

Query Match 45.4%; Score 606.5; DB 11; Length 241;
Best Local Similarity 48.4%; Pred. No. 1.2e-39;

Matches 124; Conservative 42; Mismatches 67; Indels 23; Gaps 6;

```
Qy 1 QVLAQSGGGLVPGGSLKLSGASGSDPSRYMAGWROAPGKLEWIGETINPDSSTNY 99
Db 1 QVLAQSGGGLVPGGSLKLSGASGSDPSRYMAGWROAPGKLEWIGETINPDSSTNY 99
Qy 60 NPSLDGRVITISLDTSTNOISLKLTSMTAADIAVYCAR-TVAGTSDYWGQGLTVYSSGS 118
Db 60 NPSLDGRVITISLDTSTNOISLKLTSMTAADIAVYCAR-TVAGTSDYWGQGLTVYSSGS 118
Qy 61 ADFFKGRFPLSLTASATVYLIQINNLKNEBDATVFCARGLRYPDYWGQGLTVYSSGS 117
Db 61 ADFFKGRFPLSLTASATVYLIQINNLKNEBDATVFCARGLRYPDYWGQGLTVYSSGS 117
Qy 119 ASAPTGGGSGGGGSGGGGSETTLTOSPAFMSATPDQKYSISCKASRDVDDVNW 178
Db 118 -----SGGGGSGGGGSGGGGSDIELTOSPAFMSASVETVITTCRASGNTIHWLAW 207
Qy 179 YQARGAPFIIEADATLVPGISPRFSGSGYGTDPFTLTINNIDSEDAAYFCLQHNF 238
Db 169 YQKQKSPOLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLSQEDPFGSYCCQHFVTP 267
Qy 239 LTFGGGTVEIK 250
Db 225 DNLAH-TFGGGLTLEIK 239
```

RESULT 3

```
Q7TOM2 PRELIMINARY; PRT; 243 AA.
AC Q7TOM2;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE scFv 6H8 protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/C;
RA Peter J.C., Eftekhari P., Billfeld P., Wallukat G.;
RT "scFv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAB00495.1; -.
FT NON_TER 1
FT NON_TER 243
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCE4F76 CRC64;
```

Query Match 44.0%; Score 588.5; DB 11; Length 243;
Best Local Similarity 47.0%; Pred. No. 3e-38;

Matches 118; Conservative 48; Mismatches 70; Indels 15; Gaps 4;

```
Qy 1 QVLAQSGGGLVPGGSLKLSGASGSDPSRYMAGWROAPGKLEWIGETINPDSSTNY 99
Db 1 QVLAQSGGGLVPGGSLKLSGASGSDPSRYMAGWROAPGKLEWIGETINPDSSTNY 99
Qy 60 NPSLDGRVITISLDTSTNOISLKLTSMTAADIAVYCAR-TVAGTSDYWGQGLTVYSSGS 119
Db 61 DEKFNKGLIVDSSSTAYMHLSTLASEDAVYCARGRGL-DWGAQGLTVYSSGS 115
Qy 120 SAPTGGGSGGGGSGGGGSETTLTOSPAFMSATPDQKYSISCKASRDVDDVNW 179
Db 116 -----SGGGGSGGGGSGGGGSDIELTOSPAFMSASVETVITTCRASGNTIHWLAW 207
Qy 180 QARGAPFIIEADATLVPGISPRFSGSGYGTDPFTLTINNIDSEDAAYFCLQHNF 239
Db 168 QKPKGNAPRLISGATSLTGVPSRFSGSGGTQYSLKINSLSQEDPFGSYCCQHFVTP 267
Qy 240 TFGGGLTLEIK 250
Db 227 TFGGGLTLEIK 237
```

Query Match 44.0%; Score 588.5; DB 11; Length 243;
Best Local Similarity 47.0%; Pred. No. 3e-38;

```
Qy 1 QVLAQSGGGLVPGGSLKLSGASGSDPSRYMAGWROAPGKLEWIGETINPDSSTNY 99
Db 1 QVLAQSGGGLVPGGSLKLSGASGSDPSRYMAGWROAPGKLEWIGETINPDSSTNY 99
Qy 60 NPSLDGRVITISLDTSTNOISLKLTSMTAADIAVYCAR-TVAGTSDYWGQGLTVYSSGS 119
Db 60 NPSLDGRVITISLDTSTNOISLKLTSMTAADIAVYCAR-TVAGTSDYWGQGLTVYSSGS 119
Qy 61 ADFFKGRFPLSLTASATVYLIQINNLKNEBDATVFCARGLRYPDYWGQGLTVYSSGS 117
Db 61 ADFFKGRFPLSLTASATVYLIQINNLKNEBDATVFCARGLRYPDYWGQGLTVYSSGS 117
Qy 119 ASAPTGGGSGGGGSGGGGSETTLTOSPAFMSATPDQKYSISCKASRDVDDVNW 178
Db 118 -----SGGGGSGGGGSGGGGSDIELTOSPAFMSASVETVITTCRASGNTIHWLAW 207
Qy 179 YQARGAPFIIEADATLVPGISPRFSGSGYGTDPFTLTINNIDSEDAAYFCLQHNF 238
Db 169 YQKQKSPOLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLSQEDPFGSYCCQHFVTP 267
Qy 239 LTFGGGTVEIK 250
Db 225 DNLAH-TFGGGLTLEIK 239
```

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FCG0DBAD2B39FD7 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 588;
Best Local Similarity 41.0%; Pred. No. 1.4e-31;
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

```
QY 1 QVQLQDQWAGLGLKSGTSLTCAVSGASFSGYWYMWIRPPGKGLWIGIEINHRGSTTYN 60
DB QVQLQDQWAGLGLKSGTSLTCAVSGASFSGYWYMWIRPPGKGLWIGIEINHRGSTTYN 79
QY 61 PSLDGRVITSLDSTNQISLKLTSMTAATAVYCARVAGTS-----DYMGQGT 111
DB 80 PSLKSRVITSLDSTNQISLKLTSMTAATAVYCARVAGTS-----DYMGQGT 139
QY 112 VTVSSGSASAPTLFPLVSCENSPDTSVAVGCCLAODFLPDSITPSWKYKNNSDISSTG 152
DB 140 VTVSSGSASAPTLFPLVSCENSPDTSVAVGCCLAODFLPDSITPSWKYKNNSDISSTG 199
QY 153 FMSATPGDKVSIISCKA---SRDV---DDVVMYQORPG---EAPFIIRD---ATT 196
DB 200 PPSVLRGKGYATSGVLPLSKVMOGTDEHVCKQHPRGNKKNVPLVIALPCKVSV 259
QY 197 LVP-----GISPR-----FSGSGYGT 213
DB 260 FVPRPDGFGNPRKSKLTCQATGFSFPRQIQVSWLRGKQVSGVTTDQVQAEAKSGPTT 319
QY 214 ----FTLTNNIDSEDAAYFCLQDNPFLTF 241
DB 320 YKVTSTLTIKESDMLSQSMFTC-RVDHRLTF 350
```

RESULT 5

Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFABFB7E055851 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 597;
Best Local Similarity 41.0%; Pred. No. 1.5e-31;
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

```
QY 1 QVQLQDQWAGLGLKSGTSLTCAVSGASFSGYWYMWIRPPGKGLWIGIEINHRGSTTYN 60
DB QVQLQDQWAGLGLKSGTSLTCAVSGASFSGYWYMWIRPPGKGLWIGIEINHRGSTTYN 79
QY 20 QVQLQDQWAGLGLKSGTSLTCAVSGASFSGYWYMWIRPPGKGLWIGIEINHRGSTTYN 79
DB 61 PSLDGRVITSLDSTNQISLKLTSMTAATAVYCARVAGTS-----DYMGQGT 111
```

```
DB 80 PSLKSRVITSLDSTNQISLKLTSMTAATAVYCARVAGTS-----DYMGQGT 139
QY 112 VTVSSGSASAPTLFPLVSCENSPDTSVAVGCCLAODFLPDSITPSWKYKNNSDISSTG 152
DB 140 VTVSSGSASAPTLFPLVSCENSPDTSVAVGCCLAODFLPDSITPSWKYKNNSDISSTG 199
QY 153 FMSATPGDKVSIISCKA---SRDV---DDVVMYQORPG---EAPFIIRD---ATT 196
DB 200 PPSVLRGKGYATSGVLPLSKVMOGTDEHVCKQHPRGNKKNVPLVIALPCKVSV 259
QY 197 LVP-----GISPR-----FSGSGYGT 213
DB 260 FVPRPDGFGNPRKSKLTCQATGFSFPRQIQVSWLRGKQVSGVTTDQVQAEAKSGPTT 319
QY 214 ----FTLTNNIDSEDAAYFCLQDNPFLTF 241
DB 320 YKVTSTLTIKESDMLSQSMFTC-RVDHRLTF 350
```

RESULT 6

Q96A06 PRELIMINARY; PRT; 618 AA.
AC Q96A06;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96DBDAC7C696E0A6 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 618;
Best Local Similarity 41.0%; Pred. No. 1.5e-31;
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

```
QY 1 QVQLQDQWAGLGLKSGTSLTCAVSGASFSGYWYMWIRPPGKGLWIGIEINHRGSTTYN 60
DB 20 QVQLQDQWAGLGLKSGTSLTCAVSGASFSGYWYMWIRPPGKGLWIGIEINHRGSTTYN 79
QY 61 PSLDGRVITSLDSTNQISLKLTSMTAATAVYCARVAGTS-----DYMGQGT 111
DB 80 PSLKSRVITSLDSTNQISLKLTSMTAATAVYCARVAGTS-----DYMGQGT 139
QY 112 VTVSSGSASAPTLFPLVSCENSPDTSVAVGCCLAODFLPDSITPSWKYKNNSDISSTG 152
DB 140 VTVSSGSASAPTLFPLVSCENSPDTSVAVGCCLAODFLPDSITPSWKYKNNSDISSTG 199
QY 153 FMSATPGDKVSIISCKA---SRDV---DDVVMYQORPG---EAPFIIRD---ATT 196
DB 200 PPSVLRGKGYATSGVLPLSKVMOGTDEHVCKQHPRGNKKNVPLVIALPCKVSV 259
QY 197 LVP-----GISPR-----FSGSGYGT 213
DB 260 FVPRPDGFGNPRKSKLTCQATGFSFPRQIQVSWLRGKQVSGVTTDQVQAEAKSGPTT 319
```

QY 214 ----FTLTNNIDSEDAAYVFLQHDNPLTF 241
 DB 320 YKVTSTLTIKESDWSQSMFTC-RVDHRLT 350

RESULT 7

ID Q9BOB8 PRELIMINARY; PRT; 597 AA.
 AC Q9BOB8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle, and Lymph;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AA06180.1; -
 DR EMBL; BC001872; AA01872.1; -
 DR HSSP; P01825; 7PAB.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_5.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KM Hypothetical protein.
 SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 37.6%; Score 503; DB 4; Length 597;
 Best Local Similarity 40.7%; Pred. No. 4.3e-31;
 Matches 135; Conservative 23; Mismatches 82; Indels 92; Gaps 11;

QY 1 QVQLQOMGAGLLKSGWGLSLTCAVSGASFGGYWMSWIRPPGKLEWIGELINHRGSTTYN 60
 DB 20 QVQLQOMGAGLLKPSFTLSLTGCVGSGFGGYWMSWIRPPGKLEWIGELINHSGLTYN 79
 QY 61 PSLDGRVTLSDLTSTNQISLKLSTMTADTAAYVYCARVTAAGTS-----DYWGQGLT 111
 DB 80 PSLKSRVTLSDVTSKQLSLKLSVNAADTAAYVYCARVITRASPGTDGRYGMVWGQGLT 139
 QY 112 VTVSSGSASAPV-----GGGSGGGSGSGG-----GSGGSGSETTLTQSPA 152
 DB 140 VTVSSGSASAPVTLFPLVSCENSPDTSVAVGLADFLPDSITTSWKTKNNSDISITRG 199
 QY 153 FMSATGDKVISISCKA---SRDY---DDVNMVYQRPG---EAPFIIED---ATT 196
 DB 200 FSVVLRGKGYAAATSVQLPSPKDMQGTIDRHVCKVQHPNGNKEKNVPLFVIAELPPKVS 259
 QY 197 LVP-----GISPR-----FSGSGYGTD----- 213
 DB 260 FVPPRRGFGNPKKSKYLQAGISFSPKQIQVSWMLBKGKQVSGVTTDDVQAEKESGPTT 319
 QY 214 ----FTLTNNIDSEDAAYVFLQHDNPLTF 241
 DB 320 YKVTSTLTIKESDWSQSMFTC-RVDHRLT 350

RESULT 8

ID Q925S1 PRELIMINARY; PRT; 218 AA.
 AC Q925S1;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE MRPs (Fragment).
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 RA Su C.;
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 RT the repair of intestinal epithelium after irradiation in mice.";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain.";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240168; AA03733.1; -
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 218
 SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 34.1%; Score 456; DB 11; Length 218;
 Best Local Similarity 43.8%; Pred. No. 5.9e-28;
 Matches 98; Conservative 34; Mismatches 74; Indels 18; Gaps 4;

QY 1 QVQLQOMGAGLLKSGWGLSLTCAVSGASFGGYWMSWIRPPGKLEWIGELINHRGSTTY 59
 DB 3 QVQLQOMGAGLLKPSFTLSLTGCVGSGFGGYWMSWIRPPGKLEWIGELINHSGLTY 62
 QY 60 NPSLDGRVTLSDLTSTNQISLKLSTMTADTAAYVYCARVTAAGTS-----DYWGQGLT 118
 DB 63 ABEFKGAFASLSLSASTAYLQISLNKNEEDTAYFCRMWDYDGFAYWGGITVTVS--- 119
 QY 119 ASAPVGGSGSGSGSGSGSGSGSETTLTQSPAFMSATPGDKVTSCKASRDVD--- 174
 DB 120 -----SGGSGSGSGSGSGSDIVLQSPASLASVLSGQARTISCKASBVDNIGIS 170
 QY 175 DVNMVYQRPGEAPFIIEDATTLPVPGISPRFSGSGYGTDTFTT 218
 DB 171 FNMVFOQKPGQPPPLTLTYASKQSGVPAGLLASGSGTDFSLNI 214

RESULT 9

ID Q96EYO PRELIMINARY; PRT; 613 AA.
 AC Q96EYO;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AA011857.1; -
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_5.

DR SMART, SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KM Hypothetical protein.
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 33.2%; Score 443.5; DB 4; Length 613;
 Best Local Similarity 39.2%; Pred. No. 2e-26;
 Matches 129; Conservative 24; Mismatches 85; Indels 91; Gaps 12;

QY 1 QVLOQMGAGLKSNGTSLTCAVSGASFGYWMIRPPKGLMEIGINRSGTYYN 60
 DB 20 QVLOESGPGVLPKPEETLSLTCTVSGSGSISYYWMIROPKGLMEIGITSGSTYYN 79
 QY 61 PSIDGRVTISLDTSTNOISLKLSTMTADTAAYYCAR-----TYAGTSDYWGQGLTVTV 114
 DB 80 PSLKSRVTMSVDTSKQPSLKLSTVTAADTAAYYCARQWELPTVG--LFTWGGGLTVTV 137
 QY 115 SSGSASAPT-----GGGSGSGSGSGG-----GGGSGSGSTTLTQSPAFMS 155
 DB 138 SSGSASAPTLFPLVSCENSPDTSSVAAGCLAQDPLPDSITFSWKYKNSDISSTRGFS 197
 QY 156 ATPGRKVISCKA---SRDV---DDVNMVYQQRPG---EAPFIIID---ATTLPV 199
 DB 198 VLRGGKVAATSGVLLPSPKDVMOGTDEHVYCKVQHENGKNEKVVPLVIALPPEKSVFVP 257
 QY 200 -----GISPR-----FSGSGYGTD----- 213
 DB 258 PRDGFNPRKSKLICQATGFSFPROI QVSWLREGKQVSGVTDDVQAEKSGPTTYKV 317
 QY 214 -FTLTINNIDSEDAAYFCLQDNFPLTF 241
 DB 318 TSTLTIKESDMLSQSMFTC-RVDHRLTF 345

RESULT 10

Q723Y6 PRELIMINARY; PRT; 116 AA.

AC Q723Y6:
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Rearranged VH4-34 V gene segment (Fragment).
 GN VH4-34.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hodgkin lymphoma;
 RA Tinguey M., Rosenquist R., Sundstroem C., Amin R.M., Koppers R.,
 Hansmann M.L., Braunniger A.;
 RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma
 RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
 RT cell precursor in a germinal center."
 RL Submitted (May-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ564425; CAD92032.1; -.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 116 AA; 12902 MW; CE3DA846616C908 CRC64;

Query Match 32.7%; Score 437.5; DB 4; Length 116;
 Best Local Similarity 72.0%; Pred. No. 7.6e-27;
 Matches 85; Conservative 8; Mismatches 14; Indels 11; Gaps 1;

QY 1 QVLOQMGAGLKSNGTSLTCAVSGASFGYWMIRPPKGLMEIGINRSGTYYN 60
 DB 1 QVLOQMGAGLKSNGTSLTCAVSGASFGYWMIRPPKGLMEIGINRSGTYYN 60
 QY 61 PSIDGRVTISLDTSTNOISLKLSTMTADTAAYYCARVTAGTSDYWGQGLTVTVSSGS 118
 DB 61 PSLKSRVTISVDTSKQPSLKLSTVTAADTAAYYCAR-----GEIVVPAAS 107

RESULT 11

ID 095973 PRELIMINARY; PRT; 150 AA.

AC 095973:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VH4 heavy chain variable region precursor (fragment).
 GN IGM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
 RT "Clonal proliferation of IGM secreting B cell in the synovium of
 RT Behcet's patient with arthritis."
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF103795; AAC79084.1; -.
 DR HSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW SIGNAL.

FT CHAIN 1 19 POTENTIAL.
 FT NON TER 20 >150 VH4 HEAVY CHAIN VARIABLE REGION.
 FT NON TER 150 150
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 32.7%; Score 437; DB 4; Length 150;
 Best Local Similarity 68.0%; Pred. No. 1.1e-26;
 Matches 85; Conservative 13; Mismatches 25; Indels 2; Gaps 1;

QY 1 QVLOQMGAGLKSNGTSLTCAVSGASFGYWMIRPPKGLMEIGINRSGTYYN 58
 DB 20 QVLOESGPGVLPKPEETLSLTCTVSGSGSISYYWMIROPKGLMEIGITSGSTYYN 79
 QY 59 YNPISLGRVTISLDTSTNOISLKLSTMTADTAAYYCARVTAGTSDYWGQGLTVTVSSGS 118
 DB 80 YNPISLGRVTISVDTSKQPSLKLSTVTAADTAAYYCARLGMGAPFWMGHGTVTVSSGS 139
 QY 119 ASAPT 123
 DB 140 ASAPT 144

RESULT 12

Q9UL73 PRELIMINARY; PRT; 119 AA.

AC Q9UL73:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035041; AAD56277.1; -.

DR HSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_V; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON TER 119 119
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BD8686420EA0BE CRC64;

Query Match 31.2%; Score 416.5; DB 4; Length 119;
 Best Local Similarity 70.6%; Pred. No. 3.4e-25;
 Matches 84; Conservative 6; Mismatches 26; Indels 3; Gaps 1;

QY 1 QVQLQOMGAGLTKSWGTSLTCAVSGASFSGYWMIROPKGLWIGINHRGSTTN 60
 DB 1 QVQLQESGGLVLPSETSLTCTVSGSICSYWMIROPKGLWIGIYISGSTNTT 60
 QY 61 PSLDGRVTISLDTSTNQISLKTSMTPADTAVYVCARTVAGTS---DYWGQGLTVVSS 116
 DB 61 PSLKSRVTISVDRSKNQFSLKLSLTAADTAVYFCARLSNMGPYFQDYGQGLTVVSS 119

RESULT 13

Q6KX8 PRELIMINARY; PRT; 496 AA.

AC Q96KX8; PRELIMINARY; PRT; 496 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Lung;
 RA Strassberg R.
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016369; AAH16369.1; -.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_4.
 DR SMART; SM00406; IG_V; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 31.1%; Score 415.5; DB 4; Length 496;
 Best Local Similarity 42.8%; Pred. No. 2.4e-24;
 Matches 101; Conservative 20; Mismatches 54; Indels 61; Gaps 7;

QY 1 QVQLQOMGAGLTKSWGTSLTCAVSGASFS---GYWMIROPKGLWIGINHRGSTT 58
 DB 20 QVQLQESGGLVLPSETSLTCTVSGSISSSSYWMIROPKGLWIGIYISGSTNTT 79
 QY 59 YNPISLDGRVTISLDTSTNQISLKTSMTPADTAVYVCAR-----TVAGTSDYWGQGLTV 112
 DB 80 YNPISLKSRTVITSDTISKQSLKVRVTAADTAVYFCARHGVSRSRGTALDIYWGQGLTV 139
 QY 113 TVSSGASAPFTGGGGGGGGGGGGGGGGGGSETTLTQSPAFMSATPGDYVSIKCRASRDV 172
 DB 140 TVSSASAPFTSPK-----VFPISLCTSTQPDGNNVVIACIVQ--- 172
 QY 173 DDDVMMYQGRPGAPFIETDATTLPGISPRSGSGYGTDTLTINNI--DSEDA 227
 DB 173 ---GFPQEP-----LSVTWSSGGQ---VTAARNPPSQDAS 203

RESULT 14

Q72379 PRELIMINARY; PRT; 478 AA.

AC Q72379; PRELIMINARY; PRT; 478 AA.
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein DKFZP686K04218 (Fragment).
 DN DKFZP686K04218.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Human rectum tumor;
 RA Bloeker H., Boeher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fodor G., Han M., Wiemann S.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538066; CAD97996.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 30.2%; Score 403.5; DB 4; Length 478;
 Best Local Similarity 42.9%; Pred. No. 2e-23;
 Matches 100; Conservative 28; Mismatches 46; Indels 59; Gaps 10;

QY 1 QVQLQOMGAGLTKSWGTSLTCAVSGASFS---GYWMIROPKGLWIGINHRGSTT 58
 DB 19 QVQLQESGGLVLPSETSLTCTVSGSISGSDYWMIROPKGLWIGIYISGSTNTT 78
 QY 59 YNPISLDGRVTISLDTSTNQISLKTSMTPADTAVYVCARTVAGTS---DYWGQGLTVVSS 116
 DB 79 YNPISLKSRTVITSDTISKQSLKVRVTAADTAVYFCARHGVSRSRGTALDIYWGQGLTV 138
 QY 117 GSASAPFTGGGGGGGGGGGGGGGGGGSETTLTQSPAFMSATPGD-KVISICASRDVDD 175
 DB 139 ASPTSP-----KVFPISLDTSTQPDGNNVVIACIVQ----- 167
 QY 176 VMMYQGRPGAPFIETDATTLPGISPRSGSGYGTDTLTINNI--DSEDA 227
 DB 168 -GFPQEP-----LSVTWSSGGQ---VTAARNPPSQDAS 198

RESULT 15

Q72374 PRELIMINARY; PRT; 492 AA.

AC Q72374; PRELIMINARY; PRT; 492 AA.
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein DKFZP686C02218 (Fragment).
 DN DKFZP686C02218.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Human rectum tumor;
 RA Bloeker H., Boeher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fodor G., Han M., Wiemann S.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538077; CAD98001.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 29.8%; Score 398; DB 4; Length 492;
 Best Local Similarity 41.9%; Pred. No. 5.5e-23;
 Matches 98; Conservative 23; Mismatches 53; Indels 60; Gaps 8;

QY 1 QVQLQOMGAGLTKSWGTSLTCAVSGASFS---GYWMIROPKGLWIGINHRGSTT 58

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 52.0738 Seconds
(without alignments)
1372.754 Million cell updates/sec

Title: US-10-072-301-31

Perfect score: 1348
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPPLFGGKTKVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq.29Jan04:*

- 1: geneeqp19808:*
- 2: geneeqp19908:*
- 3: geneeqp20008:*
- 4: geneeqp20018:*
- 5: geneeqp20028:*
- 6: geneeqp20038:*
- 7: geneeqp20038s:*
- 8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	844	62.6	256	3	AAY55072 Interleuk
2	844	62.6	260	3	AAY55075 Single ch
3	844	62.6	367	3	AAY55078 Single ch
4	844	62.6	381	3	AAY55079 Single ch
5	844	62.6	519	3	AAY55080 Single ch
6	844	62.6	519	3	AAY55074 Single ch
7	844	62.6	626	3	AAY55081 Single ch
8	844	62.6	640	3	AAY55082 Single ch
9	822.5	61.0	259	3	AAB09778 Antiviral
10	822.5	61.0	259	4	AAB70885 TMV 54K P
11	811.5	60.2	251	5	ABP45038 Human Bly
12	811.5	60.2	909	2	AARS0092 Humanised
13	803	59.6	248	5	ABP45149 Human Bly
14	801.5	59.5	255	5	ABP45592 Human Bly
15	800.5	59.4	249	5	ABP45310 Human Bly
16	789	58.5	248	5	ABP45865 Human Bly
17	787	58.4	240	4	AAB46044 Human TF
18	787	58.4	240	4	AAB46045 Human TF
19	787	58.4	248	5	ABP45410 Human Bly
20	786	58.3	240	4	AAB46010 Human MTC
21	781.5	58.0	243	5	ABP45924 Human Bly
22	781.5	58.0	249	5	ABP45177 Human Bly
23	779.5	57.8	272	2	AAR21260 SCFV sequ
24	779.5	57.8	285	2	AAR484810 SCFV anti
25	779	57.8	240	4	AAB46011 Human MTC

26	779	57.8	240	4	AAB46012 Human MTC
27	777	57.6	249	5	AAB75150 Amino aci
28	777	57.6	250	5	ABP45163 Human Bly
29	775	57.5	240	4	AAB46006 Human MTC
30	773	57.3	240	4	AAB45596 Human MTC
31	772	57.3	240	4	AAB46009 Human MTC
32	772	57.3	240	4	AAB46039 Human TF
33	771	57.2	240	4	AAB46031 Human MTC
34	769	57.0	240	4	AAB46018 Human MTC
35	769	57.0	240	4	AAB46021 Human MTC
36	769	57.0	266	5	ABG97826 Human Bln
37	769	57.0	266	5	ABG35329 Thrombopo
38	767	56.9	240	4	AAB46013 Human MTC
39	767	56.9	240	4	AAB45992 Human MTC
40	767	56.9	240	4	AAB46017 Human MTC
41	767	56.9	240	4	AAB46014 Human MTC
42	766	56.8	240	4	AAB46040 Human TF
43	766	56.8	667	6	ABP97414 Anti-huma
44	765	56.8	240	4	AAB45997 Human MTC
45	765	56.8	240	4	AAB46038 Human TF

ALIGNMENTS

RESULT 1
AAY55072
ID AAY55072 standard; protein; 256 AA.

AC AAY55072;
DT 25-FEB-2000 (first entry)

DE Interleukin-6 specific ScFv protein sequence.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secreted functional protein; antigenic protein;
KW protein isolation; diagnosis; interleukin-6; ScFv.

OS Synthetic.
OS Homo sapiens.

PN WO9606113-A1.
PD 25-NOV-1999.
PF 30-APR-1999; 99WO-0P002341.
PR 20-MAY-1998; 98JP-00138652.
PR 01-OCT-1998; 98JP-00279876.
(CHUS) CHUGAI SEIYAKU KK.
Tauchiya M, Saito M, Ohtomo T;
WPI, 2000-039382/03.
N-PSDB; AA240291.

Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein.

Example 1; Page 54-56; 120pp; Japanese.

This sequence represents a ScFv specific for human interleukin-6. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secreted functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for

CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein
 XX
 SQ Sequence 256 AA;

Query Match 62.6%; Score 844; DB 3; Length 256;
 Best Local Similarity 65.6%; Pred. No. 3.1e-49;
 Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRTTGEVGVWRQPPGKALEWLIYWDDEK 60
 DB 1 QVQLQESGPGIIVRSQTLSTCTVSGYSI-TSDHAWMWRQPPGKLEWIGYISGITT 59
 QY 61 YSPSLKSLTITTKDTSKKQVLTMTNVPADTATYCTHEQYYDTSGQPYFDFWGGQT 120
 DB 60 YNPSLKSRVTMLRDTSKNQFSLRLSSVTADTAVYYCAR-----SLARTAMDYWGQS 113
 QY 121 LVTWSSGGGSGGSGGSGGSGGSGNIGVTSPSLSASVGDRTVMTCRASQDIRKNLN 180
 DB 114 LVTWV-----SGGGSGGSGGSGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 168
 QY 181 WYQQRKAPKVLIIYDASDLGTGIPSRFSGSGSGTDFLITLISLQPEDIATYYCCQGSYL 240
 DB 169 WYQQRKAPKVLIIYTSRLHSGVPSRFSGSGSGTDFLTISLQPEDIATYYCCQGNLT 228
 QY 241 PLTFGGGTGVNDIK 253
 DB 229 PYTFGGGTGVNDIK 241

RESULT 2
 ID AAY55075 standard; protein; 260 AA.

XX AAY55075;

DT 25-FEB-2000 (first entry)

XX Single chain Fv protein sequence shPM1(deltaBL).

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KM antigen-binding cell; secretable functional protein; antigenic protein;
 KM protein isolation; diagnosis; ScFv.

XX Synthetic.

XX MO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Teuchiya M, Saito M, Ohtomo T;

XX WPI; 2000-039382/03.

XX N-PSDB; AA240305.

XX Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.

XX Example 7; Page 80-82; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
 CC relates to a method for isolating a gene encoding a membrane-bound
 CC protein, comprising introducing a vector into a cell, contacting an

CC antigen with the cell expressing the fused protein encoded by the vector
 CC on its surface to select an antigen-binding cell, and isolating the cDNA.
 CC The vector contains DNA encoding a secretable functional protein with
 CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
 CC of the 3' end of the coding sequence. The method can be used to isolate a
 CC membrane-bound protein for diagnosis and study. It can also be used for
 CC producing drugs treating abnormal functions of the protein. Such a
 CC technique is efficient and selective, which is different from the prior-
 CC art transmembrane trap (TMT) method wherein an epitope recognised by an
 CC antibody is carried in a fused protein
 XX
 SQ Sequence 260 AA;

Query Match 62.6%; Score 844; DB 3; Length 260;
 Best Local Similarity 65.6%; Pred. No. 3.1e-49;
 Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRTTGEVGVWRQPPGKALEWLIYWDDEK 60
 DB 20 QVQLQESGPGIIVRSQTLSTCTVSGYSI-TSDHAWMWRQPPGKLEWIGYISGITT 78
 QY 61 YSPSLKSLTITTKDTSKKQVLTMTNVPADTATYCTHEQYYDTSGQPYFDFWGGQT 120
 DB 79 YNPSLKSRVTMLRDTSKNQFSLRLSSVTADTAVYYCAR-----SLARTAMDYWGQS 132
 QY 121 LVTWSSGGGSGGSGGSGGSGGSGNIGVTSPSLSASVGDRTVMTCRASQDIRKNLN 180
 DB 133 LVTWV-----SGGGSGGSGGSGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 187
 QY 181 WYQQRKAPKVLIIYDASDLGTGIPSRFSGSGSGTDFLITLISLQPEDIATYYCCQGSYL 240
 DB 188 WYQQRKAPKVLIIYTSRLHSGVPSRFSGSGSGTDFLTISLQPEDIATYYCCQGNLT 247
 QY 241 PLTFGGGTGVNDIK 253
 DB 248 PYTFGGGTGVNDIK 260

RESULT 3
 ID AAY55078 standard; protein; 367 AA.

XX AAY55078;

DT 25-FEB-2000 (first entry)

XX Single chain Fv protein sequence shPM1-Kappa.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KM antigen-binding cell; secretable functional protein; antigenic protein;
 KM protein isolation; diagnosis; ScFv.

XX Synthetic.

XX MO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP002341.

XX 20-MAY-1998; 98JP-00138652.

XX 01-OCT-1998; 98JP-00279876.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Teuchiya M, Saito M, Ohtomo T;

XX WPI; 2000-039382/03.

XX N-PSDB; AA240308.

XX Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs treating abnormal functions of the protein.

XX Example 7; Page 86-89; 120pp; Japanese.

PS This sequence represents a single chain Fv (ScFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
XX protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein

SQ Sequence 367 AA;

Query Match 62.6%; Score 844; DB 3; Length 367;
Best Local Similarity 65.6%; Pred. No. 4, 4e-49;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFCGFSRLTTEGEGVWROPKALMIALIYMDDDR 60
DB 20 QVQLQESGPGVLRPSQTSLTCTVSGYSI-TSDHMSWRQPRGRLEWIGYISYGITT 78
QY 61 YSPSLKSRITTKDTSKQVVLMTNVPADATATYYCTHEQYYDTSGQPYYPDFWGQGT 120
DB 79 YNPSLKSRYTMDRLTSKNQPSLRSLSSVTADAVYYCAR-----SIARTTAMDYWGQGS 132
QY 121 LVTVSSGGSGSGSGSGSGSGSGSNIGVTSPLSLASVGDRLYMTTRAQODIRKNN 180
DB 133 LVTVS-----SGSGSGSGSGSGSGSDIQMTQSPSLSLASVGDRLYMTTRAQODISSYLN 187
QY 181 WTQOKRGKAPKVLIDASDLDTGIPSRFSGSGSGTDFITLISLQPEDIAATYYCCQSDYL 240
DB 188 WTQOKRGKAPKVLIIYTSRLHSGVPSRFSGSGSGDTFTTISLSLOPEDIAATYYCCQGNLT 247
QY 241 PLTFGGGTAKVDIK 253
DB 248 PYTFGGGTAKVEIK 260

RESULT 4

AAVS5079 standard; protein; 381 AA.

AAVS5079;

25-FEB-2000 (first entry)

Single chain Fv protein sequence shPM1-MCH4.

Gene isolation; membrane-bound protein; fusion protein; drug production;
antigen-binding cell; secretable functional protein; antigenic protein;
protein isolation; diagnosis; ScFv.

Synthetic.

MO9960113-A1.

25-NOV-1999.

30-APR-1999; 99WO-JP002341.

20-MAY-1998; 98JP-00138652.

01-OCT-1998; 98JP-00279876.

(CHUS) CHUGAI SEIYAKU KK.

Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AA240309.

XX Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.

PS Example 7; Page 90-94; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein

SQ Sequence 381 AA;

Query Match 62.6%; Score 844; DB 3; Length 381;
Best Local Similarity 65.6%; Pred. No. 4, 4e-49;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFCGFSRLTTEGEGVWROPKALMIALIYMDDDR 60
DB 20 QVQLQESGPGVLRPSQTSLTCTVSGYSI-TSDHMSWRQPRGRLEWIGYISYGITT 78
QY 61 YSPSLKSRITTKDTSKQVVLMTNVPADATATYYCTHEQYYDTSGQPYYPDFWGQGT 120
DB 79 YNPSLKSRYTMDRLTSKNQPSLRSLSSVTADAVYYCAR-----SIARTTAMDYWGQGS 132
QY 121 LVTVSSGGSGSGSGSGSGSGSNIGVTSPLSLASVGDRLYMTTRAQODIRKNN 180
DB 133 LVTVS-----SGSGSGSGSGSGSGSDIQMTQSPSLSLASVGDRLYMTTRAQODISSYLN 187
QY 181 WTQOKRGKAPKVLIDASDLDTGIPSRFSGSGSGTDFITLISLQPEDIAATYYCCQSDYL 240
DB 188 WTQOKRGKAPKVLIIYTSRLHSGVPSRFSGSGSGDTFTTISLSLOPEDIAATYYCCQGNLT 247
QY 241 PLTFGGGTAKVDIK 253
DB 248 PYTFGGGTAKVEIK 260

RESULT 5

AAVS5080 standard; protein; 519 AA.

AAVS5080;

25-FEB-2000 (first entry)

Single chain Fv protein sequence shPM1(deltaEL)-BVGSG3.

Gene isolation; membrane-bound protein; fusion protein; drug production;
antigen-binding cell; secretable functional protein; antigenic protein;
protein isolation; diagnosis; ScFv.

Synthetic.

MO9960113-A1.

25-NOV-1999.

30-APR-1999; 99WO-JP002341.

20-MAY-1998; 98JP-00138652.

```
PR 01-OCT-1998; 98JP-00279876.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Saito M, Ohtomo T;
XX
XX MPI; 2000-039382/03.
XX
XX N-PSDB; AAZ40312.
XX
XX Efficient and selective isolation of a gene encoding membrane protein
XX with low or no antigenic binding activity, for diagnosis, study of, and
XX production of drugs treating abnormal functions of the protein.
XX
XX Example 7; Page 95-100; 120pp; Japanese.
XX
XX This sequence represents a single chain Fv (ScFv) sequence. The invention
XX relates to a method for isolating a gene encoding a membrane-bound
XX protein, comprising introducing a vector into a cell, contacting an
XX antigen with the cell expressing the fused protein encoded by the vector
XX on its surface to select an antigen-binding cell, and isolating the cDNA.
XX The vector contains DNA encoding a secretable functional protein with
XX antigenicity and binding affinity, and a cDNA ligated to DNA downstream
XX of the 3' end of the coding sequence. The method can be used to isolate a
XX membrane-bound protein for diagnosis and study. It can also be used for
XX producing drugs treating abnormal functions of the protein. Such a
XX technique is efficient and selective, which is different from the prior-
XX art transmembrane trap (TMT) method wherein an epitope recognised by an
XX antibody is carried in a fused protein
XX
XX Sequence 519 AA;
SQ
Query Match 62.6%; Score 844; DB 3; Length 519;
Best Local Similarity 65.6%; Pred. No. 6.2e-49;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;
XX
XX 1 QVTLKSGPTLVKPTQTTLTCTFSGFSIRTTGEGVWROPFGKALEMLALTYMDDDR 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 20 QVQLQSSGGGLVFRPQGLTSLCTVSGYSI-TSDHMSWVRQPGRLGIWIGTISYGI 78
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 YSPSLKSRLLITTKDTSKKQVLTMTNVPADATATYCTHKGYYDTSGQPYFDFMGQGT 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 79 YNPSLKSRYTMLRDTSKNCFSLRLSSVTADTAVYYCAR-----SLARTTAMDYWGQS 132
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 121 LVTVSSGGGSGGGSGGGSGGSGNIGVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 133 LVTVS-----SGGSGSGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 187
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 181 WYQQRGKAPKVLITDASLETGIPSRFSGSGSGDTFILITISLSLOPEDATATYCCQSDYL 240
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 188 WYQQRGKAPKLLIYTSRLHSGVPSRFSGSGSDTFTLTISLSLOPEDATATYCCQGNLT 247
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 241 PLTFGGGTQVDIK 253
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 248 PYTFGGGTQVKEIK 260
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX RESULT 6
XX AA155074 standard; protein; 546 AA.
XX ID AAY55074;
XX AC AAY55074;
XX
XX 25-FEB-2000 (first entry)
XX
XX Single chain Fv protein sequence hPM1-BVGS3.
XX
XX Gene isolation; membrane-bound protein; fusion protein; drug production;
XX antigen-binding cell; secretable functional protein; antigenic protein;
XX protein isolation; diagnosis; ScFv.
XX
XX Synthetic.
XX
XX OS
XX
XX PN WO960113-A1.
```

```
XX
XX 25-NOV-1999.
XX
XX 30-APR-1999; 99WO-JP002341.
XX
XX 20-MAY-1998; 98JP-00138652.
XX
XX 01-OCT-1998; 98JP-00279876.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Saito M, Ohtomo T;
XX
XX MPI; 2000-039382/03.
XX
XX N-PSDB; AAZ40303.
XX
XX Efficient and selective isolation of a gene encoding membrane protein
XX with low or no antigenic binding activity, for diagnosis, study of, and
XX production of drugs treating abnormal functions of the protein.
XX
XX Example 5; Page 73-78; 120pp; Japanese.
XX
XX This sequence represents a single chain Fv (ScFv) sequence. The invention
XX relates to a method for isolating a gene encoding a membrane-bound
XX protein, comprising introducing a vector into a cell, contacting an
XX antigen with the cell expressing the fused protein encoded by the vector
XX on its surface to select an antigen-binding cell, and isolating the cDNA.
XX The vector contains DNA encoding a secretable functional protein with
XX antigenicity and binding affinity, and a cDNA ligated to DNA downstream
XX of the 3' end of the coding sequence. The method can be used to isolate a
XX membrane-bound protein for diagnosis and study. It can also be used for
XX producing drugs treating abnormal functions of the protein. Such a
XX technique is efficient and selective, which is different from the prior-
XX art transmembrane trap (TMT) method wherein an epitope recognised by an
XX antibody is carried in a fused protein
XX
XX Sequence 546 AA;
SQ
Query Match 62.6%; Score 844; DB 3; Length 546;
Best Local Similarity 65.6%; Pred. No. 6.5e-49;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;
XX
XX 1 QVTLKSGPTLVKPTQTTLTCTFSGFSIRTTGEGVWROPFGKALEMLALTYMDDDR 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 20 QVQLQSSGGGLVFRPQGLTSLCTVSGYSI-TSDHMSWVRQPGRLGIWIGTISYGI 78
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 YSPSLKSRLLITTKDTSKKQVLTMTNVPADATATYCTHKGYYDTSGQPYFDFMGQGT 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 79 YNPSLKSRYTMLRDTSKNCFSLRLSSVTADTAVYYCAR-----SLARTTAMDYWGQS 132
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 121 LVTVSSGGGSGGGSGGGSGGSGNIGVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 133 LVTVS-----SGGSGSGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 187
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 181 WYQQRGKAPKVLITDASLETGIPSRFSGSGSGDTFILITISLSLOPEDATATYCCQSDYL 240
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 188 WYQQRGKAPKLLIYTSRLHSGVPSRFSGSGSDTFTLTISLSLOPEDATATYCCQGNLT 247
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 241 PLTFGGGTQVDIK 253
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 248 PYTFGGGTQVKEIK 260
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX RESULT 7
XX AA155081 standard; protein; 626 AA.
XX ID AAY55081;
XX AC AAY55081;
XX
XX 25-FEB-2000 (first entry)
XX
XX Single chain Fv protein sequence shPM1-kappa-BVGS3.
XX
XX Gene isolation; membrane-bound protein; fusion protein; drug production;
```

KW antigen-binding cell; secretable functional protein; antigenic protein;
XX protein isolation; diagnosis; ScFv.
OS Synthetic.
XX WO960113-A1.
XX PD 25-NOV-1999.
XX PF 30-APR-1999; 99WO-JP002341.
XX PR 20-MAY-1998; 98JP-00138652.
XX PR 01-OCT-1998; 98JP-00279876.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Saito M, Ohtomo T;
XX DR WPI; 2000-039382/03.
XX DR N-PSDB; AA240316.
XX PT Efficient and selective isolation of a gene encoding membrane protein
XX with low or no antigenic binding activity, for diagnosis, study of, and
XX production of drugs treating abnormal functions of the protein.
XX Example 7; Page 103-109; 120pp; Japanese.
PS
CC This sequence represents a single chain Fv (ScFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein
XX
XX
SQ Sequence 626 AA;
Query Match 62.6%; Score 844; DB 3; Length 626;
Best Local Similarity 65.6%; Pred. No. 7.4e-49;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;
QY 1 QVTLKESGPTLVKPTQTLTLCTFGSFLRTTGEVGVWRQPPGKALEWALITYMDDDR 60
DB 20 QVQLQSSGGGLVFRPSTLSITCTVSGYST-TSDHMSWRQPRGRLEWIGYISGITT 78
QY 61 YSPSLKSRITLTITKDTISKQVLTMTNVDPAADTATYYCTHEQYYDTSGQPYYPDFWGQGT 120
DB 79 YNPSSLKSRVTMLRDTISKQFSLRLSSVTADTAVYYCAR-----SLARTTAMDYWGQGS 132
QY 121 LVTVSSGGGSGGGSGGGSGGSGGSGNIOVTPSSLSASVGDRTVMTCRASODIRKNN 180
DB 133 LVTVS-----SGGSGSGGGSGGGSGGSDIQWTPSSLSASVGDRTVITCRASODISSYNN 187
QY 181 WYQQRKGAKPKVLIYDASDLETGIPSRFSGSGGTDFTLTISLSLPEDATATYYCQSQDYL 240
DB 188 WYQQRKGAKPKVLIYTSRLHSGVSPSRFSGSGGTDFTLTISLSLPEDATATYYCQSQGNTL 247
QY 241 PLTFGGGTVDIK 253
DB 248 PYTFGGGTVEIK 260

RESULT 8
ID AA155082 standard; protein; 640 AA.
XX
AC AA155082;

XX
DT 25-FEB-2000 (first entry)
XX
DE Single chain Fv protein sequence sHPM1-MCH4-BVGS3.
KW Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
XX
OS Synthetic.
XX WO960113-A1.
XX PD 25-NOV-1999.
XX PF 30-APR-1999; 99WO-JP002341.
XX PR 20-MAY-1998; 98JP-00138652.
XX PR 01-OCT-1998; 98JP-00279876.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Saito M, Ohtomo T;
XX DR WPI; 2000-039382/03.
XX DR N-PSDB; AA240321.
XX PT Efficient and selective isolation of a gene encoding membrane protein
XX with low or no antigenic binding activity, for diagnosis, study of, and
XX production of drugs treating abnormal functions of the protein.
XX Example 7; Page 111-117; 120pp; Japanese.
PS
CC This sequence represents a single chain Fv (ScFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretable functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein
XX
XX
SQ Sequence 640 AA;
Query Match 62.6%; Score 844; DB 3; Length 640;
Best Local Similarity 65.6%; Pred. No. 7.6e-49;
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;
QY 1 QVTLKESGPTLVKPTQTLTLCTFGSFLRTTGEVGVWRQPPGKALEWALITYMDDDR 60
DB 20 QVQLQSSGGGLVFRPSTLSITCTVSGYST-TSDHMSWRQPRGRLEWIGYISGITT 78
QY 61 YSPSLKSRITLTITKDTISKQVLTMTNVDPAADTATYYCTHEQYYDTSGQPYYPDFWGQGT 120
DB 79 YNPSSLKSRVTMLRDTISKQFSLRLSSVTADTAVYYCAR-----SLARTTAMDYWGQGS 132
QY 121 LVTVSSGGGSGGGSGGGSGGSGGSGNIOVTPSSLSASVGDRTVMTCRASODIRKNN 180
DB 133 LVTVS-----SGGSGSGGGSGGGSGGSDIQWTPSSLSASVGDRTVITCRASODISSYNN 187
QY 181 WYQQRKGAKPKVLIYDASDLETGIPSRFSGSGGTDFTLTISLSLPEDATATYYCQSQDYL 240
DB 188 WYQQRKGAKPKVLIYTSRLHSGVSPSRFSGSGGTDFTLTISLSLPEDATATYYCQSQGNTL 247
QY 241 PLTFGGGTVDIK 253
DB 248 PYTFGGGTVEIK 260

Matches 156; Conservative 39; Mismatches 53; Indels 7; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTBEGVGNWROPGRKALEWLAIIYWD DDKR 60
 DB 3 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTBEGVGNWROPGRKALEWLAIIYWD DDKR 62
 QY 61 YSPSLKSRLLTTTKDTSKQVVLTMNVDPADATATYCTHBOYYTSGOPYFDFWGQGT 120
 DB 63 YNPSLRSLTITSKDTSRNVQFLRITNVDTADTATYTCARGYGNDSP-----FATWGQGT 117
 QY 121 LVTYSSGGGGGGGGGGGGGGG--GGSNIQVTSPPSLASVDRVTMTCRASQDRIKN 178
 DB 118 LITVSSGAGPTSGSGKPGPBGSTGKAPDIVLSQSPKFWSTVGDVRVSTICRASQIVRTA 177
 QY 179 LNMVQKRGKAPKULIYDASDLRTGIPSRFSGSGSGTPIILTSSLOPEDATATYCCQSD 238
 DB 178 VAMFOQKGGQSPKALIIYASNHTGTVPDRFTSGSGGTFTLITISNVQSDLDLADYCLQHW 237
 QY 239 YLPLTFGGGTGYDIK 253
 DB 238 NYPLTFGGGTGYDIK 252

RESULT 11
 ABP45038
 ID ABP45038 standard; protein; 251 AA.
 AC ABP45038;
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding acfv seq ID 1049.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN MO200202641-A1.
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMP-) CAMBRIDGE ANTI BODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI, 2002-114799/15.
 DR
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 FT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 1654-1655; 3148p; English.
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and actively such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

SQ Sequence 251 AA;
 XX
 QY Query Match 60.2%; Score 811.5; DB 5; Length 251;
 DB Beert Local Similarity 63.0%; Pred. No. 4.7e-47;
 Matches 160; Conservative 31; Mismatches 56; Indels 5; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTBEGVGNWROPGRKALEWLAIIYWD DDKR 60
 DB 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTBEGVGNWROPGRKALEWLAIIYWD DDKR 60
 QY 61 YSPSLKSRLLTTTKDTSKQVVLTMNVDPADATATYCTHBOYYTSGOPYFDFWGQGT 120
 DB 61 YSPSLKSRLLTTTKDTSKQVVLTMNVDPADATATYCTHBOYYTSGOPYFDFWGQGT 119
 QY 121 LVTYSSGGGGGGGGGGGGGGG--GGSNIQVTSPPSLASVDRVTMTCRASQDRIKN 180
 DB 120 LVTYSSGGGGGGGGGGGGGGG--ALEIVLTQSPSLASVDRVTMTCRASQDRIKN 176
 QY 181 WYQKRGKAPKULIYDASDLRTGIPSRFSGSGSGTPIILTSSLOPEDATATYCCQSD 240
 DB 177 WYQKRGKAPKULIYDASDLRTGIPSRFSGSGSGTPIILTSSLOPEDATATYCCQSD 236
 QY 241 P-LTFGGGTGYDIK 253
 DB 237 P-LTFGGGTGYDIK 250

RESULT 12
 AAR50092
 ID AAR50092 standard; protein; 909 AA.
 AC AAR50092;
 DT 25-MAR-2003 (revised)
 DT 26-OCT-1994 (first entry)
 XX
 DE Humanised anti-CEA sFv fragment-human beta-glucuronidase fusion protein.
 XX
 KW Carcinoembryonic antigen; single chain variable region; sFv fragment;
 KW fusion gene; cancer treatment; targeted drug delivery; tumour.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal_peptide
 FT Protein 20..909
 FT /label= fusion_protein
 FT /note= "humanised anti-CEA sFv fragment fused to human
 FT beta-glucuronidase"
 XX
 FN EP590530-A2.
 PD 06-APR-1994.
 XX
 PF 24-SEP-1993; 93BP-00115418.
 XX
 PR 02-OCT-1992; 92DE-04233152.
 XX
 PA (BEHM) BEHRINGWERKE AG.
 XX
 PI Gehrman M, Seemann G, Boseslet K, Czech J;

```
XX WPI; 1994-111012/14.
DR N-PSDB; AAO58896.
XX
XX PT New fusion protein contg. enzyme for prodng activation - coupled to
PT antigen binding component, esp. sFv antibody fragmant, partic. for
PT treatment of tumours.
XX
XX PS Claim 13; Page 12-15; 35pp; German.
XX
CC The sequence AAR50092 comprises a humanised sFv-fragment against CEA
CC fused to a human beta-glucuronidase. The fusion protein is useful for
CC targeting beta-glucuronidase to cancer cells expressing CEA, where the
CC enzyme is able to convert a prodng into its active form. Any fusion
CC protein not bound to tumour can be removed by internalisation via the
CC mannose-6-phosphate and galactose receptors. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX SQ Sequence 909 AA;

Query Match      60.2%; Score 811.5; DB 2; Length 909;
Best Local Similarity 63.6%; Pred. No. 1.7e-46;
Matches 161; Conservative 30; Mismatches 49; Indels 13; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGPSLRTGEGVWVROPKALFEMALIIYDDDKR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   20 QVQLQSGPGQVLRPSGTLSTCTVSGFTLSSGYSWVWRQPPGRGLEWIGYIQSGITN 78
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YSPSLKSLRTITTKDTSKKQVLTMTNVDPADTATYYCTHEQYYDTSGQPYFPDWGQGT 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   79 YNPSLKSRVTMLVDTSKQPSLRISVTADTAVVYCARBDYDH----WYFDVWGQGT 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LVTYSSGGGSGGGSGGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASQDIRKLN 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   134 YTVTVS-----SGGGSGGGSGGGSGGSDIQLTQSPSLASVGDRTVITCTSSSV-SYTH 187
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 WYQQRKGAAPKVLIDASDLETGIPSRFSGSGGTDPIITLISLQEDIAIYYCQGSDDL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   188 WYQQRKGAAPKVLIDTSNLSAGVPSRFSGSGGTDFTLTISLQEDIAIYYCQWMSY 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 PLTFGGGTGVNDIK 253
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 248 P-TFGGQTRLRIRK 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
ID ABP45349 standard; protein; 248 AA.
XX
XX AC ABP45349;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human Blys binding scFv SEQ ID 1360.
XX
XX BYs; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX OS Homo sapiens.
XX
XX PN WO200202641-A1.
XX
XX PD 10-JAN-2002.
XX
XX PF 15-JUN-2001; 2001WO-US019110.
XX
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
```

```
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX DR WPI; 2002-114799/15.
XX
XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX PS Claim 1; Page 2025-2026; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX SQ Sequence 248 AA;

Query Match      59.6%; Score 803; DB 5; Length 248;
Best Local Similarity 63.2%; Pred. No. 1.7e-46;
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGPSLRTGEGVWVROPKALFEMALIIYDDDKR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   1 QVQLQSGPGVLRPSGTLSTCTVSGSIRS--YVWSVIRQSPGKGLWIGHIYHSGSTD 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YSPSLKSLRTITTKDTSKKQVLTMTNVDPADTATYYCTHEQYYDTSGQPYFPDWGQGT 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   59 YNPSLKSRVTMISIDTSKQPSLNLISYAADTAVYCARHDYDVLTSYLAQFDWGGGT 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LVTYSSGGGSGGGSGGGSGGSGGSGGSGNIQVTPSSLSASVGDRTVMTCRASQDIRKLN 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   119 LVTYSSGGGSGGGSGGGSGGSGS---ALDIQLTQSPSSLSASVGDRTVITCRASQSIGRYLN 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 WYQQRKGAAPKVLIDASDLETGIPSRFSGSGGTDPIITLISLQEDIAIYYCQGSDDL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   176 WYQQRKGAAPKVLIDTSNLSHSDVPSRFSGSGGTDFTLTISLQEDPATIYYCQGS-YT 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 PLTFGGGTGVNDIK 253
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 235 DPTFGGQTRLRIRK 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ID ABP45592 standard; protein; 255 AA.
XX
XX AC ABP45592;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human Blys binding scFv SEQ ID 1603.
XX
XX BYs; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX
```


KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2316-2317; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumor necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 255 AA;
XX
Query Match 59.5%; Score 801.5; DB 5; Length 255;
Best Local Similarity 62.0%; Pred. No. 2.2e-46;
Matches 163; Conservative 27; Mismatches 54; Indels 19; Gaps 6;
QY 1 QVTLKESGPTLVKPTQTLTLTCTFGSFLRTGEGVGNWRPGKALEMLALITY----WD 56
DB 1 QVQLOQSGGLVSPQTLTLSCAIGSDVSGNCAAMWIRQSPRLGLMIGRTYRSQWY 60
QY 57 DDKRYSPLSLKRLTITKDTSKKQVLTMTNVPADATATYCTHEQYVD--TSQOPY--- 112
DB 61 SP--YGASVRSRITTNADTSKQPSLQNLNVTPEDTAVYVCARBSRDIILTG--YISGG 116
QY 113 --FDWGGQTLVTSVSGGGSGGGSGGGSGGSGNIGVTSQPSLSASVGDRTVMTGR 170
DB 117 GGMVYWGRTGLTVTS-----SGGGSGGGSGGGSGGSDIGMTQSPSLASIGDRVITTCR 171
QY 171 ASODIKRLNLMWQKRGKAPKULIYDASLLEFGIPSRFEGSSGNDPFIITSSLPEDIA 230
DB 172 ASEGIVHMLAWYQKRGKAPKULLIYKASSLASGAPRFSGSGSDTDFLTITSSLPDDPA 231
QY 231 TTYCCQSDVLPPLFGGGRVDIK 253
DB 232 TTYCCQYSNVPPLFGGGRVDIK 254

RESULT 15
ABP45310
ID ABP45310 standard; protein; 249 AA.
XX
XX
AC ABP45310;
XX
XX
DT 19-AUG-2002 (first entry)
XX
XX
DE Human Blys binding scFv SEQ ID 1321.
XX
XX
KW Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumor necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1979-1980; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumor necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;
XX
Query Match 59.4%; Score 800.5; DB 5; Length 249;
Best Local Similarity 64.3%; Pred. No. 2.5e-46;
Matches 164; Conservative 27; Mismatches 55; Indels 9; Gaps 4;
QY 1 QVTLKESGPTLVKPTQTLTLTCTFGSFLRTGEGVGNWRPGKALEMLALITYWDDKR 60
DB 1 QVQLOQWAGLKPSETLSTLCAYVGSF--SGYWSWIRQSPRLGLMIGISNIGSTN 58


```

Db      60  YNSVSVKGRITLISHDSSKNTFYLQNMSSLRAEDTAAYVYCGASHYFG----HWHFAMVQGT 115
Qy      121  LTVSSSGGGSGSGGGSGGGSGGGSGNSIQVTPSSLSASVGDVYTMTCRASDI----R 176
        116  LVTVS-----SRGGSGEGGGSGGGSGDIDLTSPSSLASVGDVRYITTCRASAKPVDGEGD 170
Db      177  KQNLNMYQOKRGKAPKVLIDASDLFTGIPSRPSGSGSTDTLITSSIQEPDIAITYYCOQ 236
        171  SYLNMYQOKRGKAPKVLITAASYLSSGVPSPSGSGSTDTLITSSIQEPDIAITYYCOQ 230
Qy      237  SDYLPLTFGGGTVDIK 253
        231  SHEDPYTFGGGTVEIK 247
Db

```

RESULT 5
 US-08-918-148-77
 : Sequence 77, Application US/08918148A
 : Patent No. 6342220
 : GENERAL INFORMATION:
 : APPLICANT: Adams, Camellia
 : APPLICANT: W.
 : APPLICANT: Carter, Paul J.
 : APPLICANT: Fendly, Brian M.
 : APPLICANT: Gurney, Austin L.
 : TITLE OF INVENTION: Against Anticodons
 : FILE REFERENCE: P0979
 : CURRENT APPLICATION NUMBER: US/08/918,148A
 : CURRENT FILING DATE: 1997-08-25
 : NUMBER OF SEQ ID NOS: 79
 : SEQ ID NO 77
 : LENGTH: 244
 : TYPE: PRT
 : ORGANISM: artificial
 US-08-918-148-77

Query Match	56.5%	Score 762;	DB 4;	Length 244;
Best Local Similarity	60.6%;	Pred. No. 1.9e-53;		
Matches 154;	Conservative 33;	Mismatches 51;	Indels 16;	Gaps 4

[illegible]

RESULT 6
US-08-887-352B-23
Sequence 23 Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1GE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

1
 2 CITY: South San Francisco
 3 STATE: California
 4 COUNTRY: USA
 5 ZIP: 94080
 6
 7 COMPUTER READABLE FORM:
 8 MEDIUM TYPE: 3.5 inch, 1.44 MB flo
 9 COMPUTER: IBM pc compatible
 10 OPERATING SYSTEM: PC-DOS/MS-DOS
 11 SOFTWARE: WinPatIn (Genentech)
 12 CURRENT APPLICATION DATA:
 13 APPLICATION NUMBER: US/08/887,352B
 14 FILING DATE: 03-Jul-1997
 15
 16 CLASSIFICATION: 530
 17
 18 ATTORNEY/AGENT INFORMATION:
 19 NAME: Svoboda, Craig G.
 20 REGISTRATION NUMBER: 39,044
 21 REFERENCE/DOCKET NUMBER: P1123
 22 TELECOMMUNICATION INFORMATION:
 23 TELEPHONE: 650/225-1489
 24
 25 TELEFAX: 650/952-9881
 26
 27 INFORMATION FOR SEQ ID NO: 23:
 28 SEQUENCE CHARACTERISTICS:
 29 LENGTH: 248 amino acids
 30 TYPE: Amino Acid
 31 TOPOLOGY: Linear
 32
 33 US-08-887-352B-23

Query Match	56.5%;	Score 762;	DB 2;	Length 248;
Best Local Similarity	60.3%;	Pred. No. 2e-53;		
Matches 155;	Conservative 32;	Mismatches 56;	Indels 14;	Gaps 4

QY 1 QVTLKSGSGTLYKPYQVTLTLCTFSGFSRLRTYBGEVWVRQPEKALBMLALTYMDDKR 60

Db 1 EVQLVDSGGGLVQPGGSLRLSCAVGSYSI-TSGYSMMNIRQAPKGLIEWVASIKYSGETK 59

QY 61 YSPSLKSLRTITKQDSKKQVLTMTNVDPADPATYTYCTHEBYYYDTSGGQPYYPDFMGQT 120

Db 60 YNSYVGRITTIIRSDDSKNTFYLDNMNLSLAEBPTAAYYCARSGSHYG---HHFPAWVGQT 115

QY 121 LVTWSSGGGGSGGGSGGGSGGGSGSNIQVTSQPSLSASVGDREVTMTCRASQDI----R 176

Db 116 LVTWVS-----SEGGGSEGGGSEGGGSDQLVQSPSLSASVGDNAVITITCRASKVDSQEGD 170

QY 177 KNINMTQQRKAPKAPVLIYDASDLETGIPSPRPSGGSGCTDFILTISSLQPEDIATYYCQ 236

Db 171 SYLNMTQQRKAPKRLIYYASVYLESQVSPRPSGGSGCTDFILTISSLQPEDFATYYCQ 230

QY 237 SDVLTPLTRGGGTRKVDIK 253

Db 231 SHEDPYTPGGTRKVEIK 247

```

RESULT 7
US-09-109-207C-23
: Sequence 23, Application US/09109207C
: Patent No. 6172213
: GENERAL INFORMATION:
: APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
: TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of Improving Polypeptide
: FILE REFERENCE: P1123R1
: CURRENT APPLICATION NUMBER: US/09/109,207C
: CURRENT FILING DATE: 1998-06-30
: PRIOR APPLICATION NUMBER: US 60/051,554
: PRIOR FILING DATE: 1997-07-03
: NUMBER OF SEQ ID NOS: 44
: SEQ ID NO 23
: LENGTH: 248
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: NAME/KEY: Artificial
: LOCATION: 1-248
: OTHER INFORMATION: sfp sequence derived from MAE11

```

US-09-109-207C-23

Query Match	56.5%	Score 762;	DB 3;	Length 248;
Best Local Similarity	60.3%;	Pred. No. 2e-53;		
Matches 155;	Conservative 32;	Mismatches 56;	Indels 14;	Gaps 4

QY 1 QVTLKESGPTLVKPKITQTLTLCTPBGSEFLRTTGBGVNRQPPGKALEMIALIYWDIDKR 60
Db 1 EVQLVESGGGLVQPGGSLRLISCAVGSYI -TSGYSMNRIQAPGKGLTGMVASIKTSGTK 59
QY 61 YSPSLKSRLLITTKDTSKKQVVLVTMTNVPADATATYTCHEQVYDDTSGQPYFDFWGGQT 120
Db 60 YNPVSKGRITISRDTSKNTFYLGWNSLRADETALVYYCARGSHYFG---HHHFAWGGQT 115
QY 121 LVYVSSGGGGGGGGSGGGSGGGSNNIQTQSPBSLSASVGDRTYMTGRASODI---R 176
Db 116 LVYVS-----SEGGSGEGSGEGGSDIQLQSPBSLSASVGDRTYITCRASKPVDGEGD 170
QY 177 KNLNMYOQKPKAKARVLIIYDASDETETGIPSRFSGSGSGTDFLITLTSIQPEDIAITYYQO 236
Db 171 SYLNWYQOQPKAPKRLIIYASYLESGVPSRFSGSGSGTDFTLTLSIQPEDPAITYYQO 230
QY 237 SDYLPPLFFGGGTXYDIK 253
Db 231 SHEDPYTFGGQTKEVEIK 247

RESULT 8
ITS-09-29

US-09-296-005-23

```

sequence 23; Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1998-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 23
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-248
OTHER INFORMATION: sFv sequence derived from MAE11
US-09-296-005-23

```

Query Match	56.5%;	Score 762;	DB 3;	Length 248;
Best Local Similarity	60.3%;	Pred. No. 2e-53;		
Matches 155;	Conservative 32;	Mismatches 56;	Indels 14;	Gaps 4;

[illegible]

RESULT 5

US-09-920-171-23
: Sequence 23, Application US/09920171

Patent No. 6682735
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardiou, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IGS Antibodies (as amended)

OTHER INFORMATION: sfv sequence derived from MAE11
US-09-920-171-23

[illegible]

RESULT 10
ITE-09-018

US-08-918-148-76

```

1 Sequence /6: Application US/089181A18A
2 Patent No. 6342220
3
4 GENERAL INFORMATION:
5 APPLICANT: Adams, Camellia
6 APPLICANT: W.
7 APPLICANT: Carter, Paul J.
8 APPLICANT: Applicant, Brian M.
9 APPLICANT: Gurney, Austin L.
10 TITLE OF INVENTION: Agonist Antibodies
11 FILE REFERENCE: P0979
12 CURRENT APPLICATION NUMBER: US/08/918.148A
13 CURRENT FILING DATE: 1997-08-25
14 NUMBER OF SEQ ID NOS: 79
15 SEQ ID NO 76
16 LENGTH: 245
17 TYPE: PRT
18 ORGANISM: artificial
19 US-08-918-148-76

```


STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-148

Query Match 54.5%; Score 734.5; DB 1; Length 240;
Best Local Similarity 57.9%; Pred. No. 2.9e-51;
Matches 147; Conservative 31; Mismatches 61; Indels 15; Gaps 4;

QY 1 QVTLKESGPTLVKPTOTLTLCTFGSFLRTGEGVGRQPPGKALEWIALI-YWDDK 59
DB 1 EIQLVQSGGGGLVPGSGVRISCAAGYTF--TWYGNWVRQAQKLEWNGWINTHTGP 58
QY 60 RYSPSLKSLRTITTKQTSKKQVLTMTNVPADATATYCTHEQYYDTSGOPYFDFWGG 119
DB 59 TYADSKGRFTSLDSKNTAVLIQINSLAEDTAVYFCRR-----GYDWYFDWGG 111
QY 120 TLVTVSSGGGGSGGGGGGGGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 179
DB 112 TLVTVS-----SGGGSGGGGGSGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 166
QY 180 NMYQOKRGKAPVLIYDASDLDTGIPSRPSGSGGTFILITISLOPEDATATYCCQSDY 239
DB 167 SMTQKPGAPKPLTILRANRLSGVPSRPSGSGGSDYTLTISLQYEDFGIYCCQYDE 226
QY 240 LPLTGGGTVDIK 253
DB 227 SPWTFGGGTLEMK 240

Search completed: May 13, 2004, 15:10:50
Job time: 13.8782 secs

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QY 181 WYQOKBKAARKLTYDASDIETCIPBPFEGSGSGTDFITLTSSLOPEDIATYRYCOOSDYL 240
Db 181 WYQOKBKAARKLVLYDSDLEIGPBFSGSGSGTDFITLTSSLOPEDIATYRYCOOSDYL 240
QY 241 PLTFGGGTVDIK 253
Db 241 PLTFGGGTVDIK 253

```

RESULT 2
US-10-072-301-31
: Sequence 31, Application US/10072301
: Publication No. US20030152913A1
: GENERAL INFORMATION:
: APPLICANT: Hua, Shao-bing
: APPLICANT: Pauling, Michelle H.
: APPLICANT: Zhu, Li
: TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
: TITLE OF INVENTION: VIRUS
: FILE REFERENCE: 25636-718
: CURRENT APPLICATION NUMBER: US/10/072,301
: CURRENT FILING DATE: 2002-02-08
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 31
: LENGTH: 253
: TYPE: PR1
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Clone 15.150.24 Variant
: US-10-072-301-31

```

	Query Match	100.0%	Score 1348	DB 14	Length 253
	Best Local Similarity	100.0%	Pred. No. 2e-87		
	Matches 253	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 QVTLKESGPTLVKPTQTLTLTCTESGFSRLRTGEGVMVQRPQKALEMIALIYMDDDR	60			
Db	1 QVTLKESGPTLVKPTQTLTLTCTESGFSRLRTGEGVMVQRPQKALEMIALIYMDDDR	60			
QY	61 YSPSLKSRLLTIKQDSKKQVLTMTNNDPATLAIYYCTHQQYYDDNSGQPIYDFPWGQT	120			
Db	61 YSPSLKSRLLTIKQDSKKQVLTMTNNDPATLAIYYCTHQQYYDDNSGQPIYDFPWGQT	120			
QY	121 LVTVSSGGGGSGGGSGGGSGGGSNIQVLTSPSSLASAVGDRVMTCRASODIRKNIIN	180			
Db	121 LVTVSSGGGGSGGGSGGGSGGGSNIQVLTSPSSLASAVGDRVMTCRASODIRKNIIN	180			
QY	181 WYQOKPQKAPKLIYDASDLETFGIPSPSPSGGSGTDPIILLTSSLOPEDIDAIYYCOOSDYL	240			
Db	181 WYQOKPQKAPKLIYDASDLETFGIPSPSPSGGSGTDPIILLTSSLOPEDIDAIYYCOOSDYL	240			
QY	241 PLTFGGGKTKVDIK	253			
Db	241 PLTFGGGKTKVDIK	253			

```

1  RESULT 3
2  US-10-071-866-23
3  / Sequence 23, Application US/10071866
4  / Publication No. US20030165988A1
5  / GENERAL INFORMATION:
6  / APPLICANT: Hua, Shao-bing
7  / APPLICANT: Pauling, Michelle H.
8  / APPLICANT: Zhu, Li
9  / TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
10 / TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
11 / FILE REFERENCE: 25636-717
12 / CURRENT APPLICATION NUMBER: US/10/071,866
13 / CURRENT FILING DATE: 2002-02-08
14 / NUMBER OF SEQ ID NOS: 54
15 / SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 23
;
; LENGTH: 253
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23

```

Query Match	100.0%	Score 1348	DB 14	Length 253
Best Local Similarity	100.0%	Pred. No. 2e-87		
Matches 253	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	QVTLKESGPTLVKPTQTLLTCTFSGSLRTGEGVGNVROP	PKALEMLALIYWD	DKR 60
Db	1	QVTLKESGPTLVKPTQTLLTCTFSGSLRTGEGVGNVROP	PKALEMLALIYWD	DKR 60
Qy	61	YSPSLKRLRLTTTKDTSKKQVLTMTNNDPADTALYYCTHEQYYDTS	SGQPYFDFW	GCGT 120
Db	61	YSPSLKRLRLTTTKDTSKKQVLTMTNNDPADTALYYCTHEQYYDTS	SGQPYFDFW	GCGT 120
Qy	121	LVTVSSGGGSGGGGSGGGGSGGGSNIQVOTSPSSLSASVGD	RVMTCRASODIR	KLN 180
Db	121	LVTVSSGGGSGGGGSGGGGSGGGGSGGGSNIQVOTSPSSLSASVGD	RVMTCRASODIR	KLN 180
Qy	181	WYQOKPKAKRVLIVYDASDLETGIPSRFSGSGGCTDILT	LSLQPEDIALYYCQ	GSYL 240
Db	181	WYQOKPKAKRVLIVYDASDLETGIPSRFSGSGGCTDILT	LSLQPEDIALYYCQ	GSYL 240
Qy	241	PLTFGGGT	KVDIK 253	
Db	241	PLTFGGGT	KVDIK 253	

```

RESULT 4
US-10-071-866-31
/ Sequence 31, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
/ TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Clone 15.150.24 Variant
/ US-10-071-866-31

```

	Query Match	100.0%	Score 1348	DB 14	Length 253
	Best Local Similarity	100.0%	Pred. No. 2e-87		
	Matches 253	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 QVTLKESGPTLVKKTQTLTLCTFSGSGLATTEGEGVWRPPGKALBWLAIYVDDDKR				60
Db	1 QVTLKESGPTLVKKTQTLTLCTFSGSGLATTEGEGVWRPPGKALBWLAIYVDDDKR				60
QY	61 YSPSLKSRLLITTKDTSKKQVLLMTNVDPADRTIYYCTHEQYYVYDTSGGPYVDFPWGGQT				120
Db	61 YSPSLKSRLLITTKDTSKKQVLLMTNVDPADRTIYYCTHEQYYVYDTSGGPYVDFPWGGQT				120
QY	121 LVVYSSGGSGSGSGSGSGSGSGSGNSIQVTPGSSLSASVSDRYTMTCRASQDTRKRLN				180
Db	121 LVVYSSGGSGSGSGSGSGSGSGSGNSIQVTPGSSLSASVSDRYTMTCRASQDTRKRLN				180
QY	181 WYQKPGKARKVLIIYASDLLETGIPSRFSGSGSGDTFIIITISLPEDPIATYYCQASDYL				240
Db	181 WYQKPGKARKVLIIYASDLLETGIPSRFSGSGSGDTFIIITISLPEDPIATYYCQASDYL				240

Db 181 WYQKRGKAPKVLIDASDLFTGIPSRFSGSGSDTDLTITSSLOPEDIATYYCCQSDYL 240
QY 241 PLTFGGGTRVDIK 253
Db 241 PLTFGGGTRVDIK 253

RESULT 5

US-10-360-828-23
Sequence 23, Application US/10360828
Publication No. US20030206909A1
GENERAL INFORMATION:
APPLICANT: Hua, Shaobing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727
CURRENT APPLICATION NUMBER: US/10/360,828
PRIOR FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133,978
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 253
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Clone 15.150.24
US-10-360-828-23

Query Match 100.0%; Score 1348; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVROPKALFEMALIIYWDDBR 60
Db 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVROPKALFEMALIIYWDDBR 60
QY 61 YSPSLKSLRTITKTQSKQVLTMTNVPADATATYCTHEQYYDTSGQPYFDFWGQGT 120
Db 61 YSPSLKSLRTITKTQSKQVLTMTNVPADATATYCTHEQYYDTSGQPYFDFWGQGT 120
QY 121 LVTSSGGGSGGGGSGGGGSGGSSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
Db 121 LVTSSGGGSGGGGSGGGGSGGSSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
QY 181 WYQKRGKAPKVLIDASDLFTGIPSRFSGSGSDTDLTITSSLOPEDIATYYCCQSDYL 240
Db 181 WYQKRGKAPKVLIDASDLFTGIPSRFSGSGSDTDLTITSSLOPEDIATYYCCQSDYL 240
QY 241 PLTFGGGTRVDIK 253
Db 241 PLTFGGGTRVDIK 253

RESULT 6

US-10-360-828-31
Sequence 31, Application US/10360828
Publication No. US20030206909A1
GENERAL INFORMATION:
APPLICANT: Hua, Shaobing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727
CURRENT APPLICATION NUMBER: US/10/360,828
CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133,978
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 253
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Clone 15.150.24 Variant
US-10-360-828-31

Query Match 100.0%; Score 1348; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVROPKALFEMALIIYWDDBR 60
Db 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVROPKALFEMALIIYWDDBR 60
QY 61 YSPSLKSLRTITKTQSKQVLTMTNVPADATATYCTHEQYYDTSGQPYFDFWGQGT 120
Db 61 YSPSLKSLRTITKTQSKQVLTMTNVPADATATYCTHEQYYDTSGQPYFDFWGQGT 120
QY 121 LVTSSGGGSGGGGSGGGGSGGSSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
Db 121 LVTSSGGGSGGGGSGGGGSGGSSNIQVTPSSLSASVGDRTVMTCRASQDIRKXNLN 180
QY 181 WYQKRGKAPKVLIDASDLFTGIPSRFSGSGSDTDLTITSSLOPEDIATYYCCQSDYL 240
Db 181 WYQKRGKAPKVLIDASDLFTGIPSRFSGSGSDTDLTITSSLOPEDIATYYCCQSDYL 240
QY 241 PLTFGGGTRVDIK 253
Db 241 PLTFGGGTRVDIK 253

RESULT 7

US-10-406-830-8
Sequence 8, Application US/10406830
Publication No. US20040071696A1
GENERAL INFORMATION:
APPLICANT: ADAMS, GREGORY P.
APPLICANT: WEINER, LOUIS M.
APPLICANT: HORAK, EVA M.

APPLICANT: JAMES, MARKS D.
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
FILE REFERENCE: 4077-000410US
CURRENT APPLICATION NUMBER: US/10/406,830
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/370,276
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic antibody.
US-10-406-830-8

Query Match 60.9%; Score 821.5; DB 12; Length 286;
Best Local Similarity 66.1%; Pred. No. 2.7e-50;
Matches 168; Conservative 28; Mismatches 43; Indels 15; Gaps 6;
QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVROPKALFEMALIIYWDDBR 60
Db 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVROPKALFEMALIIYWDDBR 60

```
Db 23 QVLOBSGPGVLKPSSTLSLTCTVSGGSPRS--YYMSWR-PGKGLEWIGITIFSGSTN 79
Qy 61 YPSLSKSRLLTTKDTSKKQVULMTNVPADTATYCTHEDYYDTSQPFDFWGGGT 120
Db 80 YNPSLSKSRVLTISVDTSKQVLSLCTVSGGFTSRTSYWGM:ROPKGPBEMIGNIYYTKTY 60
Qy 121 LVTVSSGGGGGGGGGGGGGSGGGSNIQVTPSPSLASVGDRTYMTCRASQDIRKUN 180
Db 135 LVTVS-----SSGGGGGGGGGGGGSDIQMTQSPSLASVGDRTYITCRASQDISVYN 189
Qy 181 WYQOKPGKAPKVLITDASDLEFGTISRFGSGSGTDFITLITSSLOPEDIATYTC-QQSDY 239
Db 190 WYQOKPGKAPKVLITDASDLEFGTISRFGSGSGTDFITLITSSLOPEDIATYTC-QQSDY 249
Qy 240 LPLTFGGGTGYDIK 253
Db 250 -PLTFGGGTGYDIK 262
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RESULT 8

```
US-09-880-748-1049
/ Sequence 1049, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1049
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1049
```

Query Match 60.2%; Score 811.5; DB 10; Length 251;

Best Local Similarity 63.0%; Pred. No. 1.2e-49;

Matches 160; Conservative 31; Mismatches 58; Indels 5; Gaps 3;

```
Qy 1 QVTLKESGPTLVKPTOTLTCTFGSFSRTTGEVGVWVROPKALEMIALIYMDDDR 60
Db 1 QVLOBSGPGVLKPSSTLSLTCTVSGGFTSRTSYWGM:ROPKGPBEMIGNIYYTKTY 60
Qy 61 YPSLSKSRLLTTKDTSKKQVULMTNVPADTATYCTHEDYYDTSQPFDFWGGGT 120
Db 61 YNPSLSKSRVLTISVDTSKQVLSLCTVSGGFTSRTSYWGM:ROPKGPBEMIGNIYYTKTY 119
Qy 121 LVTVSSGGGGGGGGGGGGGSGGGSNIQVTPSPSLASVGDRTYMTCRASQDIRKUN 180
Db 120 LVTVSSGGGGGGGGGGGGGSGGGSNIQVTPSPSLASVGDRTYMTCRASQDIRKUN 176
Qy 181 WYQOKPGKAPKVLITDASDLEFGTISRFGSGSGTDFITLITSSLOPEDIATYTC-QQSDY 240
Db 177 WYQOKPGKAPKVLITDASDLEFGTISRFGSGSGTDFITLITSSLOPEDIATYTC-QQSDY 236
Qy 241 P-LTFGGGTGYDIK 253
Db 237 P-LTFGGGTGYDIK 250
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RESULT 9

```
US-10-293-418-1049
/ Sequence 1049, Application US/10293418
/ Publication No. US20030223996A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PF523P2
/ CURRENT APPLICATION NUMBER: US/10/293,418
/ PRIOR FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1049
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-1049
```

Query Match 60.2%; Score 811.5; DB 12; Length 251;

Best Local Similarity 63.0%; Pred. No. 1.2e-49;

Matches 160; Conservative 31; Mismatches 58; Indels 5; Gaps 3;

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Qy 1 QVTLKESGPTLVKPTOTLTCTFGSFSRTTGEVGVWVROPKALEMIALIYMDDDR 60
Db 1 QVLOBSGPGVLKPSSTLSLTCTVSGGFTSRTSYWGM:ROPKGPBEMIGNIYYTKTY 60
Qy 61 YPSLSKSRLLTTKDTSKKQVULMTNVPADTATYCTHEDYYDTSQPFDFWGGGT 120
Db 61 YNPSLSKSRVLTISVDTSKQVLSLCTVSGGFTSRTSYWGM:ROPKGPBEMIGNIYYTKTY 119
Qy 121 LVTVSSGGGGGGGGGGGGGSGGGSNIQVTPSPSLASVGDRTYMTCRASQDIRKUN 180
Db 120 LVTVSSGGGGGGGGGGGGGSGGGSNIQVTPSPSLASVGDRTYMTCRASQDIRKUN 176
Qy 181 WYQOKPGKAPKVLITDASDLEFGTISRFGSGSGTDFITLITSSLOPEDIATYTC-QQSDY 240
Db 177 WYQOKPGKAPKVLITDASDLEFGTISRFGSGSGTDFITLITSSLOPEDIATYTC-QQSDY 236
Qy 241 P-LTFGGGTGYDIK 253
Db 237 P-LTFGGGTGYDIK 250
```

RESULT 10

```
US-09-880-748-1360
/ Sequence 1360, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
```


RESULT 13
US-10-293-418-1603
Sequence 1603, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1603
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1603

Query Match 59.5%; Score 801.5; DB 12; Length 255;
Best Local Similarity 62.0%; Pred. No. 6,1e-49; Indels 19; Gaps 6;
Matches 163; Conservative 27; Mismatches 54;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGPSLRTTGGVGVWVROPKALEWIALIY----WD 56
DB 1 QVQLQSGPGGLVKKSPQLSLSCAISGDSVGNAGAMWIRKQSPRGLEWIGRTYYSQWY 60
QY 57 DDKRYSPSLKRLTITKDTSKKQVVLMTNVDPADTATYCTHQQYYD-TSGQPY-- 112
DB 61 SD--YGASVRSRITINDTSKQPSLQNSVTPEDTAVYTCARSGRYDILTG--YSSG 116
QY 113 --PFWGQGLVTVSSGGGSGGGSGGSGGSGSNIOVTQSPSSLSASVGDRTVMTCR 170
DB 117 GGMVWNGRGLTVYS-----SGGGSGGGSGGGSGGSDIOMTQSPSTLSASIGDRTVITCR 171
QY 171 ASODIRKLNMYQOKPGAPKVLIVDASDLETGIPSRFSGSGSTDFILTTSSIQPEDIA 230
DB 172 ASEGIVHMLAWYQOKPGAPKVLIVKASLSLAGAPSRFSGSGSTDFILTTSSIQPEDFA 231
QY 231 TYCCQSDYLPLTFGGGTKVDIK 253
DB 232 TYCCQYSNYPLTFGGGTKLEIK 254

RESULT 14
US-09-880-748-1321
Sequence 1321, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1321
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1321

Query Match 59.4%; Score 800.5; DB 10; Length 249;
Best Local Similarity 64.3%; Pred. No. 7e-49; Indels 9; Gaps 4;
Matches 164; Conservative 27; Mismatches 55;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGPSLRTTGGVGVWVROPKALEWIALIYWD 60
DB 1 QVQLQSGPGGLVKKSPQLSLSCAISGDSVGNAGAMWIRKQSPRGLEWIGRTYYSQWY 58
QY 61 YSPSLKRLTITKDTSKKQVVLMTNVDPADTATYCTHQQYYD-TSGQPY-YFDFWQ 118
DB 59 YNPSLKRVTISVDTSKQPSLKLSTVADTAVYTCARSGRYDILTGIRIMFDFWGR 118
QY 119 GTLVTVSSGGGSGGGSGGGSGGSGGSGSNIOVTQSPSSLSASVGDRTVMTCRASQDIRKN 178
DB 119 GTLVTVS-----SGGGSGGGSGGGSGGSDIOMTQSPSTLSASVGDRTVITCRASQISSW 173
QY 179 LNWYQOKPGAPKVLIVDASDLETGIPSRFSGSGSTDFILTTSSIQPEDATYCCQSD 238
DB 174 LNWYQOKPGAPKVLIVKASLSLAGAPSRFSGSGSTDFILTTSSIQPEDATYCCQSY 233
QY 239 YLPLTFGGGTKVDIK 253
DB 234 STPWFQGGTKLEIK 248

RESULT 15
US-10-293-418-1321
Sequence 1321, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1321
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1321

Query Match 59.4%; Score 800.5; DB 12; Length 249;
 Best Local Similarity 64.3%; Pred. No. 7e-49;
 Matches 164; Conservative 27; Mismatches 55; Indels 9; Gaps 4;

```

Qy 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGEVGVWVROPKALEWLAIIYDDDR 60
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 QVQLQOQMGAGLIKPSSETLSITCAVYGGSF--SGYVSWIRPPKGLIEWIGIINSGSTN 58
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 61 YSPSLKSRLLTIKDDTSKKQVLTMTNVDPADTATYYCTHEQYYD-TSGQPY-YPDFWQ 118
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 59 YNPSLKSRVTISVDTSKNQFSLKSSVTADTAIVYICARGPRYYDILTGRYNWFDPWGR 118
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 119 GTLVTVSSGGGGSGGGSGGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 178
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 119 GTLVTVS-----SGGGSGGGSGGGSGGGSDIWMTQSPSTLSASVGDRTVITCRASQGISW 173
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 179 LNWYQQKPGKAPKVLIIYDASDLETGIPSRFSGSGSGGTFDPILTISIQPEDIAITYYCQGS 238
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 174 LAMWQQKPGRAPKVLIIYKASTLESQVPSRFSGSGSGTDPFTLTITSLQPEDPATYYCQGSY 233
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 239 YIPLTFGGGTXYDIK 253
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 234 STPWTFGGGTXYLEIK 248
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
  
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 Job time : 38.4587 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.4218 Seconds
(without alignments)
2130.694 Million cell updates/sec

Title: US-10-072-301-31

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTLTL.....CQSDYLPPLFCGGRKVDIK 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	45.3	268	2 A56446	Ig heavy chain V r
2	578.5	42.9	249	2 S41374	single chain Fv an
3	551	40.9	124	2 A49002	Ig heavy chain V r
4	538.5	39.9	138	2 S31513	Ig heavy chain - h
5	534.5	39.7	374	2 S69339	Ig heavy chain V r
6	533.5	39.6	233	2 JCS322	p53 specific singl
7	487	36.1	119	2 S18555	Ig heavy chain V r
8	485.5	36.0	125	1 MHHUMC	Ig heavy chain V-I
9	474.5	35.2	121	1 G1HUMH	Ig heavy chain V-I
10	470.5	34.9	118	2 S18556	Ig heavy chain V r
11	469.5	34.8	121	2 A36005	Ig heavy chain V r
12	468	34.7	108	1 K1HURY	Ig kappa chain V-I
13	468	34.7	129	2 S52789	Ig kappa chain V r
14	462	34.3	110	2 S44118	Ig kappa chain V-J
15	456	33.8	108	1 K1HUAU	Ig kappa chain V-I
16	456	33.8	108	2 B49047	Ig kappa chain V r
17	456	33.8	125	2 S40349	Ig kappa chain V-J
18	449	33.3	107	2 S36264	Ig lambda chain V
19	448	33.2	108	1 K1HUSW	Ig kappa chain V-I
20	447	33.2	107	2 S36269	Ig lambda chain V
21	445	33.0	122	2 S11740	Ig heavy chain pre
22	445	33.0	123	2 S40331	Ig kappa chain - h
23	443	32.9	108	2 S19674	Ig kappa chain V r
24	443	32.9	129	2 S52793	Ig kappa chain V r
25	442	32.8	108	1 K1HUGG	Ig kappa chain V-I
26	442	32.8	124	2 S40348	Ig kappa chain V-J
27	441	32.7	125	2 S40316	Ig kappa chain - h
28	441	32.7	127	2 S40367	Ig kappa chain V-J
29	440	32.6	107	2 S36262	Ig lambda chain V

30	439	32.6	129	2 S40317	Ig kappa chain - h
31	437	32.4	139	2 S40365	Ig kappa chain - h
32	435	32.3	108	1 K1HURE	Ig kappa chain V-I
33	435	32.3	108	1 K1HUMS	Ig kappa chain V-I
34	435	32.3	120	1 G1HUCO	Ig heavy chain V-I
35	434	32.2	108	2 J39154	Ig kappa chain (BR
36	432	32.0	109	2 S31981	Ig kappa chain V r
37	431	32.0	105	2 S36266	Ig lambda chain V
38	431	32.0	129	2 S52792	Ig kappa chain V r
39	430	31.9	117	2 S46376	Ig kappa chain V-J
40	429	31.8	125	2 S40350	Ig kappa chain - h
41	429	31.8	143	2 PT0174	Ig heavy chain pre
42	428	31.8	109	2 S31998	Ig heavy chain - h
43	427	31.7	108	2 S36279	Ig kappa chain V
44	427	31.7	117	2 S43528	Ig kappa chain V r
45	427	31.7	117	2 S42263	Ig kappa chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scfv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446
Rifang, P.W.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity dioxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; MUID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotrimer; immunoglobulin

Query Match 45.3%; Score 611; DB 2; Length 268;

Best Local Similarity 49.6%; Pred. No. 1.3e-34;

Matches 126; Conservative 42; Mismatches 70; Indels 16; Gaps 6;

QY	1	QVTLKESGPTLVKPTQTLTLCTCFSGFSIRTTGEGVWRQPGKALEWIALTY-WDDK	59
DB	3	QVTLKESGHELVKPGASVKSLCTSGFNKDT--YMHVKQRPBGLEWIGIAIRANGIT	60
QY	60	RYSPLKSLRLTTKDTSKKQVLTMTNVPADTATYYCTHEQYVYDTSGQPYFPFGG	119
DB	61	KVDPKFGKATITADTSSNTAVLQLSLTSEDTAVYCAS--YLTR---YENYWGQ	113
QY	120	TLVTVSSGGGSGGGSGGGSGGSGNSIQVTPSSLSASVGDVYMTCRASQDIRKL	179
DB	114	TLVTVS-----SGGGSGGGSGGGSGGSDIELQSPALMSASIGREKTVMSCRASSSV-NPI	167
QY	180	NMYQQKPKAPKPVLLVLDASDLETGIPSPFSGSGSGDFLTITSSLOPEDIATYYCQSDY	239
DB	168	YMYQQKSPASPKLWVYVYSHLPFGVPARPSGSGSGNSYSLTSSMEGDAAITVCCQPTS	227
QY	240	LPFLFEGGGRKVDIK 253	
DB	228	SPFTFGSGTKLEIK 241	

RESULT 2

S41374
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374
Rihtaenko, O.; Weiler, E.W.; Wuentz, K.; Conrad, U.

Submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibod

RESULT 6

JC5322

p53 specific single-chain antibody Pab421 - human

C:Species: Homo sapiens (man)

C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C:Accession: JC5322

R:Jannot, C.B.; Hynes, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A:Reference number: JC5322; MUID:97168950; PMID:9016757

A:Accession: JC5322

A:Molecule type: mRNA

A:Residues: 1-233 <JAN>

A:Experimental source: hybridoma cell

C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 39.6%; Score 533.5; DB 2; Length 233;

Best Local Similarity 45.5%; Pred. No. 28-29;

Matches 116; Conservative 46; Mismatches 64; Indels 29; Gaps 8;

QY 5 KESGPTLVKPTQTLLTCTFSGFSRLTGEVGVWRQPGKALEWLALE--YWDGKRY 61

DB 1 QESGAEIVRSGASVSLCTSSGFNI--NDYVMHWKKEQGLWIGRIDPENGADMTNR 58

QY 62 SPSTLSRLITIKDTSKQVVLMTNVDPADTATYCTHEQYYVDTSQGYTFDFWGGCTL 121

DB 59 SSGVKA--TMTADTSSNTAYLQLSSLTSEDTAVVYC-----NAG---MDYWGQGT 104

QY 122 VTSSGGGSGGGGGGGGSGGSGGSGNIVQTGSSSLASVGDVMTCTCRASGDIRKN--- 178

DB 105 VTVS-----SGGGSGGGRASGGGSDIELTGSPALAVSLGCRATISCRASVSSTSGS 159

QY 179 -LNMVQKPKAKVLYIDASDLETGIPRFGSGSGTDPIITLISLPEDIDATYTCQGS 237

DB 160 YNMHWQKRGQPPRLILYLVSLVESGVPARFSGSGSDTFNTINHVEEDATATYTCQII 219

QY 238 DYLPTFGGCTKVDI 252

DB 220 RELTRS-EGGTLEI 233

RESULT 7

S18555

Ig heavy chain V region precursor (VII-5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000

C:Accession: S18555

R:Shin, B.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H

EMBO J. 10, 3641-3645, 1991

A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c1

A:Reference number: S18551; MUID:92037524; PMID:1935893

A:Accession: S18555

A:Molecule type: DNA

A:Residues: 1-119 <SHI>

A:Cross-references: EMBL:X62111; NID:937839; PIDD:CAA44021.1; PID:G3580125

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>

F:134-118/Domain: immunoglobulin homology <IMM>

Query Match 36.1%; Score 487; DB 2; Length 119;

Best Local Similarity 89.9%; Pred. No. 1.5e-26;

Matches 89; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTGEVGVWRQPGKALEWLALEIYWDGK 60

DB 20 QTLKESGPTLVKPTQTLLTCTFSGFSRLTGEVGVWRQPGKALEWLALEIYWDGK 79

QY 61 YSPSLKSLRTITIKDTSKQVVLMTNVDPADTATYTCII 99

DB

80 YSPSLKSLRTITIKDTSKQVVLMTNVDPADTATYTCII 118

RESULT 8

MHHDUC

Ig heavy chain V-II region (MCE) - human

C:Species: Homo sapiens (man)

C:Date: 14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change 02-Sep-1997

C:Accession: A02092

R:Geber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W.

J. Immunol. 126, 1212-1216, 1981

A:Title: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X.

A:Reference number: A02092; MUID:81118242; PMID:6780622

A:Accession: A02092

A:Molecule type: protein

A:Residues: 1-125 <GER>

A:Note: This chain was derived from a monoclonal IgM cryoimmunoglobulin

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F:15-99/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.0%; Score 485.5; DB 1; Length 125;

Best Local Similarity 73.8%; Pred. No. 1.9e-26;

Matches 93; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTGEVGVWRQPGKALEWLALEIYWDGK 60

DB 1 QTLKESGPTLVKPTQTLLTCTFSGFSRLTGEVGVWRQPGKALEWLALEIYWDGK 60

QY 61 YSPSLKSLRTITIKDTSKQVVLMTNVDPADTATYCTHEQYYVDTSQGYTFDFWGGCT 120

DB 61 YSPSLKSLRTITIKDTSKQVVLMTNVDPADTATYCTHEQYYVDTSQGYTFDFWGGCT 119

QY 121 LVTVSS 126

DB 120 LVTVSS 125

RESULT 9

GJHUNE

Ig heavy chain V-II region (He) - human

C:Species: Homo sapiens (man)

C:Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 24-Nov-1999

C:Accession: A02093

R:Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.

Proc. Natl. Acad. Sci. U.S.A. 64, 997-1003, 1969

A:Title: Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy

A:Reference number: A02093; MUID:70114712; PMID:5264153

A:Accession: A02093

A:Molecule type: protein

A:Residues: 1-121 <GUN>

C:Comment: This gamma-1 chain was isolated from a myeloma protein.

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: blocked amino end; heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status

Query Match 35.2%; Score 474.5; DB 1; Length 121;

Best Local Similarity 71.7%; Pred. No. 1e-25;

Matches 91; Conservative 10; Mismatches 19; Indels 7; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLTGEVGVWRQPGKALEWLALEIYWDGK 59

A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52789
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 34.7%; Score 468; DB 2; Length 129;
Best Local Similarity 81.1%; Pred. No. 3.1e-25;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 143 GGGSNIQVQSPSSLSASVGDRTVMTCRASODIRKLNMYQKPGKAPKLYIDASDLET 202
DB 19 GARCDIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNMYQKPGKAPKLYIDASDLET 78

QY 203 GIPSRFGSGSGTDFITLTSSLOPEDIATYYCQQSDYLP-ITFGGGRVDIK 253
DB 79 GYPSRRSGSGSGTDFITLTSSLOPEDIATYYCQQYDNLPTFGGGRVDIK 129

RESULT 14
S4418
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S4418
R:Halling, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A:Reference number: S44105
A:Accession: S4418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <HAM>
A:Cross-references: EMBL:Z31395; NID:g472972; PIDN:CAA83270.1; PID:g940529
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 34.3%; Score 462; DB 2; Length 110;
Best Local Similarity 83.5%; Pred. No. 6.6e-25;
Matches 91; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 147 NIQVQSPSSLSASVGDRTVMTCRASODIRKLNMYQKPGKAPKLYIDASDLETGIPS 206
DB 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNMYQKPGKAPKLYIDASDLETGIPS 60

QY 207 RFGSGSGTDFITLTSSLOPEDIATYYCQQSDYLP-ITFGGGRVDIK 253
DB 61 RFGSGSGTDFITLTSSLOPEDIATYYCQYDNLPTFGGGRVDIK 109

RESULT 15
KIHUAD
Ig kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C:Accession: A91653; A01862; S02573
R:Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Suh
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653
A:Molecule type: protein
A:Residues: 1-108 <SCH>
A:Note: the C region of this chain has the Inv (3) marker
R:Fehlhammer, H.; Schliffer, M.; Bpp, O.; Colman, P.M.; Lateman, E.E.; Schwager, P.; Steil
Biophys. Struct. Mech. 1, 139-146, 1975
A:Title: The structure determination of the variable portion of the Bence-Jones protein

A:Reference number: A90729; MUID:77022433; PMID:1234024
A:Contents: annotation; X-ray crystallography
A:Note: the structure of the V region was determined by molecular replacement methods us
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substructures enhances the
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kap
bain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 33.8%; Score 456; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.7e-24;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 147 NIQVQSPSSLSASVGDRTVMTCRASODIRKLNMYQKPGKAPKLYIDASDLETGIPS 206
DB 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNMYQKPGKAPKLYIDASDLETGIPS 60

QY 207 RFGSGSGTDFITLTSSLOPEDIATYYCQQSDYLP-ITFGGGRVDIK 253
DB 61 RFGSGSGSHFTFTLTSSLOPEDIATYYCQYDNLPTFGGGRVDIK 107

Search completed: May 13, 2004, 15:08:44
Job time: 11.4218 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.1233 Seconds

(without alignments)
1849.388 Million cell updates/sec

Title: US-10-072-301-31

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPITFGGKTKVDIK 253

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485.5	36.0	125	1	HV2E_HUMAN
2	474.5	35.2	121	1	HV2E_HUMAN
3	468	34.7	108	1	KV1P_HUMAN
4	468	34.7	108	1	KV1P_HUMAN
5	456	33.8	108	1	KV1B_HUMAN
6	448	33.2	108	1	KV1Q_HUMAN
7	442	32.8	108	1	KV1Q_HUMAN
8	435	32.3	108	1	KV1Q_HUMAN
9	435	32.3	108	1	KV1Q_HUMAN
10	435	32.3	120	1	HV2B_HUMAN
11	425	31.5	108	1	KV1C_HUMAN
12	425	31.5	108	1	KV1C_HUMAN
13	423	31.4	108	1	KV1E_HUMAN
14	423	31.4	108	1	KV1E_HUMAN
15	423	31.4	129	1	KV1G_HUMAN
16	418	31.0	108	1	KV1G_HUMAN
17	418	31.0	108	1	KV1M_HUMAN
18	415	30.8	108	1	KV1R_HUMAN
19	413	30.6	108	1	KV1K_HUMAN
20	411	30.5	147	1	HV2H_HUMAN
21	408.5	30.3	107	1	KV1D_HUMAN
22	408.5	30.3	109	1	KV1T_HUMAN
23	406	30.1	129	1	KV1X_HUMAN
24	405	30.0	108	1	KV5S_MOUSE
25	404	30.0	108	1	KV1L_HUMAN
26	403	29.9	108	1	KV1N_HUMAN
27	402.5	29.9	119	1	HV2C_HUMAN
28	401	29.7	108	1	KV5Q_MOUSE
29	401	29.7	108	1	KV5T_MOUSE
30	397	29.5	108	1	KV1F_HUMAN
31	391	29.0	108	1	KV5R_MOUSE
32	389	28.9	126	1	HV2A_HUMAN
33	388	28.8	108	1	KV5O_MOUSE

34	387	28.7	108	1	KV5L_MOUSE
35	387	28.7	107	1	KV1J_HUMAN
36	386	28.6	118	1	KV5K_MOUSE
37	386	28.6	108	1	KV5M_MOUSE
38	385	28.6	108	1	KV5N_MOUSE
39	382	28.3	112	1	KV1U_HUMAN
40	381	28.3	108	1	KV5P_MOUSE
41	378	28.0	108	1	KV5J_MOUSE
42	373.5	27.7	144	1	HV43_MOUSE
43	372	27.6	117	1	KV1I_HUMAN
44	367	27.2	128	1	KV5E_MOUSE
45	363.5	27.0	133	1	KV4B_HUMAN

ALIGNMENTS

RESULT 1

HV2D_HUMAN STANDARD; PRT; 125 AA.

AC P01817;

DT 21-JUL-1986 (rel. 01, Created)

DT 21-JUL-1986 (rel. 01, Last sequence update)

DT 10-OCT-2003 (rel. 42, Last annotation update)

DE Ig heavy chain V-II region MCE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RA MEDLINE=8118242; PubMed=6780622;

RA Gerber-Jenson B., Kazin A., Kenne J.M., Scheffel C., Erickson B.W.,

RA Litman G.W.;

RT "Molecular basis for the temperature-dependent insolubility of

RT cryoglobulins. X. The amino acid sequence of the heavy chain variable

RT region of MCE."

RL J. Immunol. 126:1212-1216(1981).

CC -I- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM

CC CRYOIMMUNOGLOBULIN.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02092; MHDMC.

DR HSSP; P01825; 7PAB.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS00835; IG_LIKE; 1.

DR KX; Immunoglobulin V region; Pyrolydine carboxylic acid.

FT DOMAIN 1 113 IG-LIKE.

FT MOD RES 1 1 PYROLYDINE CARBOXYLIC ACID.

SO NON_TER 125 125

SEQUENCE 125 AA; 13783 MW; 7A1ADP4C40F47BBS CRC64;

Query Match 36.0%; Score 485.5; DB 1; Length 125;

Best Local Similarity 73.8%; Pred. No. 1.4e-31;

Matches 93; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY	1	QVTLKESGPTLVKPTQTTLTCTFSGFSRTGEGVGRQPPGRALFWLALTYDDDR	60
QY	1	: : : : : : : : :	60
DB	1	QVTLKESGPTLVKPTQTTLTCTFSGFSRTGEGVGRQPPGRALFWLALTYDDDR	60
QY	61	YSPSLKSRITTKDYSKQVVLVTMTNVPADATATYCTHBOXYTSGPYFFDFWQGT	120
QY	61	: : : : : : : :	120
DB	61	YSPSLKSRITTKDYSKQVVLVTMTNVPADATATYCTHBOXYTSGPYFFDFWQGT	120
QY	121	LVTVSS 126	
QY	121		
DB	120	LVTVSS 125	
DB	120		

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RESULT 2
HV2E_HUMAN          STANDARD;          PRT;          121 AA.
ID   HV2E_HUMAN
AC   P01818;
DT   21-JUL-1986 (Rel. 01, Created)
DR   21-JUL-1986 (Rel. 01, Last sequence update)
DE   10-OCT-2003 (Rel. 42, Last annotation update)
DS   Ig heavy chain V-II region HE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RX   NCB1_Taxid=9606;
RN   [1]
RP   SEQUENCE.
RA   MEDLINE=70114712; PubMed=5264153;
RT   Cunningham B.A., Pflum M.N., Rutschauser U., Edelman G.M.,
RL   "Subgroups of amino acid sequences in the variable regions of
RU   immunoglobulin heavy chains."
RU   Proc. Natl. Acad. Sci. U.S.A. 64:997-1003 (1969).
CC   -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC   PROTEIN.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02093; GIHHE.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG-LIKE; 1.
DR   Immunoglobulin V region; Pyrrrolidone carboxylic acid.
FT   DOMAIN 1 120
FT   MOD RES 1 121
FT   NON TER 121 121
FT   SEQUENCE 121 AA; 13483 MW; 88A5082C27375B4 CRC64;
SQ
Query Match          35.2%; Score 474.5; DB 1; Length 121;
Best Local Similarity 71.7%; Pred. No. 1e-30;
Matches 91; Conservative 10; Mismatches 19; Indels 7; Gaps 2;
QY 1 QVTLKESGPTLVPTOTLTCTFSGSPSRTGEGVGMVROPGRKALEWLA-LITWDDK 59
DB 1 QVTLKNGPTLVPTETLTCTLSGLSTLTDVAAGMTRGGRLEWLA-LITWDDK 60
QY 60 RYSPSLKSRITLTQTSKQVLTMTNVPADATAYCTHEQYVYDTSGQPYFDFMGOG 119
DB 61 RYSPSLKSRITLVTRDTSKQVLTMTNMDPVATATYCVHRH-----PRTIAFDVWGOG 114
QY 120 TLVTYVS 126
DB 115 TKVAVSS 121

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RT Cum.)";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080 (1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hillebrand N., Barnikol H.U., Hess M., Langer B., Ponatting H.,
RL Steimerz-Kayne M., Suter U., Watanabe S.;
RL (in) Finek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A91638; KIHURY.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG-LIKE; 1.
DR   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN 1 23
FT   DOMAIN 24 34
FT   DOMAIN 35 49
FT   DOMAIN 50 56
FT   DOMAIN 57 88
FT   DOMAIN 89 97
FT   DOMAIN 98 107
FT   DISULFID 23 88
FT   NON TER 108 108
FT   SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;
SQ
Query Match          34.7%; Score 468; DB 1; Length 108;
Best Local Similarity 84.1%; Pred. No. 2.8e-30;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 147 NIQVTPSSLSASVGRVMTTCASODIRKLNMTQKRGKAPKVIYASDLEFGIPS 206
DB 1 DIQVTPSSLSASVGRVITTCASODISIFLNMTQKRGKAPKVIYASDLEAGVPS 60
QY 207 RFSGSGSGTDFILITSLQPEDIATYCCQSDVPLTFGGGTAVDIX 253
DB 61 RFSGTSGTDFITFISLQPEDIATYCCQFNDPLTFGGTAVDIX 107

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RESULT 4
KVLY_HUMAN          STANDARD;          PRT;          108 AA.
ID   KVLY_HUMAN
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DR   01-NOV-1995 (Rel. 32, Last sequence update)
DE   28-FEB-2003 (Rel. 41, Last annotation update)
DS   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RX   NCB1_Taxid=9606;
RN   [1]
RP   SEQUENCE. AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RA   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers."
RT   Biochemistry 33:14848-14857 (1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;

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RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human Ki Bence Jones protein Mat.,"
 RL J. Mol. Biol. 147:185-193(1981).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB: 1MTL; 01-NOV-94.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 RT DOMAIN 1 23
 CC COMPLEMENTARITY-DETERMINING-1.
 FT 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT 23 88
 FT 30 31
 FT 4 7
 FT 10 13
 FT 15 16
 FT 19 25
 FT 30 31
 FT 33 38
 FT 40 41
 FT 45 49
 FT 50 52
 FT 53 54
 FT 56 57
 FT 60 61
 FT 62 67
 FT 68 69
 FT 70 75
 FT 80 82
 FT 84 90
 FT 98 98
 FT 102 106
 FT 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
 Query Match 34.7%; Score 468; DB 1; Length 108;
 Best Local Similarity 84.1%; Pred. No. 2.8e-30;
 Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 147 NIQTQSSSSLSASVGDVMTTCRASODIRKRLNMYOQKPGKAPVLLYDASDLTGIPS 206
 DB 1 DIQMTQSSSSLSASVGDVMTTCRASODITWVNFQORPGQAPVLLYDASDLTGIPS 60
 QY 207 RFGSGSGTDFILTTSSLOPEDIAITYYCOQSDYLPFTGGGKVDIK 253
 DB 61 RFGSGSGTDFILTTSSLOPEDIAITYYCOQSDYLPFTGGGKVDIK 107
 RESULT 5
 ID KV1B HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;

RA Schlecht H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au).",
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RN X-RAY CRYSTALLOGRAPHY.
 RP MEDLINE=77022433; PubMed=1234024;
 RX Pehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.B.,
 RA Selwager P., Steigemann W., Schramm H.U.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au.",
 CC "The structure of the kappa chain of the variable portion of the
 CC Bence-Jones protein Au.",
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
 DR PIR; A91653; KIHUAV.
 DR PDB; 1JVS; 30-JAN-02.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 RT DOMAIN 1 23
 CC COMPLEMENTARITY-DETERMINING-1.
 FT 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT 23 88
 FT 30 31
 FT 4 7
 FT 10 13
 FT 15 16
 FT 19 25
 FT 30 31
 FT 33 38
 FT 40 41
 FT 45 49
 FT 50 52
 FT 53 54
 FT 56 57
 FT 60 61
 FT 62 67
 FT 68 69
 FT 70 75
 FT 80 82
 FT 84 90
 FT 98 98
 FT 102 106
 FT 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E801187BE6FEF9 CRC64;
 Query Match 33.8%; Score 456; DB 1; Length 108;
 Best Local Similarity 81.3%; Pred. No. 2.5e-29;
 Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 147 NIQTQSSSSLSASVGDVMTTCRASODIRKRLNMYOQKPGKAPVLLYDASDLTGIPS 206
 DB 1 DIQMTQSSSSLSASVGDVMTTCRASODISDLYNMYOQKPGKAPVLLYDASDLTGIPS 60
 QY 207 RFGSGSGTDFILTTSSLOPEDIAITYYCOQSDYLPFTGGGKVDIK 253
 DB 61 RFGSGSGTDFILTTSSLOPEDIAITYYCOQSDYLPFTGGGKVDIK 107
 RESULT 6
 ID KV10 HUMAN STANDARD; PRT; 108 AA.
 AC P01609;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region SCW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059271; PubMed=4435756;
 RA Bulitz M., Hilschmann N.;
 RT "The primary structure of a human immunoglobulin L-chain of
 RT kappa-type (Bence-Jones protein SCW).",
 RT and the complete amino acid sequence.",
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).

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CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01875; KIHUSM.
DR HSSP; P01607; 1RET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE, 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 25 35 FRAMEWORK-2.
FT DOMAIN 36 46 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 47 57 FRAMEWORK-3.
FT DOMAIN 58 68 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 69 79 FRAMEWORK-4.
FT DOMAIN 80 90 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11764 MM; 32CECDDE9644414 CRC64;

Query Match
Best Local Similarity 33.2%; Score 448; DB 1; Length 108;
Matches 84; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 147 NIQVTPSSLSASVGDRTVMTCRASODIRKLNLMYQOKPKAPKLLIYDASDLETGIPS 206
DB 1 DIQMTQSPSSLSASVGRVITTCASQDIRKHLNLMYQOKPKAPKLLIYDASDLETGIPS 60
QY 207 RFSGSGGTDFLTISLQPEDIAITYCOQDYLPRTFGGSTRVDIK 253
DB 61 RFSGSGGTDFLTISLQPEDIAITYCOQDYLPRTFGGSTRVDIK 107
DB 61 RFSGSGGTDFLTISLQPEDIAITYCOQDYLPRTFGGSTRVDIK 107

RESULT 7
KV10_HUMAN
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX MEDLINE=69234734; PubMed=4893682;
RA Tiltani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RT J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUNG.
DR HSSP; P01607; 1RET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE, 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.

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FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MM; E3B3B246C18F0C4F CRC64;

Query Match
Best Local Similarity 32.8%; Score 442; DB 1; Length 108;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 147 NIQVTPSSLSASVGDRTVMTCRASODIRKLNLMYQOKPKAPKLLIYDASDLETGIPS 206
DB 1 DIQMTQSPSSLSASVGRVITTCASQDIRKHLNLMYQOKPKAPKLLIYDASDLETGIPS 60
QY 207 RFSGSGGTDFLTISLQPEDIAITYCOQDYLPRTFGGSTRVDIK 253
DB 61 RFSGSGGTDFLTISLQPEDIAITYCOQDYLPRTFGGSTRVDIK 107
DB 61 RFSGSGGTDFLTISLQPEDIAITYCOQDYLPRTFGGSTRVDIK 107

RESULT 8
KV10_HUMAN
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type J-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RX [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein RFI refined at 2.0-A resolution."
RT Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A9163; KIHUR2.
DR PDB; 1AR1; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-97.
DR PDB; 1BWW; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE, 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

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FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 988143B118BCE2A CRC64;

Query Match 32.3%; Score 435; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 1.1e-27;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 147 NIQTQSPSSLSASVGVDRVTMTCRASQDRIKRLNMYQOKPGKAPVLIYDASDLFTGIPS 206
DB 1 DIQMTQSPSSLSASVGVDRVTITCRASQDRIKRLNMYQOKPGKAPVLIYDASDLFTGIPS 60

QY 207 RFGSGSGTDFLTITSSLPEDPATYTCQOSDYLPRTFGGTRKVDI 252
DB 61 RFGSGSGTDFLTITSSLPEDPATYTCQOSDYLPRTFGGTRKVDI 106

RESULT 9
KV15_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR HSSP; P01877; KIHUMS.
DR HSSP; P01877; KIHUMS.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 97 FRAMEWORK-4.
FT DISULFID 98 107
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60B45 CRC64;

Query Match 32.3%; Score 435; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 1.1e-27;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 147 NIQTQSPSSLSASVGVDRVTMTCRASQDRIKRLNMYQOKPGKAPVLIYDASDLFTGIPS 206
DB 1 DIQMTQSPSSLSASVGVDRVTITCRASQDRIKRLNMYQOKPGKAPVLIYDASDLFTGIPS 60

QY 207 RFGSGSGTDFLTITSSLPEDPATYTCQOSDYLPRTFGGTRKVDI 253
DB 61 RFGSGSGTDFLTITSSLPEDPATYTCQOSDYLPRTFGGTRKVDI 107

RESULT 10
HV2B_HUMAN STANDARD; PRT; 120 AA.
AC P01815;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press R.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02089; GIHICO.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT DOMAIN 1 110
FT MOD RES 1 1
FT CARBOHYD 22 94
FT CARBOHYD 62 62
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EB98 CRC64;

Query Match 32.3%; Score 435; DB 1; Length 120;
Best Local Similarity 69.0%; Pred. No. 1.2e-27;
Matches 87; Conservative 10; Mismatches 23; Indels 6; Gaps 2;

QY 1 QVTLKSGPTLVKPTQLTLCFSGFSRTTSGGVGWVROPGKALEWLIYDDDKR 60
DB 1 QVTLKSGPTLVKPTQLTLCFSGFSRTTSGGVGWVROPGKALEWLIYDDDKR 60

QY 61 YPSLSKRLITTKDTSKQVVLVTNVPADPATYTCHEQVYDTSQPYVDFWGGQT 120
DB 61 YNTSLFTLTITSKDTSKQVVLVTNVPADPATYTCHEQVYDTSQPYVDFWGGQT 114

OY 121 LYTSS 126
 DB 115 PVTSS 120

RESULT 11

KVIC_HUMAN STANDARD; PRT; 108 AA.
 AC P01595;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region B1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73029807; PubMed=4563064;
 RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
 RT "Principle of antibody structure. The primary structure of a
 RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
 RT B1). 3. The complete amino acid sequence and the genetic
 RT significance of the variability principles for the mechanism of
 RT antibody formation.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01863; KIHUB1.
 DR HSSP; P01607; 1RET.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR KIM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match 31.5%; Score 425; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 6.7e-27;
 Matches 82; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

OY 147 NIQVTPSSSLASVGDVRYMTTCRASODIRKXLMWYQKPGKAPKLYIDASDLETGIS 206
 DB 1 DIQMTSPSPSLASVSDSVITTCQASQDIRKSLIMYQKPGKAPKLYIDAEMLIGVPS 60
 OY 207 RFGSGSGTDFLITLSSLOPEDIAITYYCCQSDYLPFTFGGKTVDIK 253
 DB 61 RFGSGSGTDFLITLSSLOPEDPATIYYCQYVNLPTFGGTLEIK 107

RESULT 12
 KVIC_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Matanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01868; KIHUHU.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR KIM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 31.5%; Score 425; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 6.7e-27;
 Matches 82; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

OY 147 NIQVTPSSSLASVGDVRYMTTCRASODIRKXLMWYQKPGKAPKLYIDASDLETGIS 206
 DB 1 DIQMTSPSPSLASVSDSVITTCQASQDIRKSLIMYQKPGKAPKLYIDAEMLIGVPS 60
 OY 207 RFGSGSGTDFLITLSSLOPEDIAITYYCCQSDYLPFTFGGKTVDIK 253
 DB 61 RFGSGSGTDFLITLSSLOPEDPATIYYCQYVNLPTFGGTLEIK 107

RESULT 13

KVIC_HUMAN STANDARD; PRT; 108 AA.
 AC P01597;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region DEB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72053133; PubMed=5124396;
 RA Milstein C.P.; Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain.";
 RL Biochem. J. 123:945-958(1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01865; KIHUDE.
 DR HSSP; P01607; 1RET.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 24 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 147 NIQTQSPSSLSASVGRVTMTCSRASQDIRKRLNLYQOKRPGAKPKVLIYDASDLEIGPS 206
DB 1 BIZMTQSPSSLSASVGRVTITCRAGQSYNKYLNWYQOKRPGAKPKVLIYDASDLEIGPS 60
QY 207 RFGSGSGTDFLTITSSLPEDIAITYYCOQSDYLPPLFPGGGRKVDK 252
DB 61 RFGSGSGTDFLTITSSLPEDIPATYYCOQSYTTPYTFPGGGRKVDK 106

RESULT 14
KV1V HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
OX [1]
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA D'wulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSSP; P80362; 1MTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV, 1.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 24 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
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```
QY 147 NIQTQSPSSLSASVGRVTMTCSRASQDIRKRLNLYQOKRPGAKPKVLIYDASDLEIGPS 206
DB 1 BIZMTQSPSSLSASVGRVTITCRAGQSYNKYLNWYQOKRPGAKPKVLIYDASDLEIGPS 60
QY 207 RFGSGSGTDFLTITSSLPEDIAITYYCOQSDYLPPLFPGGGRKVDK 253
DB 61 RFGSGSGTDFLTITSSLPEDIPATYYCOQSYTTPYTFPGGGRKVDK 107

RESULT 15
KV1V HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
DR EMBL; X00965; CA25477.1; ALT_TERM.
DR PIR; A01883; KIHOMK.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV, 1.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 22 IG KAPPA CHAIN V-I REGION WALKER.
FT SIGNAL 23 129
FT DOMAIN 23 46 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 46 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 FRAMEWORK-3.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 129;
Matches 83; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 143 GGSNIQTQSPSSLSASVGRVTMTCSRASQDIRKRLNLYQOKRPGAKPKVLIYDASDLEIGPS 202
DB 19 GARCDIQMTQSPSSLSASVGRVTITCRAGQSYNKYLNWYQOKRPGAKPKVLIYDASDLEIGPS 78
QY 203 GIPSRFGSGSGTDFLTITSSLPEDIAITYYCOQSDYLPPLFPGGGRKVDK 253
DB 61 GIPSRFGSGSGTDFLTITSSLPEDIPATYYCOQSYTTPYTFPGGGRKVDK 107
```

Mon May 17 11:03:45 2004

us-10-072-301-31.rsp

Page 8

Db 79 GVTNRFGSGGCTDPTLTITISLQPEDSATYCCQSYSTLITFGQCTRLBIK 129

Search completed: May 13, 2004, 15:02:06
Job time : 7.1233 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 34.0199 Seconds
(without alignments)
2346.453 Million cell updates/sec

Title: US-10-072-301-31
Perfect score: 1348
Sequence: 1 QVTLKESGPTLVKPTQTLL.....CQSDYLPITFGGGRVDIK 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 10170411

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :
SPRMBML_25:*
1: sp. archaea:*
2: sp. bacteria:*
3: sp. fungi:*
4: sp. human:*
5: sp. invertebrate:*
6: sp. mammal:*
7:
8: sp. mhc:*
9: sp. organelle:*
10: sp. phage:*
11: sp. plant:*
12: sp. rodent:*
13: sp. virus:*
14: sp. vertebrate:*
15: sp. unclassified:*
16: sp. virus:*
17: sp. bacteriophage:*
18: sp. archaeop:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	674.5	50.0	298	11	Q9GYF0	Q9GYF0 mus musculi
2	652	48.4	241	11	Q9Z1A6	Q9Z1A6 mus musculi
3	621	46.1	243	11	Q7TGM2	Q7TGM2 mus musculi
4	549.5	40.8	121	4	Q9UL96	Q9UL96 homo sapien
5	496.5	36.8	218	11	Q9Z5S1	Q9Z5S1 mus musculi
6	450	33.4	118	11	Q811U5	Q811U5 mus musculi
7	448.5	33.3	107	4	Q966A9	Q966A9 homo sapien
8	429	31.8	108	4	Q9UL77	Q9UL77 homo sapien
9	424.5	31.5	107	4	Q9UL81	Q9UL81 homo sapien
10	423	31.4	108	4	Q966P6	Q966P6 homo sapien
11	419	31.1	116	4	Q9UL70	Q9UL70 homo sapien
12	416	30.9	236	4	Q7Z3Y4	Q7Z3Y4 homo sapien
13	390	28.9	233	11	Q91W59	Q91W59 mus musculi
14	387	28.7	234	4	Q7Z473	Q7Z473 homo sapien
15	384	28.5	37	4	O43Z34	O43Z34 homo sapien
16	383	28.4	108	4	Q9UL79	Q9UL79 homo sapien

17	373	27.7	214	11	Q9RIA5	Q9IA95 mus musculus
18	373	27.7	236	11	Q7TS98	Q9IA98 mus musculus
19	371	27.5	234	11	Q91WF8	Q91F8 mus musculus
20	371	27.5	234	11	Q8R062	Q8I062 mus musculus
21	369.5	27.4	109	4	Q9UL78	Q9UL78 homo sapien
22	368	27.3	108	4	Q9UL85	Q9UL83 homo sapien
23	367.5	27.3	109	4	Q9UL85	Q9UL85 homo sapien
24	367	27.2	236	11	Q7TKK3	Q7TKK3 mus musculus
25	363	26.9	121	11	Q99NG4	Q99NG4 mus musculus
26	362	26.9	234	11	Q8VCP0	Q8VCP0 mus musculus
27	359	26.6	109	11	Q920E6	Q920E6 mus musculus
28	354	26.3	107	11	Q9UL84	Q9J184 mus musculus
29	354	26.3	108	11	Q8VJ70	Q8VJ70 mus musculus
30	353	26.2	111	11	Q920E9	Q920E9 mus musculus
31	351.5	26.1	492	4	Q7Z374	Q7Z374 homo sapien
32	348.5	25.9	119	4	Q9UL73	Q9UL73 homo sapien
33	347	25.7	111	11	Q8I106	Q8I106 mus musculus
34	346.5	25.7	131	11	Q811C3	Q811C3 mus musculus
35	343.5	25.5	114	11	Q8K1F1	Q8K1F1 mus musculus
36	343	25.4	496	4	Q96KX8	Q96KX8 homo sapien
37	338.5	25.1	134	11	Q8VDD0	Q8VDD0 mus musculus
38	337	25.0	127	11	Q925S9	Q925S9 mus musculus
39	335	24.9	234	11	Q8R028	Q8R028 mus musculus
40	334.5	24.8	109	4	Q9UL86	Q9UL86 homo sapien
41	333	24.7	482	11	Q91X92	Q91X92 mus musculus
42	329.5	24.4	112	11	Q8K1F2	Q8K1F2 mus musculus
43	328	24.3	107	11	Q9ER29	Q9ER29 mus musculus
44	328	24.3	613	4	Q96EV0	Q96EV0 homo sapien
45	327.5	24.3	112	11	Q8K1F3	Q8K1F3 mus musculus

ALIGNMENTS

RESULT 1	
Q9QYF0	
ID Q9QYF0	PRELIMINARY; PRT; 298 AA

DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=2018331; PubMed=10706631;
RA Shiohara N., Demura T., Fukuda H.;
RT Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method.
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
RL EMBL; AB036341; BAA88633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PR00047; IG: 2.
DR SMART; SM00406; IGV_2.
DR PROSITE; PSS0835; IG_LIKE; 2.
QO SEQUENCE 298 AA; 31667 MW; 80F96BBA17004317 CRC64;

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Db      40 QVTLQSGGGLVPGSLKLSKASGSDF--SRYMMSWVRQAPDKGLWIGINPDSTI 97
QY      60 RYSPSLKSRLLTIKDTSKKQVLTMTNVDPADATATYCTHEQYVYDTSQPPYFDWGGG 119
Db      98 NYTPSLKDKFTISRDNKNTLTLYLQMSKVSSEDTALYTCARASYGHSA-----YWGQ 150
QY      120 TLVTSSGGGGSGGGSGGGSGGGSGNIQVTPSPSLASVGDRTVMTCRASODIRKRL 179
Db      151 TTVTVS-----SGGGSGGGSGGGSGGGSDIELTQSPSLASVGEYITITICRASGNINHTL 205
QY      180 NMYQOKPGAPKVLITDASDLFTGIRSRPSSGSGTDFILITISLQPEDIAITYCQSDY 239
Db      206 AMYQOKGSPQLLVNNAKTLADGVSRFSGSGTQYSLKINSLOPEDFGSYCCQHFMT 265
QY      240 LPLTFGGGTXYDIX 253
Db      266 TPTTFGGGTKEIK 279

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RESULT 2

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ID      0921A6 PRELIMINARY; PRT; 241 AA.
AC      0921A6;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE      Anti-CBA 79 single chain Fv fragment (Fragment).
OC      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98170165; PubMed=9509426;
RA      Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA      Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT      "Cloning and characterization of cDNAs encoding VH and VL of a
RT      monoclonal anti-CBA antibody (CBA 79) cross-reactive with NCA-95 and
RL      generation of a single-chain Fv molecule (scfv).";
RL      Mol. Cells 7:816-819(1997).
DR      EMBL; U88067; AAB8044.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig_2.
DR      SMART; SM00406; IGV_2.
DR      PROSITE; PS50835; IG_Like; 2.
FT      NON_TER 1
FT      NON_TER 241
SQ      SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

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Query Match 48.4%; Score 652; DB 11; Length 241;

Best Local Similarity 51.2%; Pred. No. 3.6e-48;

Matches 132; Conservative 41; Mismatches 61; Indels 24; Gaps 7;

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QY      1 QVTLKESGTLVKTPTOTLTLTCTFSGFSLRITGEGVWVROPFGKALEMLALI-YWDDK 59
Db      1 QVTLQSGSELKPKGFTVXISKASGYTF--TDYGMNWKQAPGKGLKMGMINITYGEP 58
QY      60 RYSPSLKSRLLTIKDTSKKQVLTMTNVDPADATATYCTHEQYVYDTSQPPYFDWGGG 119
Db      59 TYADDFKGFAPSLSTASTAYLQINLNKNEDTATYFCARKKL-----RYFYWGQ 111
QY      120 TLVTSSGGGGSGGGSGGGSGGGSGNIQVTPSPSLASVGDRTVMTCRASODIRKRL 179
Db      112 TTVTVS-----SGGGSGGGSGGGSGGGSDIELTQSPSLASVGEYITITICRASQDINKI 166
QY      160 NMYQOKPGAPK---VLITYDASDLFTGIRSRPSSGSGTDFILITISLQPEDIAITYCQ 235
Db      167 AMYQOKPGKPGSPASMTLHIY----IQPGIPSRFSGSGSGRDYSPSISNLEPEDIAITYCL 222
QY      236 QSDYLPPLTFGGGTXYDIX 253
Db      223 HYDNLH-TFGGGTKLEIK 239

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RESULT 3

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ID      07TQM2 PRELIMINARY; PRT; 243 AA.
AC      07TQM2;
DT      01-OCT-2003 (TREMBLrel. 25, Created)
DT      01-OCT-2003 (TREMBLrel. 25, last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE      scfv 6H8 protein (Fragment).
GN      scfv 6H8.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Balb/C;
RA      Peter J.C., Fetherhart P., Billfeld P., Wallukat G.;
RT      "scfv single chain antibody variable fragment as inverse agonist for
RT      the beta-2 adrenergic receptor";
RL      Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ574851; CAE00495.1; -.
FT      NON_TER 1
FT      NON_TER 1
SQ      SEQUENCE 243 AA; 25976 MW; BEFF64D2DC4F76 CRC64;

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Query Match 46.1%; Score 621; DB 11; Length 243;

Best Local Similarity 50.8%; Pred. No. 1.7e-45;

Matches 129; Conservative 40; Mismatches 67; Indels 18; Gaps 6;

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QY      1 QVTLKESGTLVKTPTOTLTLTCTFSGFSLRITGEGVWVROPFGKALEMLALI-YWDDK 59
Db      1 QVTLQSGSELVPRPASVXLSCKASGYFTT--YMHMVKRHHQGLEMINIYVSGIT 58
QY      60 RYSPSLKSRLLTIKDTSKKQVLTMTNVDPADATATYCTHEQYVYDTSQPPYFDWGGG 119
Db      59 NYDEKFNKGLIYDTSSTAYMHLSLASEDSAYYCAR-----GGRG--LDVWGAG 109
QY      120 TLVTSSGGGGSGGGSGGGSGGGSGNIQVTPSPSLASVGDRTVMTCRASODIRKRL 179
Db      110 TTVTVS-----SGGGSGGGSGGGSGGGSDIQVTPSPSLASVGEYITITICRASEDITVRL 164
QY      160 NMYQOKPGAPKVLITDASDLFTGIRSRPSSGSGTDFILITISLQPEDIAITYCQSDY 239
Db      165 AMYQOKPGNAPRLISGATSLFTGVPSRFSGSGGKDYTLISLTQEDVATYYCQY-W 223
QY      240 LPLTFGGGTXYDIX 253
Db      224 STRTFGGGTKEIK 237

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RESULT 4

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ID      09UL96 PRELIMINARY; PRT; 121 AA.
AC      09UL96;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE      Myosin-reactive immunoglobulin heavy chain variable region
DE      (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035018; AAD56254.1; -.

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DR HSPB; P01825; 7FAB.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 121
FT NON_TER 121
SQ SEQUENCE 121 AA; 13695 MW; D582DA50596BD35 CRC64;

Query Match 40.8%; Score 549.5; DB 4; Length 121;
Best Local Similarity 82.5%; Pred. No. 1e-39;
Matches 104; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

Qy 1 QVTLKESGPTLVKPTQTLTLTCTFSGFSLRTGEGVGVWROPKALMLALTYWDDDKR 60
Db 1 QVTLKESGPTLVKPTQTLTLTCTFSGFSLRTGEGVGVWROPKALMLALTYWDDDKR 60
Qy 61 YSPSLKSLRTITKDTSKQVLTMTNVPADPATATYCTHEQYVYDTSQGYFDFMGQGT 120
Db 61 YSPSLKSLRTITKDTSKQVLTMTNVPADPATATYCTHEQYVYDTSQGYFDFMGQGT 115
Qy 121 LVTVSS 126
Db 116 LVTVSS 121

RESULT 5

Q925S1 PRELIMINARY; PRT; 218 AA.

AC Q925S1 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice."
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK3733.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 218
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 36.8%; Score 496.5; DB 11; Length 218;
Best Local Similarity 44.8%; Pred. No. 7.8e-35;
Matches 103; Conservative 42; Mismatches 66; Indels 19; Gaps 6;

Qy 1 QVTLKESGPTLVKPTQTLTLTCTFSGFSLRTGEGVGVWROPKALMLALTYWDDDKR 59
Db 3 QVTLKESGPTLVKPTQTLTLTCTFSGFSLRTGEGVGVWROPKALMLALTYWDDDKR 60

Qy 60 RYPSLKSRLITTKDTSKQVLTMTNVPADPATATYCTHEQYVYDTSQGYFDFMGQGT 119
Db 61 KYAEFKRGRFAPSLETSASTAYLQISNLKNEBTATYPCM--RWDVDCG-----FAYKQGG 113
Qy 120 TLVTVSSGG 176
Db 114 TTVTVS-----SCGG 168
Qy 177 -KNLWYQOKKPKAPKVLITYDASLETGIPSPFSSGGSGTPIILYSSIQ 225
Db 169 ISFMWFOOKPQKPKLITYASKQSGVPAGLASGDTPIILYPMWE 218

RESULT 6

Q811U5 PRELIMINARY; PRT; 118 AA.

AC Q811U5 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Anti-human Fc gamma receptor III 368 gamma heavy chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Bruenke J., Valerieus T., Repp R., Fey G.H.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY13025; AAO18227.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12979 MW; F57BB0703742E99 CRC64;

Query Match 33.4%; Score 450; DB 11; Length 118;
Best Local Similarity 66.7%; Pred. No. 3.6e-31;
Matches 84; Conservative 17; Mismatches 17; Indels 8; Gaps 1;

Qy 1 QVTLKESGPTLVKPTQTLTLTCTFSGFSLRTGEGVGVWROPKALMLALTYWDDDKR 60
Db 1 QVTLKESGPTLVKPTQTLTLTCTFSGFSLRTGEGVGVWROPKALMLALTYWDDDKR 60
Qy 61 YSPSLKSLRTITKDTSKQVLTMTNVPADPATATYCTHEQYVYDTSQGYFDFMGQGT 120
Db 61 YSPSLKSLRTITKDTSKQVLTMTNVPADPATATYCTHEQYVYDTSQGYFDFMGQGT 112
Qy 121 LVTVSS 126
Db 113 LVTVSS 118

RESULT 7

Q96SA9 PRELIMINARY; PRT; 107 AA.

AC Q96SA9 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Anti-streptococcal/anti-amyosin immunoglobulin kappa light chain
variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Qy	147	NIGTQSPSSLSASVGDRTVTTCRASODIRKUNLWYQQCPGKAPKTLIYDASDLFTGIS	206
Dd	1	:DIQMTPSSLSASVGDRVTITTCRASQSISSYLMNYYOQPKGRAPMLLIYAASSLSGGVPS	60
Qy	207	RFSGSGSGTDFTLTITSLQPEDIAATYVCCQSDYLPLTFGGGTGRVDIK	253
Dd	61	RFSGSGSGTDFTLTITSLQPEDPATYVCCQGSISTMTPEGTRKEIK	107
RESULT 9			
ID	Q9UL81	PRELIMINARY;	PRT; 107 AA.
AC	Q9UL81:		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Mycosin-reactive immunoglobulin light chain variable region (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OK	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RX	Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.,		
RT	"Mycosin-reactive autoantibodies in rheumatic carditis and normal fetus";		
RL	Clin. Immunol. Immunopathol. 87:184-192.(1998).		
DR	EMBL; AF035033; AAD56269.1; -.		
DR	HSSP; P01607; IRR1.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig_1.		
DR	Pfam; SM00406; IGV; 1.		
DR	PROSITE; PS00835; IG_LIKE; 1.		
FT	NON_TER	1	
FT	NON_TER	1	
SQ	SEQUENCE	107 AA; 11501 MW; 070549FDE0754748 CRC64;	
Query Match			
Beat Local Similarity 31.5%; Score 424.5; DB 4; Length 107;			
Matches 84; Conservative 8; Mismatches 14; Indels 1; Gaps 1			
Qy	147	NIGTQSPSSLSASVGDRTVTTCRASQDIRKUNLWYQQCPGKAPKTLIYDASDLFTGIS	206
Dd	1	:DIQMTPSSLSASVGDRVTITTCRASQSISSYLMNYYOQPKGRAPMLLIYAASSLSGGVPS	60
Qy	207	RFSGSGSGTDFTLTITSLQPEDIAATYVCCQSDYLPLTFGGGTGRVDIK	253
Dd	61	RFSGSGSGTDFTLTITSLQPEDPATYVCCQGSYSTMTPEGTRKEIK	106
RESULT 10			
ID	Q96PF6	PRELIMINARY;	PRT; 116 AA.
AC	Q96PF6:		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Kappa 1 light chain variable region (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OK	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21361171; PubMed=11466171;		
RX	Cuenca R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.,		
RA	"The tropism of Organ Involvement in primary systemic amyloidosis:		

RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden."
RL Blood 98:714-720(2001).
DR EMBL, AF361758; AKS1465.1; -.
DR InterPro: IPR007110; Ig_1-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFC57 CRC64;

Query Match 31.1%; Score 423; DB 4; Length 116;
Best Local Similarity 74.8%; Pred. No. 7.4e-29;
Matches 80; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 147 NIQVTSBSSLSASVGDRTVMTCRASQDIRKNLMWYQKPGKAPKVLIVDASDLDTGIPS 206
DB 1 DIQMTQSPSSLSASVGDRTVTCQASQDIANHLNMYQKPGKAPKFLIVDSFLLTGVS 60
QY 207 RPSGSGSTDFLTITSSLOPEDIAITYYCOQSDYLPPLTFGGGTRKVDIK 253
DB 61 RPSGSGSATNFTVITSSLOPEDFATYYCQYVHHLPTFGPGTRKVDIFK 107

RESULT 11
Q0UL70 PRELIMINARY; PRT; 108 AA.
ID Q0UL70;
AC Q0UL70;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL, AF035044; AAD56280.1; -.
DR PIR: P0863; P0863.
DR HSP, P01607; IREI.
DR InterPro: IPR007110; Ig_1-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 31.1%; Score 419; DB 4; Length 108;
Best Local Similarity 75.7%; Pred. No. 1.5e-28;
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 147 NIQVTSBSSLSASVGDRTVMTCRASQDIRKNLMWYQKPGKAPKVLIVDASDLDTGIPS 206
DB 1 DIQMTQSPSSLSASVGDRTVTCQASQDIANHLNMYQKPGKAPKFLIVDSFLLTGVS 60
QY 207 RPSGSGSTDFLTITSSLOPEDIAITYYCOQSDYLPPLTFGGGTRKVDIK 253
DB 61 RPSGSGSATNFTVITSSLOPEDFATYYCQYVHHLPTFGPGTRKVDIFK 107

RESULT 12

Q723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4;
AC Q723Y4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheimen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC005332; AAH05332.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7F8F84ED230848C6 CRC64;

Query Match 30.9%; Score 416; DB 4; Length 236;
Best Local Similarity 73.0%; Pred. No. 7.4e-28;
Matches 81; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 143 GGSNIOVTSBSSLSASVGDRTVMTCRASQDIRKNLMWYQKPGKAPKVLIVDASDLDT 202
DB 19 GARCIDQMTQSPSSLSASVGDRTVTCQASQDIANHLNMYQKPGKAPKFLIVDSFLLTGVS 78
QY 203 GIPSRPSGSGSTDFLTITSSLOPEDIAITYYCOQSDYLPPLTFGGGTRKVDIK 253
DB 79 GVQSKFSGSGSTDFLTITSSLOPEDFATYYCQYVHHLPTFGPGTRKVDIFK 129

RESULT 13
Q91WS9 PRELIMINARY; PRT; 233 AA.
ID Q91WS9;
AC Q91WS9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

